

SEQUENCE LISTING

<110> CODEXIS, INC.
Vroom, Jonathan
Galanie, Stephanie Sue
Alvizo, Oscar

<120> ENZYMATIC GLYCOSYLATION OF STEVIOL GLYCOSIDES AND OTHER COMPOUNDS WITH
GLUCOSE-1-PHOSPHATE

<130> CX8-155USP1

<140> NOT YET ASSIGNED

<141> 2016-06-15

<160> 32

<210> 1

<211> 1326

<212> DNA

<213> Artificial Sequence

<220>

<223> Wild type UDP-glycosyltransferase 76G1 from Stevia

<400> 1

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ttcagtatca ccatctttca caccaacttc aacaaaccca aaacatctaa ttaccctcac 180
ttcactttca gattcatcct cgacaacgac ccacaagacg aacgcatttc caatctaccg 240
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ttacgacgcg aactggaact gttgatgtta gcttctgaag aagatgaaga ggtatcgtgt 360
ttaatcacgg atgctctttg gtacttcgcg caatctgttg ctgacagtct taacctccga 420
cggcttgttt tgatgacaag cagcttgttt aattttcatg cacatgtttc acttcctcag 480
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aaagagatat tagggaagat gataaaacaa acaagagcat cttcaggagt catctggaac 660
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gggtgggaaa gaggagagat agcaaatgca ataagaagag ttatggtgga tgaagaagga 1260
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<210> 2

<211> 442

<212> PRT

<213> Artificial Sequence

<220>

<223> Wild type UDP-glycosyltransferase 76G1 from Stevia

<400> 2

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			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				
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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
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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
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> 1203
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Wild type macrolide glycosyltransferase from Streptomyces

<400> 3

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atgaccagtc gctcgacat cgccatgttc tccatcgccg cccacgggca cgtgaacccg 60
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cccgtcttcg ccgggaaggt cgccgaggcc ggccgaggag tgaagctctg gaactccacc 180
ctgccctcgc ccgacgacga cccacaggca tggggcacga ccctgctgga caacgtggag 240
ccgttcctgg ccgacgcgat ccaggcgctc ccgcagctga tcgaggcgta cgaaggggac 300
gagcccgacc tcgtgctgca cgacatcacc tcctaccggg cccgcgtcct ggcccaccgc 360
tggggcgtgc ccgcggtctc cctgtcgccg aacctcgtcg cctgggaggg ctacgagaag 420
gaggtggccg agccgatgtg ggccgagccg aagcggaccg agcgcgggcg ggcctactac 480
gcccgttcc acgcctggct ggaggagaac ggcgtaacc tgcacccgga cgacttcgtg 540
ggccgccccg cccgctgtct cgtcctgatc ccgaaggcgc tgcagcccaa cgccgaccgg 600
gtggacgagg gcgtgtactc cttcgtgggc gcctgccagg gtgaccgcgg cgcggagggg 660
gagtggcggc ggcccgccgg cgccgagaag gtcgccctgg tctcgtcgg gtcctccttc 720
accaagcagc cggacttcta ccgggagtg gtcaggcggt tcggcgagct gccgggctgg 780
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gcccggccgc tcgacaccga ggaggcgacc gccaggccc tcagggcggc cgccctcgtc 1080
ctcgtcgacg accccgaagt ggcccgtcgg gcgcgggaca tccaggctca gatggcgggg 1140
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tag 1203
  
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<210> 4
 <211> 400
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Wild type macrolide glycosyltransferase from Streptomyces

<400> 4

Met Thr Ser Arg Ser His Ile Ala Met Phe Ser Ile Ala Ala His Gly
1 5 10 15

<210> 5
<211> 1248
<212> DNA
<213> Artificial Sequence

<220>

<223> Wild type macrolide glycosyltransferase from Streptomyces

<400> 5

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gccattccgc ccgtcttcgc cgacaaggtg gccgccaccg gcgcccggcc cgtcctctac 180
cactccaccc tgcccggccc cgacgccgac ccggaggcat ggggaagcac cctgctggac 240
aacgtcgaac cgttcctgaa cgacgcgac caggcgctcc cgcagctcgc cgatgcctac 300
gccgacgaca tccccgatct cgtcctgcac gacatcacct cctaccgggc ccgcgtcctg 360
gcccggcgct ggggcggtccc ggcggtctcc ctctccccga acctcgtcgc ctggaagggt 420
tacgaggagg aggtcgccga gccgatgtgg cgcaacccc ggagaccga gcgcggacgg 480
gcctactacg cccgggtcga ggcatggctg aaggagaacg ggatcaccga gcaccggac 540
acgttcgcca gtcacccgcc gcgctccctg gtgctcatcc cgaaggcgct ccagccgcac 600
gccgaccggg tggacgaaga cgtgtacacc ttcgtcggcg cctgccaggg agaccgcgc 660
gaggaaggcg gctggcagcg gcccggcggc gcggagaagg tcgtcctggt gtcgctcggc 720
tcggcgttca ccaagcagcc cgcttctac cgggagtgcg tgcgcgcctt cgggaacctg 780
cccggctggc acctcgtcct ccagatcggc cggaaggtag ccccgccga actgggggag 840
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gatctgttcg tcaccacgc gggcgccggc ggagccagg aggggctggc caccgcgacg 960
cccatgatcg ccgtaccgca ggccgtcgac cagttcggca acgccgacat gctccaaggg 1020
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cgccacgagc ggcaggagcc ggtgggcgac cgaccaacg gtgggtga 1248
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<210> 6

<211> 415

<212> PRT

<213> Artificial Sequence

<220>

<223> Wild type macrolide glycosyltransferase from Streptomyces

<400> 6

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

<210> 7

<211> 894

<212> DNA

<213> Artificial Sequence

<220>

<223> Wild type laminaribiose phosphorylase from *Paenibacillus*

<400> 7

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ctggcgttat acgtcgtttt ttatttcgga ccatcggtgt tgaccgtgat ttattcgttt 120
acggatgtga aaaacatccc cggcagctcc atgaacttcg tcgggctcga taattataaa 180
gacttgtttt ttgccggaaa ttccggggaa cgctgggttt ccatcaaaaa cacgttaatt 240
ttcatgttta tcgtcaccat cgtgcagaac ggagtggcgt tgtttgtggc tgtgctgata 300
aaccaacggc tgcgcggcga ttatttttac cgggccgtat tttttcttcc ggtcgtgctt 360
ggggtggccg ttgttgcgct cgtttggggc atgatgttcg atccgatgag cgggccgggt 420
aacatgctgt atcaatcgct gttcggatat aaagacatgt ttttctccag ctttacgcac 480
gcgttcggct acattatttt cgttcaaadc tggatgtaca tgggctattc aatgctgatt 540
tttctcgccg gcctacaatc cgtgccaaaa gatctgtacg aagcggggta catcgacggt 600

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acgaaccgct ggcaatcggt caagaatatt acgttcccgc tgatcgcccc gtctttttacg 660
gtcaatatgc tgcttttcgat catcggggcg atgtccacgt tcgatattat cctcgccacg 720
acggacggca agttcaacac cagaacgatg gcttacgacg tatataagga aacgttccgc 780
ggcagctctgg aaatgggctt gccttcggcg ctgtccgtgg tccagttcct gatcattttg 840
gtgtttgtta tcgtggccgt cagacagacg cgtaagagag aggtggaata ttaa      894

```

<210> 8

<211> 297

<212> PRT

<213> Artificial Sequence

<220>

<223> Wild type laminaribiose phosphorylase from Paenibacillus

<400> 8

```

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

```

<210> 9

<211> 1374

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of UDP-glycosyltransferase 76G1 from Stevia

<400> 9

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tttagcatca ccatTTTTtca 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
cgtctgggtt tgatgaccag cagcctgttt aacttccacg cgcacgtgag cctgccgcag 480
tttgacgagc tgggctacct ggatccggac gataaaaccc gtctggagga acaagcgagc 540
ggtttcccga tgctgaagggt taaagatatc aagagcgcgt atagcaactg gcagatcctg 600
aaagaaattc tgggcaagat gatcaagcag acccgtgcga gcagcgggtgt gatttggaaac 660
agctttaaag agctggagga aagcgagctg gaaaccgtta tccgtgaaat tccggcgccg 720
agcttcttga ttccgctgcc gaagcacctg accgcgagca gcagcagcct gctggaccac 780
gatcgtaccg tgttccagtg gctggaccag caaccgccga gcagcgtgct gtacgttagc 840
tttggcagca ccagcgaggt ggacgaaaag gatttcctgg agattgcgcg tggctctggtt 900
gacagcaaac aaagctttct gtgggtgggt cgtccgggct tctggaaggg tagcacctgg 960
gttgagccgc tgccggatgg ttttctgggc gaacgtgggt gtatcgtgaa gtgggttccg 1020
caacaagaag tgctggcgca cggcgcgatt ggtgcgttct ggaccacag cggttggaac 1080
agcaccctgg agagcgtgtg cgaaggcgtt ccgatgatct ttagcgactt cggctctggat 1140
cagccgctga acgcgcgtta catgagcgat gttctgaaag tgggcgttta tctggagaac 1200
ggctgggagc gtgggtgaaat cgcgaaacgc attcgtcgtg tgatggttga cgaggaaggt 1260
gagtacatcc gtcagaacgc gcgtgttctg aagcaaaaag cggatgttag cctgatgaag 1320
ggtggcagca gctacgagag cctggaaagc ctggttagct atattagcag cctg 1374
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<210> 10

<211> 458

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of UDP-glycosyltransferase 76G1 from Stevia

<400> 10

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

<210> 11

<211> 1203

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of macrolide glycosyltransferase from Streptomyces

<400> 11

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ccggttttcg ccggtaaaagt tgctgaagcg ggcgccgaag tgaaactgtg gaacagcacg 180
ctgccgtctc cggatgacga tccgcaggcg tggggtagca cgctgctgga taatgttgaa 240
ccgtttctgg cagacgctat tcaggctctg ccgcaactga tcgaagcgta tgaaggcgac 300
gaaccggatc tggtcctgca tgatatcacc tcatatccgg ctctgtttct ggccccatcgc 360
tgggggtgtc cggccgtgtc actgtcgccg aatctgggtg cctgggaagg ctacgaaaaa 420
gaagtgcgtg aaccgatgtg ggcggaaccg aaacgtaccg aacgtgggtc cgcctattac 480
gcacgctttc atgcctggct ggaagaaaac ggtgttacgc tgcattccgga tgattttgtt 540
ggctgtccgg cacgttgctt ggtgctgatt ccgaaagccc tgcagccgaa tgcagaccgt 600
gtggatgaag gtgtttatag ctttgtcggc gcctgtcaag gcgctgcggg tgcagagggt 660
gaatggcgct gcccgcgagg tgcagaaaaa gttgccctgg tctctctggg cagctctttt 720
accaaacagc cggatttcta ccgtgaatgc gtgcgcgcct tcggtgaatt accgggctgg 780
catctgggtc tgcaaattgg tcgcatgtg gaccgggccc atctgggtga tgtgccggaa 840
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gcagtgcgcg aggcagttga tcaattcggg aatgcagaca tgctgcaggg tctgggtgtt 1020
gcccgtcgcc tggataccga agaagcaacc gctgaagcgc tgcgtgcagc ggcgctggcg 1080
ctggttgatg atccggaagt tgctcgtcgc gcgcgcgata ttcaggcgca gatggcgggt 1140
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taa 1203
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<210> 12

<211> 400

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of macrolide glycosyltransferase from Streptomyces

<400> 12

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

<210> 13

<211> 2733

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of laminaribiose phosphorylase from *Paenibacillus*

<400> 13

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gagcacaaca gctacctgta ttttccgctg gtgaacgaag cgggtatgat gagcgcggtt 120
accccgaacc tgcacggcga gatcaccagc ggtcacaaca ccttcctgat ggaaccggtg 180
agcgcgggaga gcctgcacaa cagcaaggcg agccgtaact tttgggtgtt cattgaaggt 240
tatggtgctg ggagcgtagt cggcaacagc gcgcgtcaga acgcggcgcg ttttaccggt 300
gaggaagagc gtagcgcggt ggaggcgggt ttcctgtggc acgcgggttac ccgtgaaaac 360
gagaaggcgg gtctgaaagc gcgtaccgtg agcttcgtgc cggttaccga cgataagatc 420
gaactgatgc gtgttaccct gaccaacacc ggcaacgcgc cgctgaaact gaccccgacc 480
gcggcgattc cgctgtatgg tcgtagcgcg gacgatctgc gtgatcaccg tcacgtgacc 540
agcctgctgc accgtatctt taccagcgaa tacggcattg aggttcagcc ggcgctgagc 600

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ttcgacgaac	gtggtcaccg	tgtgaacaag	gttacctatg	gcgtgttttg	tgcggaggcg	660
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gcgctggact	ggccggaagc	ggtggttgcg	aaccgtgagc	cggatgcgca	ggcgggcacc	780
gcggtggaag	gttatgaggc	ggttggcgcg	ctgcgttttg	cgccggtgga	gctggcgccg	840
ggcaaaagcg	tgagctatgt	ggttgcatg	gttatcagcg	gcgaccgtat	tgatgttggt	900
cgttacgcgg	cggattatct	ggcggcgggt	cgttttgacg	cgctgctgga	gcagaaccgt	960
gcgtactggc	gtgacaagct	ggataccgtg	cgtttcagca	gcggtgatgg	cgagcaggac	1020
ctgtggatga	aatgggttac	cctgcaaccg	attctgcgtc	gtctgtatgg	taacagcttc	1080
ctgccgtacc	acgattatgg	tcgtgggtggc	cgtggctggc	gtgatctgtg	gcaagactgc	1140
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gcggatcgta	acaacatccc	gcgtgttttg	atggaccatg	gtgcgtggcc	gctgatgacc	1320
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cagagcaaag	agggctacgc	gtggtttaac	ggttactata	acaacgacgg	tgaacgtgtg	1980
gagggcgatc	acccggacgg	tgttcgtatg	accctgaccg	gtcaagtgtt	cgcgatcatg	2040
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ggtcgtgcgt	tcggctttgc	gttcggtcac	aaggagaacg	gtgcgatgtt	cagccacatg	2220
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tggctgctgc	tgaccaact	gaccgaagtg	tatggcgtta	agggtcgttt	cggcgatctg	2460
cgtctggagc	cgaaactggt	gcaggcgcaa	tttgacggca	gcggtgaagc	ggcggttgag	2520
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ggtcaatatc	gtgtggatag	cgttagcctg	aacggtcaga	gcgttgattg	ccaaaacgac	2640
ggcgcgggtt	gcctgatcgg	tcgtagcctg	attgaagcgc	tgccggcgga	tggtgtgcat	2700
gagctgatcg	ttaccctggg	tcgtaacatt	agc			2733

<210> 14

<211> 911

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of laminaribiose phosphorylase from *Paenibacillus*

<400> 14

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

			420					425					430			
His	Gly	Ala	Trp	Pro	Leu	Met	Thr	Thr	Leu	Leu	Tyr	Leu	His	Gln	Ser	
		435					440					445				
Gly	Asp	Leu	Asp	Leu	Leu	Phe	Gln	Pro	Gln	Ser	Tyr	Phe	Arg	Asp	Val	
	450					455					460					
Phe	Val	Lys	Arg	Cys	Arg	Glu	Arg	Asp	Ala	Ser	Trp	Thr	Pro	Glu	Gln	
465					470					475					480	
Gly	Asn	Lys	Leu	Leu	Thr	Ala	Asp	Gly	Gln	Ile	Tyr	Glu	Gly	Thr	Ile	
				485					490					495		
Leu	Glu	His	Ile	Leu	Leu	Gln	Asn	Ile	Val	Pro	Phe	Phe	Asn	Val	Gly	
			500					505					510			
Glu	His	Gly	Asn	Ile	Lys	Leu	Glu	Gly	Ala	Asp	Trp	Asn	Asp	Gly	Leu	
		515					520					525				
Asp	Leu	Ala	Pro	Glu	Arg	Gly	Glu	Ser	Val	Ala	Phe	Thr	Ala	Phe	Tyr	
	530					535					540					
Ala	Ser	Asn	Leu	Met	Glu	Leu	Ser	Glu	Leu	Leu	Glu	Leu	Gln	Lys		
545					550				555					560		
Arg	Thr	Gly	Lys	Asp	Ser	Leu	Asp	Ile	Ala	Glu	Glu	Met	Ala	Leu	Leu	
				565					570					575		
Leu	Asp	Thr	Leu	Gly	Lys	Pro	Ile	Ser	Tyr	Asp	Ser	Ile	Gln	Glu	Lys	
			580					585					590			
Arg	Ser	Leu	Leu	Asp	Arg	Tyr	Tyr	Asp	Ala	Val	Thr	Pro	Arg	Val	Ser	
		595					600					605				
Gly	Lys	Lys	Leu	Leu	Leu	Asp	Ile	Arg	Lys	Val	Ala	Glu	Asp	Leu	Lys	
	610					615					620					
Arg	Lys	Ala	Asp	Trp	Ala	Val	Ala	His	Leu	Arg	Gly	Ser	Glu	Trp	Ile	
625					630					635					640	
Gln	Ser	Lys	Glu	Gly	Tyr	Ala	Trp	Phe	Asn	Gly	Tyr	Tyr	Asn	Asn	Asp	
				645					650					655		
Gly	Glu	Arg	Val	Glu	Gly	Asp	His	Pro	Asp	Gly	Val	Arg	Met	Thr	Leu	
			660					665					670			
Thr	Gly	Gln	Val	Phe	Ala	Ile	Met	Gly	Gly	Val	Ala	Thr	Asp	Glu	Gln	
		675					680					685				
Thr	Glu	Lys	Ile	Ser	Gln	Ala	Val	Asn	Arg	Tyr	Leu	Lys	Asp	Glu	Arg	
	690					695					700					
Ile	Gly	Tyr	Arg	Leu	Asn	Ser	Arg	Phe	Gly	Gly	Ile	Gln	Gln	Asn	Leu	
705					710					715					720	
Gly	Arg	Ala	Phe	Gly	Phe	Ala	Phe	Gly	His	Lys	Glu	Asn	Gly	Ala	Met	
				725					730					735		
Phe	Ser	His	Met	Thr	Val	Met	Tyr	Ala	Asn	Ala	Leu	Tyr	Lys	Arg	Gly	
			740					745					750			
Phe	Val	Gln	Glu	Gly	Phe	Glu	Val	Leu	Asp	Ser	Ile	Tyr	Arg	Leu	Ser	
		755					760					765				
Ala	Asp	Phe	Glu	Asn	Ser	Arg	Ile	Tyr	Pro	Gly	Val	Pro	Glu	Tyr	Ile	
	770					77										

850		855		860
Val Asp Ser Val Ser	Leu Asn Gly Gln Ser	Val Asp Cys Gln Asn Asp		
865	870	875	880	
Gly Ala Gly Cys Leu Ile Gly Arg Ser	Leu Ile Glu Ala Leu Pro Ala			
	885	890	895	
Asp Gly Val His Glu Leu Ile Val Thr	Leu Gly Arg Asn Ile Ser			
	900	905	910	

<210> 15
 <211> 1476
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sucrose phosphorylase from Leuconostoc

<400> 15
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 ctgccgttct ttccgagcac cggatgatcg ggcttcgcgc cgagcgacta caccctgtgt 180
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 ttcgacttta tgatcaacca cattagccgt gaaagcgta tgtaccagga cttcaagaaa 300
 aaccacgatg agagcaagta taaagacttc tttatccgtt gggagaaaatt ttgggcgaaa 360
 gcgggtgaaa accgtccgac ccaggcggac gtggatctga tctacaagcg taaagataag 420
 gcgccgaccc aagagattac cttcgacgat ggtaccaccg aaaacctgtg gaacaccttt 480
 ggcgacgagc aaatcgacat tgatgttaac agcgcgatcg cgaaagagtt cattaagacc 540
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 aacgaagtgc gtgaaattct gaccccgctg aaggcggaga tcctgccgga gattcacgaa 720
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 aagatgagcc cgatgaagca attcaccacc ctggacaccc acgatggtat cggcgtgggt 900
 gacgcgcgtg atgtgctgac cgacgaggaa attgattacg cgagcgagga actgtataag 960
 gttggcgca acgtgaagaa aacctacagc agcgcgagct ataacgacct ggatatctac 1020
 caaattaaca gcacctacta tagcgcgctg ggtaacgacg atgcggcgta tctgctgagc 1080
 cgtatcttcc aggtttttgc gccgggcatc ccgcaaattt actatgtggg tctgctggcg 1140
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 tactatagcg ttgacgaagt gaaagaggaa gttaagcgtc cgggtggttg gaaactgctg 1260
 aagctgctga gctggcgtaa caacttcgcg gcgtttgacc tggatggtag cattgatgtg 1320
 gaaaccccga gcgacaccac catcaagatt acccgtaaag ataagagcgg cgagaacgtg 1380
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<210> 16
 <211> 492
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Sucrose phosphorylase from Leuconostoc

<400> 16

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

<223> Sucrose phosphorylase from Bifidobacterium

<400> 18

```

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

```


<213> Artificial Sequence

<220>

<223> Sucrose phosphorylase from uncultured bacterium

<400> 20

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

Thr	Asn	Asp	Met	Asp	Leu	Leu	Gly	Arg	Ser	Gly	Val	Gly	Arg	Asp	Ile
385					390					395					400
Asn	Arg	His	Tyr	Tyr	Thr	Asp	Ala	Glu	Ile	Asp	Ala	Ala	Leu	Ala	Arg
			405						410						415
Pro	Leu	Val	Arg	Thr	Leu	Ile	Ala	Leu	Ile	Arg	Leu	Arg	Asn	Thr	His
			420					425						430	
Pro	Ala	Phe	Ala	Gly	Glu	Phe	Asp	Val	Ser	Val	Pro	Ala	Ala	Thr	Gln
		435					440					445			
Ile	Arg	Leu	Arg	Trp	Gln	Arg	Gln	Glu	His	Trp	Ile	Glu	Leu	His	Val
	450				455						460				
Asp	Leu	Ser	Ile	Pro	Lys	Ala	Ser	Ile	Thr	Gly	Thr	Gly	Ile	His	Pro
465					470					475					480
Ile	Thr	Ile	Pro	Gly	Ala	Ala	Asp	Ala	Gly	Ala	Pro	Ser			
				485					490						

<210> 21

<211> 1467

<212> DNA

<213> Artificial Sequence

<220>

<223> Sucrose phosphorylase from *Oenococcus*

<400> 21

atgccggtga	agaacaaagc	gatgctgatac	acctacagcg	atagcatggg	taaaaacatc	60
aaggaactgc	agtacattct	ggacaaatat	atcggcgatg	cgattgggtg	cgttcacctg	120
ctgccgttct	ttccgagcac	cggatgatcgt	ggcttcgcgc	cgagcgacta	taccctgtgtg	180
aacccggact	ttgggtgattg	ggaggacgtt	gaggaactgg	gcaagaaata	ctatctgatg	240
ttcgacttta	tgatcaacca	cattagccgt	gaaagcatta	tgtaccagga	cttcaaagag	300
aagaaagatg	cgagcagcta	taaggacttc	tttatccgtt	gggaaaaatt	ttggccgaag	360
ggctcgtccga	ccaaggcgga	catcgatctg	atttacaagc	gtaaagataa	ggcgccgatc	420
cagggtatta	ccttcgcgga	cggcagccaa	gaacacctgt	ggaacacctt	tggtgacgag	480
caaatcgata	ttaacgtgaa	aagcaagggt	gcgcaggagt	tctttaaaga	taccctgcaa	540
agcatggtga	agcacggcgc	ggacctgatt	cgtctggatg	cgttcgcgta	cgcgatcaag	600
aaaattgata	ccaacgactt	ctttatcgaa	ccggagattt	gggatctgct	ggaaagcggt	660
cgtaaaattc	tggacccgct	gcatgcggag	atcctgccgg	aaatttacga	gcactatacc	720
atcccggcga	agattaacga	atacggttat	ttcacctacg	actttgtgct	gccgctgggt	780
atcctgtaca	ccctgtatag	cggcaaccgg	aaacagctgg	cgaaatggct	gaagatgagc	840
ccgaagaaac	aattcaccac	cctggatacc	cacgacggta	tcggcgtggg	tgatgcgcgt	900
gacatcctga	ccgacgagga	aattgattac	accagcagcg	agctgtataa	agtgggtgcg	960
aacgttaagc	gtacctacag	cagcgcgggc	tataacaacc	tgacatcta	ccagattaac	1020
agcacctact	atagcgcgct	gggtaacgac	gataaagcgt	atctgctggc	gcgtgcgatc	1080
cagatTTTTG	cgccgggcat	cccgcaaat	tactatgcgg	gtctgctggc	gggcgaaaac	1140
gacctggatc	tgctggaaaa	aaccaaagag	ggtcgtaaca	ttaaccgtca	ctactatagc	1200
gaggaagagg	tggcgaacga	ggttcaacgt	ccgatcgttg	cgtgcctgct	gaagctgctg	1260
gcgtggcgta	accgtagcgc	ggcgttcgac	ctgcagggtg	atattcaagt	tagcgcgacc	1320
gataaaaacg	aaatcaagat	cattcgtacc	agcaccaacg	gtcaagacac	cgcggagctg	1380
accgcgaacg	tggcgtgtaa	aacctttacc	atcaaagaaa	acgacaagat	cattctgatt	1440
gaggatcaaa	ccgacaccaa	ggatatc				1467

<210> 22

<211> 489

<212> PRT

<213> Artificial Sequence

<220>

<223> Sucrose phosphorylase from *Oenococcus*

<400> 22

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

370		375		380
Leu Glu Lys Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser				
385		390		395
Glu Glu Glu Val Ala Asn Glu Val Gln Arg Pro Ile Val Ala Cys Leu				
	405		410	415
Leu Lys Leu Leu Ala Trp Arg Asn Arg Ser Ala Ala Phe Asp Leu Gln				
	420		425	430
Gly Asp Ile Gln Val Ser Ala Thr Asp Lys Asn Glu Ile Lys Ile Ile				
	435		440	445
Arg Thr Ser Thr Asn Gly Gln Asp Thr Ala Glu Leu Thr Ala Asn Val				
	450		455	460
Ala Leu Lys Thr Phe Thr Ile Lys Glu Asn Asp Lys Ile Ile Leu Ile				
465		470		475
Glu Asp Gln Thr Asp Thr Lys Asp Ile				480
	485			

<210> 23

<211> 1446

<212> DNA

<213> Artificial Sequence

<220>

<223> Sucrose phosphorylase from Enterococcus

<400> 23

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ctgccgttct ttccgagcac cggtgatcgt ggcttcgcgc cgagcgacta taccgtggtt 180
gatagcgcgt ttggtacctg gcaagagggt gaagcgctgg gcgagaagta ctacctgatg 240
ttcgacttca tgatcaacca catcagccgt gaaagcaaat tctttcagga tttcaagcaa 300
aaccacgagg cgagcccgtg caaggaaatg tttattcgta tccacgagtt ctttccggaa 360
aaccgtccga ccccgaggga cattgatctg atctataagc gtaaagacaa ggcgccgttc 420
caggaagtga cttttgcgga tgggtaccac gaacagggtt ggaacacctt cggcgaggaa 480
caaattgacc tggatgtgaa caaagaagtt accaagcaat tcatcaagga caccctgaag 540
gatatggcga gccacggttg cagcctgatt cgtctggacg cgttcgcgta cgcgatcaag 600
aaactggaca ccaacgattt ctttgtggag ccggaattt gggacctgct ggatgagggt 660
cgtgaggaag cggcgaaata caactgcgaa ctgctgccgg agatccacga acactatacc 720
attcagatga agatcgcgga ccacgattac tatgtgtacg acttcgcgct gccgatgatc 780
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ccgatgaagc aatttaccac cctggacacc cacgatggta ttggcgtggt tgacgcgaaa 900
gatctgctga ccgacgagga actggattac accagcgagg aactgtataa agtgggcgcg 960
aacgttaaga aaatctacag cagcgcgagc tataacaacc tggacattta ccagatcaac 1020
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1446

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<210> 24
 <211> 482
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Sucrose phosphorylase from Enterococcus

<400> 24

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

<211> 480
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Sucrose phosphorylase from Streptococcus

<400> 26

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

Gln	Val	Tyr	Tyr	Val	Gly	Phe	Leu	Ala	Gly	Lys	Asn	Asp	Leu	Glu	Leu
370						375					380				
Leu	Glu	Asn	Thr	Lys	Glu	Gly	Arg	Asn	Ile	Asn	Arg	His	Tyr	Tyr	Ser
385					390					395					400
Asn	Glu	Glu	Ile	Ala	Gln	Glu	Val	Glu	Arg	Pro	Val	Val	Lys	Ser	Leu
				405					410					415	
Leu	Lys	Leu	Phe	Ser	Phe	Arg	Asn	Asn	Ser	Gln	Ala	Phe	Asp	Leu	Glu
			420					425					430		
Gly	Ser	Ile	Glu	Val	Glu	Thr	Pro	Asp	Glu	His	Thr	Ile	Val	Ile	Thr
	435						440					445			
Arg	Gln	Asn	Lys	Asp	Gln	Thr	Ala	Thr	Ala	Val	Ala	Arg	Ile	Asn	Leu
	450					455					460				
Ala	Asp	Gly	Thr	Tyr	Gln	Val	Thr	Glu	Asn	Gly	Gln	Asp	Ile	Glu	Phe
465					470					475					480

<210> 27

<211> 1509

<212> DNA

<213> Artificial Sequence

<220>

<223> Sucrose phosphorylase from Scardovia

<400> 27

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agcctgaccg atgtgctgcg tacccgtttc gatggcggtt atgaaggtgt gcacattctg 120
ccgttcttta ccccgttcga cggcgcggtg gcgggttttg acccgatcga tcacaccaag 180
gttgacccgc gtctgggtag ctgggacgat gtggcgggagc tgagcaaac ccacgacatc 240
atggttgatg cgattgtgaa ccacatgagc tggcaaacgc aacagtttca agatgttatg 300
aagaaaggtg aaggcagcga atactatccg atgttcctga ccatgagcgc ggtgtttccg 360
gaggtgacga ccgaggaaga cctggcggtt atttatcgtc cgcgtccggg tctgccgttc 420
accactata cctggggtgg caagaccgtt ctggtttgga ccacctttac cccgcagcaa 480
gtggacatcg ataccgagc cgacgaaggt tggcggtacc tgatgagcat cctggatcag 540
atgagcaaaa gccacgttag cttcattcgt ctggacgcgg tgggttatgg cgcgaagcgt 600
gcgaaaacca gctgcttcat gaccccggtg acctttgatc tgatcagccg tattaaagag 660
gagagcgcgc gtcgtggcat ggagaccctg atcgaagttc acagctacta taagaaacaa 720
gtggagattg cgaacaaggt ggaccgtgtt tacgattttg cgatcccggc gctgctgctg 780
catgcgctga gcaccggtaa aaccggtccg ctggcgact ggctgggtgt gcgtccggtt 840
aacgcggtga acgttctgga caccacgat ggtatcggcg tgattgatgt tggcagcgac 900
cagatggatc gtagcctgaa gggctctggt ccggacgatg aagttgacca actggtggag 960
accattaaag aaaacagcca tggtgaaagc gcggaagcga ccggtgcggc ggcgagcaac 1020
ctggatctgt accaggttaa ctgcacctac tatagcgcgc tgggctgcga cgatcaaaaa 1080
tacatcgca gccgtgcggt gcagttctat atgccgggtg tgccgcaagt ttactatgtg 1140
ggcgcgctgg cgggcaagaa cgacatggag ctgctgaaac gtaccaacgt tggctcgtgat 1200
atcaaccgtc actactatac cgtggcggtg attgacgaaa acctgcgtcg tccggtggtt 1260
caggcgctga acgcgctggg ccgtttccgt aacaccctgg aggcgtttga cggtgatttc 1320
agctttaccg aaaacggtgg cagcctggcg atgacctgga ccggtcaaag caccagcacc 1380
accctgacct ttgcgccggg caagggtgcg ggtagcagcg gcgtgccggt ttgcaccatc 1440
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gcggcgag                                     1509

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<210> 28

<211> 503
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Sucrose phosphorylase from Scardovia

<400> 28

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

Phe	Tyr	Met	Pro	Gly	Val	Pro	Gln	Val	Tyr	Tyr	Val	Gly	Ala	Leu	Ala
370						375					380				
Gly	Lys	Asn	Asp	Met	Glu	Leu	Leu	Lys	Arg	Thr	Asn	Val	Gly	Arg	Asp
385					390				395						400
Ile	Asn	Arg	His	Tyr	Tyr	Thr	Val	Ala	Glu	Ile	Asp	Glu	Asn	Leu	Arg
			405						410					415	
Arg	Pro	Val	Val	Gln	Ala	Leu	Asn	Ala	Leu	Gly	Arg	Phe	Arg	Asn	Thr
		420						425					430		
Leu	Glu	Ala	Phe	Asp	Gly	Asp	Phe	Ser	Phe	Thr	Glu	Asn	Gly	Gly	Ser
	435					440						445			
Leu	Ala	Met	Thr	Trp	Thr	Gly	Gln	Ser	Thr	Ser	Thr	Thr	Leu	Thr	Phe
450						455					460				
Ala	Pro	Gly	Lys	Gly	Ala	Gly	Ser	Ser	Gly	Val	Pro	Val	Cys	Thr	Ile
465					470					475					480
Ala	Trp	Lys	Asp	Ala	Ser	Gly	Glu	His	Val	Thr	Asp	Asp	Ile	Ile	Ala
			485					490						495	
Asn	Pro	Pro	Ala	Ala	Ala	Gln									
			500												

<210> 29

<211> 1506

<212> DNA

<213> Artificial Sequence

<220>

<223> Sucrose phosphorylase from Parascardovia

<400> 29

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agcctgaccg acgtgctgcg taccggtttt gatggtgttt acgaaggcgt gcacattctg 120
ccgttcttta ccccgttcga cgggtcggat gcgggctttg acccgattga tcacaccaag 180
gttgatccgc gtctgggtac ctgggacgat atcgcggagc tgagcaaaac ccacgacatc 240
atggttgatg cgattgtgaa ccacatgagc tgggagagca agcagttcca agacgttatg 300
aaaaacggtg aagcgagccc gtactatggc atgttcctga ccatgagcgc ggtgtttccg 360
gatggtgcga ccgaggaaga tctggcgggt atctatcgtc cgcgtccggg tctgccgttc 420
accactata actggggtgg caagaccgt ctggtttgga ccacctttac cccgcagcaa 480
gtggacatca acaccgatag cattgaaggc tgggactacc tgatgagcat cctggatcag 540
atgagccaaa gccacgttag cttcattcgt ctggacgcgg tgggttatgg cgcgaagcag 600
gcgaaaacca cctgcttcat gacccgaag acctttgagc tgatcggtcg tattaagag 660
gagagcgcg aacgtggcat ggagaccctg atcgaagttc acagccacta catgaagcaa 720
gtggaaattg cgggtaaagt ggaccgtgtt tatgattttg cgattccggg tctgctgctg 780
catgcgctga ccaccggtaa aaccggtccg ctggcgcgtt ggatggaagt gcgtccgggt 840
aacgcggtga acgttctgga caccacgat ggtattggcg ttatcgatat tggtagcgac 900
cagatggatc gtagcctgaa gggtctggtg ccggacgagg aagttgatca actggtggag 960
accatcaaag aaaacagcca cggtgaaagc gcggcggcga ccggcgcggc ggcgagcaac 1020
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tatattgcgg cgcgtgcggt gcagttcttt atgccgggcg tgccgcaagt ttactatgtg 1140
ggtgcgctgg cgggcgagaa cgacatgcag ctgctgaagg aaaccaacgt tggctctgat 1200
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accctgacct ttacccggc gcaaggtgtt ggcaaagatg aggcgccggt gtgcagcctg 1440
cgttggaagg acagcgcggg tgatcacaaa accgatgac tgattgcgga accgccggcg 1500

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<210> 30

<211> 502

<212> PRT

<213> Artificial Sequence

<220>

<223> Sucrose phosphorylase from Parascardovia

<400> 30

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

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Ala	Ala	Ser	Asn	Leu	Asp	Leu	Tyr	Gln	Val	Asn	Cys	Thr	Tyr	Tyr	Ser
			340					345					350		
Ala	Leu	Gly	Cys	Asp	Asp	Gln	Lys	Tyr	Ile	Ala	Ala	Arg	Ala	Val	Gln
		355					360					365			
Phe	Phe	Met	Pro	Gly	Val	Pro	Gln	Val	Tyr	Tyr	Val	Gly	Ala	Leu	Ala
		370				375					380				
Gly	Glu	Asn	Asp	Met	Gln	Leu	Leu	Lys	Glu	Thr	Asn	Val	Gly	Arg	Asp
385					390					395					400
Ile	Asn	Arg	His	Tyr	Tyr	Ser	Leu	Glu	Glu	Ile	Asp	Gln	Asn	Leu	Glu
			405						410					415	
Arg	Pro	Val	Val	Lys	Ala	Leu	Asn	Ala	Leu	Cys	Arg	Phe	Arg	Asn	Gly
			420					425					430		
Leu	Glu	Ala	Phe	Asp	Gly	Asp	Phe	Ser	Phe	Ala	Gln	Asn	Gly	Asp	Ser
		435					440						445		
Leu	Thr	Phe	Ala	Trp	Thr	Gly	Lys	Glu	Thr	Glu	Ala	Thr	Leu	Thr	Phe
		450				455					460				
Thr	Pro	Ala	Gln	Gly	Val	Gly	Lys	Asp	Glu	Ala	Pro	Val	Cys	Ser	Leu
465					470					475					480
Arg	Trp	Lys	Asp	Ser	Ala	Gly	Asp	His	Lys	Thr	Asp	Asp	Leu	Ile	Ala
			485						490					495	
Glu	Pro	Pro	Ala	Val	Ala										
			500												

<210> 31

<211> 1500

<212> DNA

<213> Artificial Sequence

<220>

<223> Sucrose phosphorylase from Alloscardovia

<400> 31

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ccgttcttta ccccgttcga tgggtgcggac gcgggctttg atccggttga ccacacaaaa 180
gtggaccgcg gtctgggtag ctgggacgat gtggcggaac tgagcaccac ccacgatatc 240
atggttgaca ccattgtgaa ccacatgagc tgggagagcg aacagttcca agatgttatg 300
gcgaagggcg aggacagcga atactatccg atgttcctga ccatgagcag catttttccg 360
gatggtgtga ccgaggaaga cctgaccgcg atctatcgct cgcgccggg tctgccgttc 420
accactata actggggtgg caaaaccgt ctggtttgga ccacctttac cccgcagcaa 480
gtggacattg ataccgacag cgagatgggt tggaactacc tgctgagcat cctggatcag 540
ctgagccaaa gccacgttag ccaaattcgt ctggacgcgg tgggttatgg cgcgaggag 600
aaaaacagca gctgcttcat gaccccgaag accttaaac tgatcgaacg tattaaggcg 660
gaggtgaaa aacgtggcct ggagaccctg atcgaagttc acagctacta taagaaacag 720
gtggagattg cgagcaaggt ggatcgtgtt tacgactttg cgatcccggg tctgctgctg 780
catgcgctgg aatttggaac aaccgatgcg ctggcgcaat ggattgacgt tcgtccgaac 840
aacgcggtga acgttctgga taccacgac ggtatcggcg ttatcgatat tggtagcgat 900
cagatggacc gtagcctggc gggctctggtg ccggatgagg aagttgacgc gctggttgag 960
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ctggacctgt accaagttaa ctgcacctac tatgcggcgc tgggtagcga cgatcagaaa 1080
tatattgcgg cggtgcggt gcagttcttt atgccgggcg tgccgcaagt ttactatgtg 1140
gggtgcgtgg cgggcagcaa cgatatggac ctgctgaagc gtaccaacgt gggtcgtgat 1200
atcaaccgtc actactatag cgcggcgga gtaggcgagc aggtggaacg tccggtggtt 1260

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caggcgctga acgcgctggg ccgtttccgt aacaccctga gcgcgttcga tggatgaattt 1320
agctacagca acgcggacgg cgttctgacc atgacctggg cggatgatgc gacccgtgcg 1380
accctgacct ttgcgccgaa ggcgaacagc aacgggtgcga gcgtggcgcg tctggagtgg 1440
accgatgcgg cgggtgaaca tgcgaccgac gatctgatcg cgaaccgcc ggtggttgcg 1500

<210> 32
<211> 500
<212> PRT
<213> Artificial Sequence

<220>
<223> Sucrose phosphorylase from Alloscardovia

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

305					310					315					320	
Ser	Ile	His	Arg	Asn	Ser	Lys	Gly	Glu	Ser	Gln	Glu	Ala	Thr	Gly	Ala	
				325					330					335		
Ala	Ala	Ser	Asn	Leu	Asp	Leu	Tyr	Gln	Val	Asn	Cys	Thr	Tyr	Tyr	Ala	
				340					345					350		
Ala	Leu	Gly	Ser	Asp	Asp	Gln	Lys	Tyr	Ile	Ala	Ala	Arg	Ala	Val	Gln	
				355					360					365		
Phe	Phe	Met	Pro	Gly	Val	Pro	Gln	Val	Tyr	Tyr	Val	Gly	Ala	Leu	Ala	
				370					375					380		
Gly	Ser	Asn	Asp	Met	Asp	Leu	Leu	Lys	Arg	Thr	Asn	Val	Gly	Arg	Asp	
385					390					395					400	
Ile	Asn	Arg	His	Tyr	Tyr	Ser	Ala	Ala	Glu	Val	Ala	Ser	Glu	Val	Glu	
				405					410					415		
Arg	Pro	Val	Val	Gln	Ala	Leu	Asn	Ala	Leu	Gly	Arg	Phe	Arg	Asn	Thr	
				420					425					430		
Leu	Ser	Ala	Phe	Asp	Gly	Glu	Phe	Ser	Tyr	Ser	Asn	Ala	Asp	Gly	Val	
				435					440					445		
Leu	Thr	Met	Thr	Trp	Ala	Asp	Asp	Ala	Thr	Arg	Ala	Thr	Leu	Thr	Phe	
				450					455					460		
Ala	Pro	Lys	Ala	Asn	Ser	Asn	Gly	Ala	Ser	Val	Ala	Arg	Leu	Glu	Trp	
465					470					475					480	
Thr	Asp	Ala	Ala	Gly	Glu	His	Ala	Thr	Asp	Asp	Leu	Ile	Ala	Asn	Pro	
				485					490					495		
Pro	Val	Val	Ala													
				500												