SEQUENCE LISTING

<110> Evolva SA

<120> 14-2083-WO

<130> PRODUCTION OF STEVIOL GLYCOSIDES IN RECOMBINANT HOSTS

<150> US 62/110,207
<151> 2015-01-30

<160> 220

<170> PatentIn version 3.5

<210> 1
<211> 473
<212> PRT
<213> Artificial Sequence

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<223> UGT91D2e V286C

<400> 1

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Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
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Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30


Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45


Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60


Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80


Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95


Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
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            100                 105                 110

His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Cys Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300
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Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320


Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335


Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350


Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365


Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380


Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400


Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415


Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430


Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445


Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460


Arg Ala Val Ala Ile Asp His Glu Ser
465                 470
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<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e G384W

<400> 2

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Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
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Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30


Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45


Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60


Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80


Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95


Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110


His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125


Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140


Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160


Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175


Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
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            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Trp
    370                 375                 380
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Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400


Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415


Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430


Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445


Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460


Arg Ala Val Ala Ile Asp His Glu Ser
465                 470


<210>  3
<211>  1383
<212>  DNA
<213>  Stevia rebaudiana

<400>  3
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caaggacata tcaacccatt catacaattt gggaaaagat tgattagtaa gggtgtaaag      120

acaacactgg taaccactat ccacactttg aattctactc tgaaccactc aaatactact      180

actacaagta tagaaattca agctatatca gacggatgcg atgagggtgg ctttatgtct      240

gccggtgaat cttacttgga aacattcaag caagtgggat ccaagtctct ggccgatcta      300

atcaaaaagt tacagagtga aggcaccaca attgacgcca taatctacga ttctatgaca      360

gagtgggttt tagacgttgc tatcgaattt ggtattgatg gaggttcctt tttcacacaa      420

gcatgtgttg tgaattctct atactaccat gtgcataaag ggttaatctc tttaccattg      480

ggtgaaactg tttcagttcc aggttttcca gtgttacaac gttgggaaac cccattgatc      540

ttacaaaatc atgaacaaat acaatcacct tggtcccaga tgttgtttgg tcaattcgct      600
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attgaatgga ctaggaagat ctggaatttg aaagtcattg gtccaacatt gccatcaatg 720

tatttggaca aaagacttga tgatgataaa gataatggtt tcaatttgta caaggctaat 780

catcacgaat gtatgaattg gctggatgac aaaccaaagg aatcagttgt atatgttgct 840

ttcggctctc ttgttaaaca tggtccagaa caagttgagg agattacaag agcacttata 900

gactctgacg taaacttttt gtgggtcatt aagcacaaag aggaggggaa actgccagaa 960

aacctttctg aagtgataaa gaccggaaaa ggtctaatcg ttgcttggtg taaacaattg 1020

gatgttttag ctcatgaatc tgtaggctgt tttgtaacac attgcggatt caactctaca 1080

ctagaagcca tttccttagg cgtacctgtc gttgcaatgc ctcagttctc cgatcagaca 1140

accaacgcta aacttttgga cgaaatacta ggggtgggtg tcagagttaa agcagacgag 1200

aatggtatcg tcagaagagg gaacctagct tcatgtatca aaatgatcat ggaagaggaa 1260

agaggagtta tcataaggaa aaacgcagtt aagtggaagg atcttgcaaa ggttgccgtc 1320

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taa 1383

<210> 4
<211> 460
<212> PRT
<213> Stevia rebaudiana

<400> 4

Met Ala Glu Gln Gln Lys Ile Lys Lys Ser Pro His Val Leu Leu Ile
1 5 10 15

Pro Phe Pro Leu Gln Gly His Ile Asn Pro Phe Ile Gln Phe Gly Lys
20 25 30

Arg Leu Ile Ser Lys Gly Val Lys Thr Thr Leu Val Thr Thr Ile His
35 40 45

Thr Leu Asn Ser Thr Leu Asn His Ser Asn Thr Thr Thr Thr Ser Ile

```
    50                  55                  60

Glu Ile Gln Ala Ile Ser Asp Gly Cys Asp Glu Gly Gly Phe Met Ser
65                  70                  75                  80

Ala Gly Glu Ser Tyr Leu Glu Thr Phe Lys Gln Val Gly Ser Lys Ser
                85                  90                  95

Leu Ala Asp Leu Ile Lys Lys Leu Gln Ser Glu Gly Thr Thr Ile Asp
            100                 105                 110

Ala Ile Ile Tyr Asp Ser Met Thr Glu Trp Val Leu Asp Val Ala Ile
        115                 120                 125

Glu Phe Gly Ile Asp Gly Gly Ser Phe Phe Thr Gln Ala Cys Val Val
    130                 135                 140

Asn Ser Leu Tyr Tyr His Val His Lys Gly Leu Ile Ser Leu Pro Leu
145                 150                 155                 160

Gly Glu Thr Val Ser Val Pro Gly Phe Pro Val Leu Gln Arg Trp Glu
                165                 170                 175

Thr Pro Leu Ile Leu Gln Asn His Glu Gln Ile Gln Ser Pro Trp Ser
            180                 185                 190

Gln Met Leu Phe Gly Gln Phe Ala Asn Ile Asp Gln Ala Arg Trp Val
        195                 200                 205

Phe Thr Asn Ser Phe Tyr Lys Leu Glu Glu Glu Val Ile Glu Trp Thr
    210                 215                 220

Arg Lys Ile Trp Asn Leu Lys Val Ile Gly Pro Thr Leu Pro Ser Met
225                 230                 235                 240

Tyr Leu Asp Lys Arg Leu Asp Asp Asp Lys Asp Asn Gly Phe Asn Leu
                245                 250                 255
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```
Tyr Lys Ala Asn His His Glu Cys Met Asn Trp Leu Asp Asp Lys Pro
            260                 265                 270

Lys Glu Ser Val Val Tyr Val Ala Phe Gly Ser Leu Val Lys His Gly
        275                 280                 285

Pro Glu Gln Val Glu Glu Ile Thr Arg Ala Leu Ile Asp Ser Asp Val
    290                 295                 300

Asn Phe Leu Trp Val Ile Lys His Lys Glu Glu Gly Lys Leu Pro Glu
305                 310                 315                 320

Asn Leu Ser Glu Val Ile Lys Thr Gly Lys Gly Leu Ile Val Ala Trp
                325                 330                 335

Cys Lys Gln Leu Asp Val Leu Ala His Glu Ser Val Gly Cys Phe Val
            340                 345                 350

Thr His Cys Gly Phe Asn Ser Thr Leu Glu Ala Ile Ser Leu Gly Val
        355                 360                 365

Pro Val Val Ala Met Pro Gln Phe Ser Asp Gln Thr Thr Asn Ala Lys
    370                 375                 380

Leu Leu Asp Glu Ile Leu Gly Val Gly Val Arg Val Lys Ala Asp Glu
385                 390                 395                 400

Asn Gly Ile Val Arg Arg Gly Asn Leu Ala Ser Cys Ile Lys Met Ile
                405                 410                 415

Met Glu Glu Glu Arg Gly Val Ile Ile Arg Lys Asn Ala Val Lys Trp
            420                 425                 430

Lys Asp Leu Ala Lys Val Ala Val His Glu Gly Gly Ser Ser Asp Asn
        435                 440                 445

Asp Ile Val Glu Phe Val Ser Glu Leu Ile Lys Ala
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450 455 460

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<211> 1586
<212> DNA
<213> Stevia rebaudiana

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caaagccaca ttaaagccat gctcaaacta gcacaacttc tccaccacaa aggactccag 120

ataaccttcg tcaacaccga cttcatccac aaccagtttc ttgaatcatc gggcccacat 180

tgtctagacg gtgcaccggg tttccggttc gaaaccattc cggatggtgt ttctcacagt 240

ccggaagcga gcatcccaat cagagaatca ctcttgagat ccattgaaac caacttcttg 300

gatcgtttca ttgatcttgt aaccaaactt ccggatcctc cgacttgtat tatctcagat 360

gggttcttgt cggttttcac aattgacgct gcaaaaaagc ttggaattcc ggtcatgatg 420

tattggacac ttgctgcctg tgggttcatg ggtttttacc atattcattc tctcattgag 480

aaaggatttg caccacttaa agatgcaagt tacttgacaa atgggtattt ggacaccgtc 540

attgattggg ttccgggaat ggaaggcatc cgtctcaagg atttcccgct ggactggagc 600

actgacctca atgacaaagt tttgatgttc actacggaag ctcctcaaag gtcacacaag 660

gtttcacatc atattttcca cacgttcgat gagttggagc ctagtattat aaaaactttg 720

tcattgaggt ataatcacat ttacaccatc ggcccactgc aattacttct tgatcaaata 780

cccgaagaga aaaagcaaac tggaattacg agtctccatg gatacagttt agtaaaagaa 840

gaaccagagt gtttccagtg gcttcagtct aaagaaccaa attccgtcgt ttatgtaaat 900

tttggaagta ctacagtaat gtctttagaa gacatgacgg aatttggttg gggacttgct 960

aatagcaacc attatttcct ttggatcatc cgatcaaact tggtgatagg ggaaaatgca 1020

gttttgcccc ctgaacttga ggaacatata aagaaaagag gctttattgc tagctggtgt 1080

tcacaagaaa aggtcttgaa gcacccttcg gttggagggt tcttgactca ttgtgggtgg 1140

ggatcgacca tcgagagctt gtctgctggg gtgccaatga tatgctggcc ttattcgtgg 1200

gaccagctga ccaactgtag gtatatatgc aaagaatggg aggttgggct cgagatggga 1260

accaaagtga aacgagatga agtcaagagg cttgtacaag agttgatggg agaaggaggt 1320

cacaaaatga ggaacaaggc taaagattgg aaagaaaagg ctcgcattgc aatagctcct 1380

aacggttcat cttctttgaa catagacaaa atggtcaagg aaatcaccgt gctagcaaga 1440

aactagttac aaagttgttt cacattgtgc tttctattta agatgtaact ttgttctaat 1500

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tgaaataatg gtcattaggg gtgagt 1586

<210> 6
<211> 1446
<212> DNA
<213> Artificial Sequence

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ataactttcg tgaataccga cttcatccat aatcaatttc tggaatctag tggccctcat 180

tgtttggacg gagccccagg gtttagattc gaaacaattc ctgacggtgt ttcacattcc 240

ccagaggcct ccatcccaat aagagagagt ttactgaggt caatagaaac caacttttg 300

gatcgtttca ttgacttggt cacaaaactt ccagacccac caacttgcat aatctctgat 360

ggctttctgt cagtgtttac tatcgacgct gccaaaaagt tgggtatccc agttatgatg 420

tactggactc ttgctgcatg cggtttcatg ggtttctatc acatccattc tcttatcgaa 480

aagggttttg ctccactgaa agatgcatca tacttaacca acggctacct ggatactgtt 540

attgactggg taccaggtat ggaaggtata agacttaaag attttccttt ggattggtct 600

acagacctta atgataaagt attgatgttt actacagaag ctccacaaag atctcataag 660

gtttcacatc atatctttca cacctttgat gaattggaac catcaatcat caaaaccttg 720

tctctaagat acaatcatat ctacactatt ggtccattac aattacttct agatcaaatt 780

cctgaagaga aaaagcaaac tggtattaca tccttacacg gctactcttt agtgaaagag 840

gaaccagaat gttttcaatg gctacaaagt aaagagccta attctgtggt ctacgtcaac 900

ttcggaagta caacagtcat gtccttggaa gatatgactg aatttggttg gggccttgct 960

aattcaaatc attactttct atggattatc aggtccaatt tggtaatagg ggaaaacgcc 1020

gtattacctc cagaattgga ggaacacatc aaaaagagag gtttcattgc ttcctggtgt 1080

tctcaggaaa aggtattgaa acatccttct gttggtggtt tccttactca ttgcggttgg 1140

ggctctacaa tcgaatcact aagtgcagga gttccaatga tttgttggcc atattcatgg 1200

gaccaactta caaattgtag gtatatctgt aaagagtggg aagttggatt agaaatggga 1260

acaaaggtta aacgtgatga agtgaaaaga ttggttcagg agttgatggg ggaaggtggc 1320

cacaagatga gaaacaaggc caaagattgg aaggaaaaag ccagaattgc tattgctcct 1380

aacgggtcat cctctctaaa cattgataag atggtcaaag agattacagt cttagccaga 1440

aactaa 1446

<210> 7
<211> 481
<212> PRT
<213> Stevia rebaudiana

<400> 7

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1 5 10 15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
20 25 30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
35 40 45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
50 55 60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65 70 75 80

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Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
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        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480
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Asn

<210> 8
<211> 1377
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized UGT76G1

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ttttctatta caatctttca caccaatttc aacaaaccaa aaacatccaa ttacccacat 180

ttcacattca gattcatact tgataatgat ccacaagatg aacgtatttc aaacttacct 240

acccacggtc ctttagctgg aatgagaatt ccaatcatca atgaacatgg tgccgatgag 300

cttagaagag aattagagtt acttatgttg gcatccgaag aggacgagga agtctcttgt 360

ctgattactg acgctctatg gtactttgcc caatctgtgg ctgatagttt gaatttgagg 420

agattggtac taatgacatc cagtctgttt aactttcacg ctcatgttag tttaccacaa 480

tttgacgaat tgggatactt ggaccctgat gacaagacta ggttagagga acaggcctct 540

ggttttccta tgttgaaagt caaagatatc aagtctgcct attctaattg gcaaatcttg 600

aaagagatct taggaaagat gatcaaacag acaaaggctt catctggagt gatttggaac 660

agtttcaaag agttagaaga gtctgaattg gagactgtaa tcagagaaat tccagcacct 720

tcattcctga taccattacc aaaacatttg actgcttcct cttcctcttt gttggatcat 780

gacagaacag tttttcaatg gttggaccaa caaccaccta gttctgtttt gtacgtgtca 840

tttggtagta cttctgaagt cgatgaaaag gacttccttg aaatcgcaag aggcttagtc 900

gatagtaagc agtcattcct ttgggtcgtg cgtccaggtt tcgtgaaagg ctcaacatgg 960

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caacaggaag ttttagctca tggcgctatt ggggcattct ggactcattc cggatggaat 1080

tcaactttag aatcagtatg cgaaggggta cctatgatct tttcagattt tggtcttgat 1140

caaccactga acgcaagata catgtctgat gttttgaaag tgggtgtata tctagaaaat 1200

ggctgggaaa ggggtgaaat agctaatgca ataagacgtg ttatggttga tgaagagggg 1260

gagtatatca gacaaaacgc aagagtgctg aagcaaaagg ccgacgtttc tctaatgaag 1320

ggaggctctt catacgaatc cttagaatct cttgtttcct acatttcatc actgtaa 1377

<210> 9
<211> 458
<212> PRT
<213> Stevia rebaudiana

<400> 9

Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Arg Ile Ile
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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

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

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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 Lys 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
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<210> 10
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized UGT91D2e

<400> 10
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tggcttgctt tcggtcatat actgccttac ctacaactat caaaactgat agctgaaaaa 120

ggacataaag tgtcattcct ttcaacaact agaaacattc aaagattatc ttcccacata 180

tcaccattga ttaacgtcgt tcaattgaca cttccaagag tacaggaatt accagaagat 240

gctgaagcta caacagatgt gcatcctgaa gatatccctt acttgaaaaa ggcatccgat 300

ggattacagc ctgaggtcac tagattcctt gagcaacaca gtccagattg gatcatatac 360

gactacactc actattggtt gccttcaatt gcagcatcac taggcatttc tagggcacat 420

ttcagtgtaa ccacaccttg ggccattgct tacatgggtc catccgctga tgctatgatt 480

aacggcagtg atggtagaac taccgttgaa gatttgacaa ccccaccaaa gtggtttcca 540

tttccaacta aagtctgttg gagaaaacac gacttagcaa gactggttcc atacaaggca 600

ccaggaatct cagacggcta tagaatgggt ttagtcctta aagggtctga ctgcctattg 660

tctaagtgtt accatgagtt tgggacacaa tggctaccac ttttggaaac attacaccaa 720

gttcctgtcg taccagttgg tctattacct ccagaaatcc ctggtgatga gaaggacgag 780

acttgggttt caatcaaaaa gtggttagac gggaagcaaa aaggctcagt ggtatatgtg 840

gcactgggtt ccgaagtttt agtatctcaa acagaagttg tggaacttgc cttaggtttg 900

gaactatctg gattgccatt tgtctgggcc tacagaaaac caaaaggccc tgcaaagtcc 960

gattcagttg aattgccaga cggctttgtc gagagaacta gagatagagg gttggtatgg 1020

acttcatggg ctccacaatt gagaatcctg agtcacgaat ctgtgtgcgg tttcctaaca 1080

cattgtggtt ctggttctat agttgaagga ctgatgtttg gtcatccact tatcatgttg 1140

ccaatctttg gtgaccagcc tttgaatgca cgtctgttag aagataaaca agttggaatt 1200

gaaatcccac gtaatgagga agatggatgt ttaaccaagg agtctgtggc cagatcatta 1260

cgttccgttg tcgttgaaaa ggaaggcgaa atctacaagg ccaatgcccg tgaactttca 1320

aagatctaca atgacacaaa agtagagaag gaatatgttt ctcaatttgt agattaccta 1380

gagaaaaacg ctagagccgt agctattgat catgaatcct aa 1422

<210> 11
<211> 473
<212> PRT
<213> Stevia rebaudiana

<400> 11

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val

```
1               5                   10                  15

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30

Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110

His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205
```

```
Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
```

405 410 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
420 425 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
435 440 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
450 455 460

Arg Ala Val Ala Ile Asp His Glu Ser
465 470

<210> 12
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized UGT91D2e-b

<400> 12
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tggttggctt tcggtcatat tttgccatac ttgcaattgt ccaagttgat tgctgaaaag 120

ggtcacaagg tttcattctt gtctaccacc agaaacatcc aaagattgtc ctctcatatc 180

tccccattga tcaacgttgt tcaattgact ttgccaagag tccaagaatt gccagaagat 240

gctgaagcta ctactgatgt tcatccagaa gatatccctt acttgaaaaa ggcttccgat 300

ggtttacaac cagaagttac tagattcttg gaacaacatt ccccagattg gatcatctac 360

gattatactc attactggtt gccatccatt gctgcttcat tgggtatttc tagagcccat 420

ttctctgtta ctactccatg ggctattgct tatatgggtc catctgctga tgctatgatt 480

aacggttctg atggtagaac taccgttgaa gatttgacta ctccaccaaa gtggtttcca 540

tttccaacaa aagtctgttg gagaaaacac gatttggcta gattggttcc atacaaagct 600

ccaggtattt ctgatggtta cagaatgggt atggttttga aaggttccga ttgcttgttg 660

tctaagtgct atcatgaatt cggtactcaa tggttgcctt tgttggaaac attgcatcaa 720

gttccagttg ttccagtagg tttgttgcca ccagaaattc caggtgacga aaaagacgaa 780

acttgggttt ccatcaaaaa gtggttggat ggtaagcaaa agggttctgt tgtttatgtt 840

gctttgggtt ccgaagcttt ggtttctcaa accgaagttg ttgaattggc tttgggtttg 900

gaattgtctg gtttgccatt tgtttgggct tacagaaaac ctaaaggtcc agctaagtct 960

gattctgttg aattgccaga tggtttcgtt gaaagaacta gagatagagg tttggtttgg 1020

acttcttggg ctccacaatt gagaattttg tctcatgaat ccgtctgtgg tttcttgact 1080

cattgtggtt ctggttctat cgttgaaggt ttgatgtttg gtcacccatt gattatgttg 1140

ccaatctttg gtgaccaacc attgaacgct agattattgg aagataagca agtcggtatc 1200

gaaatcccaa gaaatgaaga agatggttgc ttgaccaaag aatctgttgc tagatctttg 1260

agatccgttg tcgttgaaaa agaaggtgaa atctacaagg ctaacgctag agaattgtcc 1320

aagatctaca acgataccaa ggtcgaaaaa gaatacgttt cccaattcgt tgactacttg 1380

gaaaagaatg ctagagctgt tgccattgat catgaatctt ga 1422

<210> 13
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e-b

<400> 13

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1 5 10 15

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
20 25 30

Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
35 40 45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile

```
    50                  55                  60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110

His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Met Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255
```

```
Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Ala Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
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450 455 460

Arg Ala Val Ala Ile Asp His Glu Ser
465 470

<210> 14
<211> 1389
<212> DNA
<213> Oryza sativa

<400> 14
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ccgtggctcg ccttcggcca cctgctcccg tgcctcgacc tcgcccagcg cctcgcgtcg 120

cggggccacc gcgtgtcgtt cgtctccacg ccgcggaaca tatcccgcct cccgccggtg 180

cgccccgcgc tcgcgccgct cgtcgccttc gtggcgctgc cgctcccgcg cgtcgagggg 240

ctccccgacg gcgccgagtc caccaacgac gtcccccacg acaggccgga catggtcgag 300

ctccaccgga gggccttcga cgggctcgcc gcgcccttct cggagttctt gggcaccgcg 360

tgcgccgact gggtcatcgt cgacgtcttc caccactggg ccgcagccgc cgctctcgag 420

cacaaggtgc catgtgcaat gatgttgttg ggctctgcac atatgatcgc ttccatagca 480

gacagacggc tcgagcgcgc ggagacagag tcgcctgcgg ctgccgggca gggacgccca 540

gcggcggcgc caacgttcga ggtggcgagg atgaagttga tacgaaccaa aggctcatcg 600

ggaatgtccc tcgccgagcg cttctccttg acgctctcga ggagcagcct cgtcgtcggg 660

cggagctgcg tggagttcga gccggagacc gtcccgctcc tgtcgacgct ccgcggtaag 720

cctattacct tccttggcct tatgccgccg ttgcatgaag gccgccgcga ggacggcgag 780

gatgccaccg tccgctggct cgacgcgcag ccggccaagt ccgtcgtgta cgtcgcgcta 840

ggcagcgagg tgccactggg agtggagaag gtccacgagc tcgcgctcgg gctggagctc 900

gccgggacgc gcttcctctg ggctcttagg aagcccactg gcgtctccga cgccgacctc 960

ctccccgccg gcttcgagga gcgcacgcgc ggccgcggcg tcgtggcgac gagatgggtt 1020

cctcagatga gcatactggc gcacgccgcc gtgggcgcgt tcctgaccca ctgcggctgg 1080

aactcgacca tcgaggggct catgttcggc cacccgctta tcatgctgcc gatcttcggc 1140

gaccagggac cgaacgcgcg gctaatcgag gcgaagaacg ccggattgca ggtggcaaga 1200

aacgacggcg atggatcgtt cgaccgagaa ggcgtcgcgg cggcgattcg tgcagtcgcg 1260

gtggaggaag aaagcagcaa agtgtttcaa gccaaagcca agaagctgca ggagatcgtc 1320

gcggacatgg cctgccatga gaggtacatc gacggattca ttcagcaatt gagatcttac 1380

aaggattga 1389

<210> 15
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized EUGT11

<400> 15
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ccttggttgg cctttggtca cctgttacca tgtctggatt tagcccaaag actggcctca 120

agaggccata gagtatcatt tgtgtctact cctagaaata tctctcgttt accaccagtc 180

agacctgctc tagctcctct agttgcattc gttgctcttc cacttccaag agtagaagga 240

ttgccagacg gcgctgaatc tactaatgac gtaccacatg atagacctga catggtcgaa 300

ttgcatagaa gagcctttga tggattggca gctccatttt ctgagttcct gggcacagca 360

tgtgcagact gggttatagt cgatgtattt catcactggg ctgctgcagc cgcattggaa 420

cataaggtgc cttgtgctat gatgttgtta gggtcagcac acatgatcgc atccatagct 480

gatagaagat tggaaagagc tgaaacagaa tccccagccg cagcaggaca aggtaggcca 540

gctgccgccc caacctttga agtggctaga atgaaattga ttcgtactaa aggtagttca 600

gggatgagtc ttgctgaaag gttttctctg acattatcta gatcatcatt agttgtaggt 660

agatcctgcg tcgagttcga acctgaaaca gtacctttac tatctacttt gagaggcaaa 720

cctattactt tccttggtct aatgcctcca ttacatgaag gaaggagaga agatggtgaa 780

gatgctactg ttaggtggtt agatgcccaa cctgctaagt ctgttgttta cgttgcattg 840

ggttctgagg taccactagg ggtggaaaag gtgcatgaat tagcattagg acttgagctg 900

gccggaacaa gattcctttg ggctttgaga aaaccaaccg gtgtttctga cgccgacttg 960

ctaccagctg ggttcgaaga gagaacaaga ggccgtggtg tcgttgctac tagatgggtc 1020

ccacaaatga gtattctagc tcatgcagct gtaggggcct ttctaaccca ttgcggttgg 1080

aactcaacaa tagaaggact gatgtttggt catccactta ttatgttacc aatctttggc 1140

gatcagggac ctaacgcaag attgattgag gcaaagaacg caggtctgca ggttgcacgt 1200

aatgatggtg atggttcctt tgatagagaa ggcgttgcag ctgccatcag agcagtcgcc 1260

gttgaggaag agtcatctaa agttttccaa gctaaggcca aaaaattaca agagattgtg 1320

gctgacatgg cttgtcacga aagatacatc gatggtttca tccaacaatt gagaagttat 1380

aaagactaa 1389

<210> 16
<211> 462
<212> PRT
<213> Oryza sativa

<400> 16

Met Asp Ser Gly Tyr Ser Ser Ser Tyr Ala Ala Ala Ala Gly Met His
1 5 10 15

Val Val Ile Cys Pro Trp Leu Ala Phe Gly His Leu Leu Pro Cys Leu
20 25 30

Asp Leu Ala Gln Arg Leu Ala Ser Arg Gly His Arg Val Ser Phe Val
35 40 45

Ser Thr Pro Arg Asn Ile Ser Arg Leu Pro Pro Val Arg Pro Ala Leu
50 55 60

Ala Pro Leu Val Ala Phe Val Ala Leu Pro Leu Pro Arg Val Glu Gly
65 70 75 80

Leu Pro Asp Gly Ala Glu Ser Thr Asn Asp Val Pro His Asp Arg Pro
85 90 95

```
Asp Met Val Glu Leu His Arg Arg Ala Phe Asp Gly Leu Ala Ala Pro
            100                 105                 110

Phe Ser Glu Phe Leu Gly Thr Ala Cys Ala Asp Trp Val Ile Val Asp
        115                 120                 125

Val Phe His His Trp Ala Ala Ala Ala Ala Leu Glu His Lys Val Pro
    130                 135                 140

Cys Ala Met Met Leu Leu Gly Ser Ala His Met Ile Ala Ser Ile Ala
145                 150                 155                 160

Asp Arg Arg Leu Glu Arg Ala Glu Thr Glu Ser Pro Ala Ala Ala Gly
                165                 170                 175

Gln Gly Arg Pro Ala Ala Ala Pro Thr Phe Glu Val Ala Arg Met Lys
            180                 185                 190

Leu Ile Arg Thr Lys Gly Ser Ser Gly Met Ser Leu Ala Glu Arg Phe
        195                 200                 205

Ser Leu Thr Leu Ser Arg Ser Ser Leu Val Val Gly Arg Ser Cys Val
    210                 215                 220

Glu Phe Glu Pro Glu Thr Val Pro Leu Leu Ser Thr Leu Arg Gly Lys
225                 230                 235                 240

Pro Ile Thr Phe Leu Gly Leu Met Pro Pro Leu His Glu Gly Arg Arg
                245                 250                 255

Glu Asp Gly Glu Asp Ala Thr Val Arg Trp Leu Asp Ala Gln Pro Ala
            260                 265                 270

Lys Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Pro Leu Gly Val
        275                 280                 285

Glu Lys Val His Glu Leu Ala Leu Gly Leu Glu Leu Ala Gly Thr Arg
```

```
    290                 295                 300

Phe Leu Trp Ala Leu Arg Lys Pro Thr Gly Val Ser Asp Ala Asp Leu
305                 310                 315                 320

Leu Pro Ala Gly Phe Glu Glu Arg Thr Arg Gly Arg Gly Val Val Ala
                325                 330                 335

Thr Arg Trp Val Pro Gln Met Ser Ile Leu Ala His Ala Ala Val Gly
            340                 345                 350

Ala Phe Leu Thr His Cys Gly Trp Asn Ser Thr Ile Glu Gly Leu Met
        355                 360                 365

Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly Asp Gln Gly Pro
    370                 375                 380

Asn Ala Arg Leu Ile Glu Ala Lys Asn Ala Gly Leu Gln Val Ala Arg
385                 390                 395                 400

Asn Asp Gly Asp Gly Ser Phe Asp Arg Glu Gly Val Ala Ala Ala Ile
                405                 410                 415

Arg Ala Val Ala Val Glu Glu Glu Ser Ser Lys Val Phe Gln Ala Lys
            420                 425                 430

Ala Lys Lys Leu Gln Glu Ile Val Ala Asp Met Ala Cys His Glu Arg
        435                 440                 445

Tyr Ile Asp Gly Phe Ile Gln Gln Leu Arg Ser Tyr Lys Asp
    450                 455                 460
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<210> 17
<211> 465
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e-b-EUGT11 chimera 3

<400> 17

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Met Asp Ser Gly Tyr Ser Ser Ser Tyr Ala Ala Ala Ala Gly Met His
1               5                  10                  15

Val Val Ile Cys Pro Trp Leu Ala Phe Gly His Leu Leu Pro Cys Leu
            20                  25                  30

Asp Leu Ala Gln Arg Leu Ala Ser Arg Gly His Arg Val Ser Phe Val
        35                  40                  45

Ser Thr Pro Arg Asn Ile Ser Arg Leu Pro Pro Val Arg Pro Ala Leu
    50                  55                  60

Ala Pro Leu Val Ala Phe Val Ala Leu Pro Leu Pro Arg Val Glu Gly
65                  70                  75                  80

Leu Pro Asp Gly Ala Glu Ser Thr Asn Asp Val Pro His Asp Arg Pro
                85                  90                  95

Asp Met Val Glu Leu His Arg Arg Ala Phe Asp Gly Leu Ala Ala Pro
            100                 105                 110

Phe Ser Glu Phe Leu Gly Thr Ala Cys Ala Asp Trp Val Ile Val Asp
        115                 120                 125

Val Phe His His Trp Ala Ala Ala Ala Ala Leu Glu His Lys Val Pro
    130                 135                 140

Cys Ala Met Met Leu Leu Gly Ser Ala His Met Ile Ala Ser Ile Ala
145                 150                 155                 160

Asp Arg Arg Leu Glu Arg Ala Glu Thr Glu Ser Pro Ala Ala Ala Gly
                165                 170                 175

Gln Gly Arg Pro Ala Ala Ala Pro Thr Phe Glu Val Ala Arg Met Lys
            180                 185                 190
```

```
Leu Ile Arg Thr Lys Gly Ser Ser Gly Met Ser Leu Ala Glu Arg Phe
        195                 200                 205

Ser Leu Thr Leu Ser Arg Ser Ser Leu Val Val Gly Arg Ser Cys Val
    210                 215                 220

Glu Phe Glu Pro Glu Thr Val Pro Leu Leu Ser Thr Leu Arg Gly Lys
225                 230                 235                 240

Pro Ile Thr Phe Leu Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp Glu
                245                 250                 255

Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys Gln
            260                 265                 270

Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Ala Leu Val Ser
        275                 280                 285

Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly Leu
    290                 295                 300

Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser Asp
305                 310                 315                 320

Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg Gly
                325                 330                 335

Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His Glu
            340                 345                 350

Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val Glu
        355                 360                 365

Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly Asp
    370                 375                 380

Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile Glu
```

385 390 395 400

Ile Ala Arg Asn Asp Gly Asp Gly Ser Phe Asp Arg Glu Gly Val Ala
405 410 415

Ala Ala Ile Arg Ala Val Ala Val Glu Glu Glu Ser Ser Lys Val Phe
420 425 430

Gln Ala Lys Ala Lys Lys Leu Gln Glu Ile Val Ala Asp Met Ala Cys
435 440 445

His Glu Arg Tyr Ile Asp Gly Phe Ile Gln Gln Leu Arg Ser Tyr Lys
450 455 460

Asp
465

<210> 18
<211> 470
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e-b-EUGT11 chimera 7

<400> 18

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1 5 10 15

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
20 25 30

Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
35 40 45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
50 55 60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp

```
65                  70                  75                  80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110

His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Met Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Met Pro Pro Leu His Glu Gly Arg
                245                 250                 255

Arg Glu Asp Gly Glu Asp Ala Thr Val Arg Trp Leu Asp Ala Gln Pro
            260                 265                 270
```

```
Ala Lys Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Pro Leu Gly
        275                 280                 285

Val Glu Lys Val His Glu Leu Ala Leu Gly Leu Glu Leu Ala Gly Thr
    290                 295                 300

Arg Phe Leu Trp Ala Leu Arg Lys Pro Thr Gly Val Ser Asp Ala Asp
305                 310                 315                 320

Leu Leu Pro Ala Gly Phe Glu Glu Arg Thr Arg Gly Arg Gly Val Val
                325                 330                 335

Ala Thr Arg Trp Val Pro Gln Met Ser Ile Leu Ala His Ala Ala Val
            340                 345                 350

Gly Ala Phe Leu Thr His Cys Gly Trp Asn Ser Thr Ile Glu Gly Leu
        355                 360                 365

Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly Asp Gln Gly
    370                 375                 380

Pro Asn Ala Arg Leu Ile Glu Ala Lys Asn Ala Gly Leu Gln Val Pro
385                 390                 395                 400

Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val Ala Arg Ser
                405                 410                 415

Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr Lys Ala Asn
            420                 425                 430

Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val Glu Lys Glu
        435                 440                 445

Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala Arg Ala Val
    450                 455                 460

Ala Ile Asp His Glu Ser
```

465 470

<210> 19
<211> 1086
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized GGPPS

<400> 19
atggctttgg taaacccaac cgctcttttc tatggtacct ctatcagaac aagacctaca 60

aacttactaa atccaactca aaagctaaga ccagtttcat catcttcctt accttctttc 120

tcatcagtta gtgcgattct tactgaaaaa catcaatcta atccttctga gaacaacaat 180

ttgcaaactc atctagaaac tcctttcaac tttgatagtt atatgttgga aaaagtcaac 240

atggttaacg aggcgcttga tgcatctgtc ccactaaaag acccaatcaa aatccatgaa 300

tccatgagat actctttatt ggcaggcggt aagagaatca gaccaatgat gtgtattgca 360

gcctgcgaaa tagtcggagg taatatcctt aacgccatgc cagccgcatg tgccgtggaa 420

atgattcata ctatgtcttt ggtgcatgac gatcttccat gtatggataa tgatgacttc 480

agaagaggta aacctatttc acacaaggtc tacggggagg aaatggcagt attgaccggc 540

gatgctttac taagtttatc tttcgaacat atagctactg ctacaaaggg tgtatcaaag 600

gatagaatcg tcagagctat aggggagttg gcccgttcag ttggctccga aggtttagtg 660

gctggacaag ttgtagatat cttgtcagag ggtgctgatg ttggattaga tcacctagaa 720

tacattcaca tccacaaaac agcaatgttg cttgagtcct cagtagttat tggcgctatc 780

atgggaggag gatctgatca gcagatcgaa aagttgagaa aattcgctag atctattggt 840

ctactattcc aagttgtgga tgacattttg gatgttacaa aatctaccga agagttgggg 900

aaaacagctg gtaaggattt gttgacagat aagacaactt acccaaagtt gttaggtata 960

gaaaagtcca gagaatttgc cgaaaaactt aacaaggaag cacaagagca attaagtggc 1020

tttgatagac gtaaggcagc tcctttgatc gcgttagcca actacaatgc gtaccgtcaa 1080

aattga 1086

<210> 20
<211> 361
<212> PRT
<213> Stevia rebaudiana

<400> 20

```
Met Ala Leu Val Asn Pro Thr Ala Leu Phe Tyr Gly Thr Ser Ile Arg
1               5                   10                  15


Thr Arg Pro Thr Asn Leu Leu Asn Pro Thr Gln Lys Leu Arg Pro Val
            20                  25                  30


Ser Ser Ser Ser Leu Pro Ser Phe Ser Ser Val Ser Ala Ile Leu Thr
        35                  40                  45


Glu Lys His Gln Ser Asn Pro Ser Glu Asn Asn Asn Leu Gln Thr His
    50                  55                  60


Leu Glu Thr Pro Phe Asn Phe Asp Ser Tyr Met Leu Glu Lys Val Asn
65                  70                  75                  80


Met Val Asn Glu Ala Leu Asp Ala Ser Val Pro Leu Lys Asp Pro Ile
                85                  90                  95


Lys Ile His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg
            100                 105                 110


Ile Arg Pro Met Met Cys Ile Ala Ala Cys Glu Ile Val Gly Gly Asn
        115                 120                 125


Ile Leu Asn Ala Met Pro Ala Ala Cys Ala Val Glu Met Ile His Thr
    130                 135                 140


Met Ser Leu Val His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe
145                 150                 155                 160


Arg Arg Gly Lys Pro Ile Ser His Lys Val Tyr Gly Glu Glu Met Ala
                165                 170                 175
```

```
Val Leu Thr Gly Asp Ala Leu Leu Ser Leu Ser Phe Glu His Ile Ala
            180                 185                 190

Thr Ala Thr Lys Gly Val Ser Lys Asp Arg Ile Val Arg Ala Ile Gly
        195                 200                 205

Glu Leu Ala Arg Ser Val Gly Ser Glu Gly Leu Val Ala Gly Gln Val
    210                 215                 220

Val Asp Ile Leu Ser Glu Gly Ala Asp Val Gly Leu Asp His Leu Glu
225                 230                 235                 240

Tyr Ile His Ile His Lys Thr Ala Met Leu Leu Glu Ser Ser Val Val
                245                 250                 255

Ile Gly Ala Ile Met Gly Gly Gly Ser Asp Gln Gln Ile Glu Lys Leu
            260                 265                 270

Arg Lys Phe Ala Arg Ser Ile Gly Leu Leu Phe Gln Val Val Asp Asp
        275                 280                 285

Ile Leu Asp Val Thr Lys Ser Thr Glu Glu Leu Gly Lys Thr Ala Gly
    290                 295                 300

Lys Asp Leu Leu Thr Asp Lys Thr Thr Tyr Pro Lys Leu Leu Gly Ile
305                 310                 315                 320

Glu Lys Ser Arg Glu Phe Ala Glu Lys Leu Asn Lys Glu Ala Gln Glu
                325                 330                 335

Gln Leu Ser Gly Phe Asp Arg Arg Lys Ala Ala Pro Leu Ile Ala Leu
            340                 345                 350

Ala Asn Tyr Asn Ala Tyr Arg Gln Asn
        355                 360
```

<210> 21
<211> 1029
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized GGPPS

<400> 21
atggctgagc aacaaatatc taacttgctg tctatgtttg atgcttcaca tgctagtcag 60

aaattagaaa ttactgtcca aatgatggac acataccatt acagagaaac gcctccagat 120

tcctcatctt ctgaaggcgg ttcattgtct agatacgacg agagaagagt ctctttgcct 180

ctcagtcata atgctgcctc tccagatatt gtatcacaac tatgtttttc cactgcaatg 240

tcttcagagt tgaatcacag atggaaatct caaagattaa aggtggccga ttctccttac 300

aactatatcc taacattacc atcaaaagga attagaggtg cctttatcga ttccctgaac 360

gtatggttgg aggttccaga ggatgaaaca tcagtcatca aggaagttat tggtatgctc 420

cacaactctt cattaatcat tgatgacttc caagataatt ctccacttag aagaggaaag 480

ccatctaccc atacagtctt cggccctgcc caggctatca atactgctac ttacgttata 540

gttaaagcaa tcgaaaagat acaagacata gtgggacacg atgcattggc agatgttacg 600

ggtactatta caactatttt ccaaggtcag gccatggact tgtggtggac agcaaatgca 660

atcgttccat caatacagga atacttactt atggtaaacg ataaaaccgg tgctctcttt 720

agactgagtt tggagttgtt agctctgaat tccgaagcca gtatttctga ctctgcttta 780

gaaagtttat ctagtgctgt ttccttgcta ggtcaatact tccaaatcag agacgactat 840

atgaacttga tcgataacaa gtatacagat cagaaaggct tctgcgaaga tcttgatgaa 900

ggcaagtact cactaacact tattcatgcc ctccaaactg attcatccga tctactgacc 960

aacatccttt caatgagaag agtgcaagga aagttaacgg cacaaaagag atgttggttc 1020

tggaaatga 1029

<210> 22
<211> 342
<212> PRT
<213> Gibberella fujikuroi

<400> 22

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Met Ala Glu Gln Gln Ile Ser Asn Leu Leu Ser Met Phe Asp Ala Ser
1               5                  10                  15

His Ala Ser Gln Lys Leu Glu Ile Thr Val Gln Met Met Asp Thr Tyr
            20                  25                  30

His Tyr Arg Glu Thr Pro Pro Asp Ser Ser Ser Ser Glu Gly Gly Ser
        35                  40                  45

Leu Ser Arg Tyr Asp Glu Arg Arg Val Ser Leu Pro Leu Ser His Asn
    50                  55                  60

Ala Ala Ser Pro Asp Ile Val Ser Gln Leu Cys Phe Ser Thr Ala Met
65                  70                  75                  80

Ser Ser Glu Leu Asn His Arg Trp Lys Ser Gln Arg Leu Lys Val Ala
                85                  90                  95

Asp Ser Pro Tyr Asn Tyr Ile Leu Thr Leu Pro Ser Lys Gly Ile Arg
            100                 105                 110

Gly Ala Phe Ile Asp Ser Leu Asn Val Trp Leu Glu Val Pro Glu Asp
        115                 120                 125

Glu Thr Ser Val Ile Lys Glu Val Ile Gly Met Leu His Asn Ser Ser
    130                 135                 140

Leu Ile Ile Asp Asp Phe Gln Asp Asn Ser Pro Leu Arg Arg Gly Lys
145                 150                 155                 160

Pro Ser Thr His Thr Val Phe Gly Pro Ala Gln Ala Ile Asn Thr Ala
                165                 170                 175

Thr Tyr Val Ile Val Lys Ala Ile Glu Lys Ile Gln Asp Ile Val Gly
            180                 185                 190
```

```
His Asp Ala Leu Ala Asp Val Thr Gly Thr Ile Thr Thr Ile Phe Gln
        195                 200                 205


Gly Gln Ala Met Asp Leu Trp Trp Thr Ala Asn Ala Ile Val Pro Ser
    210                 215                 220


Ile Gln Glu Tyr Leu Leu Met Val Asn Asp Lys Thr Gly Ala Leu Phe
225                 230                 235                 240


Arg Leu Ser Leu Glu Leu Leu Ala Leu Asn Ser Glu Ala Ser Ile Ser
                245                 250                 255


Asp Ser Ala Leu Glu Ser Leu Ser Ser Ala Val Ser Leu Leu Gly Gln
            260                 265                 270


Tyr Phe Gln Ile Arg Asp Asp Tyr Met Asn Leu Ile Asp Asn Lys Tyr
        275                 280                 285


Thr Asp Gln Lys Gly Phe Cys Glu Asp Leu Asp Glu Gly Lys Tyr Ser
    290                 295                 300


Leu Thr Leu Ile His Ala Leu Gln Thr Asp Ser Ser Asp Leu Leu Thr
305                 310                 315                 320


Asn Ile Leu Ser Met Arg Arg Val Gln Gly Lys Leu Thr Ala Gln Lys
                325                 330                 335


Arg Cys Trp Phe Trp Lys
            340
```

<210> 23
<211> 903
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized GGPPS

<400> 23

atggaaaaga ctaaggagaa agcagaacgt atcttgctgg agccatacag atacttatta 60

caactaccag gaaagcaagt ccgttctaaa ctatcacaag cgttcaatca ctggttaaaa 120

gttcctgaag ataagttaca aatcattatt gaagtcacag aaatgctaca caatgcttct 180

ttactgatcg atgatataga ggattcttcc aaactgagaa gaggttttcc tgtcgctcat 240

tccatatacg gggtaccaag tgtaatcaac tcagctaatt acgtctactt cttgggattg 300

gaaaaagtat tgacattaga tcatccagac gctgtaaagc tattcaccag acaacttctt 360

gaattgcatc aaggtcaagg tttggatatc tattggagag acacttatac ttgcccaaca 420

gaagaggagt acaaagcaat ggttctacaa aagactggcg gtttgttcgg acttgccgtt 480

ggtctgatgc aacttttctc tgattacaag gaggacttaa agcctctgtt ggataccttg 540

ggcttgtttt tccagattag agatgactac gctaacttac attcaaagga atattcagaa 600

aacaaatcat tctgtgaaga tttgactgaa gggaagttta gttttccaac aatccacgcc 660

atttggtcaa gaccagaatc tactcaagtg caaaacattc tgcgtcagag aacagagaat 720

attgacatca aaaagtattg tgttcagtac ttggaagatg ttggttcttt tgcttacaca 780

agacatacac ttagagaatt agaggcaaaa gcatacaagc aaatagaagc ctgtggaggc 840

aatccttctc tagtggcatt ggttaaacat ttgtccaaaa tgttcaccga ggaaaacaag 900

taa 903

<210> 24
<211> 300
<212> PRT
<213> Mus musculus

<400> 24

Met Glu Lys Thr Lys Glu Lys Ala Glu Arg Ile Leu Leu Glu Pro Tyr
1 5 10 15

Arg Tyr Leu Leu Gln Leu Pro Gly Lys Gln Val Arg Ser Lys Leu Ser
20 25 30

Gln Ala Phe Asn His Trp Leu Lys Val Pro Glu Asp Lys Leu Gln Ile
35 40 45

```
Ile Ile Glu Val Thr Glu Met Leu His Asn Ala Ser Leu Leu Ile Asp
    50                  55                  60

Asp Ile Glu Asp Ser Ser Lys Leu Arg Arg Gly Phe Pro Val Ala His
65                  70                  75                  80

Ser Ile Tyr Gly Val Pro Ser Val Ile Asn Ser Ala Asn Tyr Val Tyr
                85                  90                  95

Phe Leu Gly Leu Glu Lys Val Leu Thr Leu Asp His Pro Asp Ala Val
            100                 105                 110

Lys Leu Phe Thr Arg Gln Leu Leu Glu Leu His Gln Gly Gln Gly Leu
        115                 120                 125

Asp Ile Tyr Trp Arg Asp Thr Tyr Thr Cys Pro Thr Glu Glu Glu Tyr
    130                 135                 140

Lys Ala Met Val Leu Gln Lys Thr Gly Gly Leu Phe Gly Leu Ala Val
145                 150                 155                 160

Gly Leu Met Gln Leu Phe Ser Asp Tyr Lys Glu Asp Leu Lys Pro Leu
                165                 170                 175

Leu Asp Thr Leu Gly Leu Phe Phe Gln Ile Arg Asp Asp Tyr Ala Asn
            180                 185                 190

Leu His Ser Lys Glu Tyr Ser Glu Asn Lys Ser Phe Cys Glu Asp Leu
        195                 200                 205

Thr Glu Gly Lys Phe Ser Phe Pro Thr Ile His Ala Ile Trp Ser Arg
    210                 215                 220

Pro Glu Ser Thr Gln Val Gln Asn Ile Leu Arg Gln Arg Thr Glu Asn
225                 230                 235                 240
```

```
Ile Asp Ile Lys Lys Tyr Cys Val Gln Tyr Leu Glu Asp Val Gly Ser
                245                 250                 255

Phe Ala Tyr Thr Arg His Thr Leu Arg Glu Leu Glu Ala Lys Ala Tyr
            260                 265                 270

Lys Gln Ile Glu Ala Cys Gly Gly Asn Pro Ser Leu Val Ala Leu Val
        275                 280                 285

Lys His Leu Ser Lys Met Phe Thr Glu Glu Asn Lys
    290                 295                 300
```

<210> 25
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized GGPPS

<400> 25

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atggcaagat tctattttct taacgcacta ttgatggtta tctcattaca atcaactaca       60

gccttcactc cagctaaact tgcttatcca acaacaacaa cagctctaaa tgtcgcctcc      120

gccgaaactt ctttcagtct agatgaatac ttggcctcta agataggacc tatagagtct      180

gccttggaag catcagtcaa atccagaatt ccacagaccg ataagatctg cgaatctatg      240

gcctactctt tgatggcagg aggcaagaga attagaccag tgttgtgtat cgctgcatgt      300

gagatgttcg gtggatccca agatgtcgct atgcctactg ctgtggcatt agaaatgata      360

cacacaatgt ctttgattca tgatgatttg ccatccatgg ataacgatga cttgagaaga      420

ggtaaaccaa caaaccatgt cgttttcggc gaagatgtag ctattcttgc aggtgactct      480

ttattgtcaa cttccttcga gcacgtcgct agagaaacaa aaggagtgtc agcagaaaag      540

atcgtggatg ttatcgctag attaggcaaa tctgttggtg ccgagggcct tgctggcggt      600

caagttatgg acttagaatg tgaagctaaa ccaggtacca cattagacga cttgaaatgg      660

attcatatcc ataaaaccgc tacattgtta caagttgctg tagcttctgg tgcagttcta      720

ggtggtgcaa ctcctgaaga ggttgctgca tgcgagttgt ttgctatgaa tataggtctt      780
```

gcctttcaag ttgccgacga tatccttgat gtaaccgctt catcagaaga tttgggtaaa 840

actgcaggca aagatgaagc tactgataag acaacttacc caaagttatt aggattagaa 900

gagagtaagg catacgcaag acaactaatc gatgaagcca aggaaagttt ggctcctttt 960

ggagatagag ctgccccttt attggccatt gcagatttca ttattgatag aaagaattga 1020

<210> 26
<211> 339
<212> PRT
<213> Thalassiosira pseudonana

<400> 26

Met Ala Arg Phe Tyr Phe Leu Asn Ala Leu Leu Met Val Ile Ser Leu
1 5 10 15

Gln Ser Thr Thr Ala Phe Thr Pro Ala Lys Leu Ala Tyr Pro Thr Thr
20 25 30

Thr Thr Ala Leu Asn Val Ala Ser Ala Glu Thr Ser Phe Ser Leu Asp
35 40 45

Glu Tyr Leu Ala Ser Lys Ile Gly Pro Ile Glu Ser Ala Leu Glu Ala
50 55 60

Ser Val Lys Ser Arg Ile Pro Gln Thr Asp Lys Ile Cys Glu Ser Met
65 70 75 80

Ala Tyr Ser Leu Met Ala Gly Gly Lys Arg Ile Arg Pro Val Leu Cys
85 90 95

Ile Ala Ala Cys Glu Met Phe Gly Gly Ser Gln Asp Val Ala Met Pro
100 105 110

Thr Ala Val Ala Leu Glu Met Ile His Thr Met Ser Leu Ile His Asp
115 120 125

Asp Leu Pro Ser Met Asp Asn Asp Asp Leu Arg Arg Gly Lys Pro Thr

```
    130                 135                 140

Asn His Val Val Phe Gly Glu Asp Val Ala Ile Leu Ala Gly Asp Ser
145                 150                 155                 160

Leu Leu Ser Thr Ser Phe Glu His Val Ala Arg Glu Thr Lys Gly Val
                165                 170                 175

Ser Ala Glu Lys Ile Val Asp Val Ile Ala Arg Leu Gly Lys Ser Val
            180                 185                 190

Gly Ala Glu Gly Leu Ala Gly Gly Gln Val Met Asp Leu Glu Cys Glu
        195                 200                 205

Ala Lys Pro Gly Thr Thr Leu Asp Asp Leu Lys Trp Ile His Ile His
    210                 215                 220

Lys Thr Ala Thr Leu Leu Gln Val Ala Val Ala Ser Gly Ala Val Leu
225                 230                 235                 240

Gly Gly Ala Thr Pro Glu Glu Val Ala Ala Cys Glu Leu Phe Ala Met
                245                 250                 255

Asn Ile Gly Leu Ala Phe Gln Val Ala Asp Asp Ile Leu Asp Val Thr
            260                 265                 270

Ala Ser Ser Glu Asp Leu Gly Lys Thr Ala Gly Lys Asp Glu Ala Thr
        275                 280                 285

Asp Lys Thr Thr Tyr Pro Lys Leu Leu Gly Leu Glu Glu Ser Lys Ala
    290                 295                 300

Tyr Ala Arg Gln Leu Ile Asp Glu Ala Lys Glu Ser Leu Ala Pro Phe
305                 310                 315                 320

Gly Asp Arg Ala Ala Pro Leu Leu Ala Ile Ala Asp Phe Ile Ile Asp
                325                 330                 335
```

Arg Lys Asn

<210> 27
<211> 1068
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized GGPPS

<400> 27
atgcacttag caccacgtag agtccctaga ggtagaagat caccacctga cagagttcct 60

gaaagacaag gtgccttggg tagaagacgt ggagctggct ctactggctg tgcccgtgct 120

gctgctggtg ttcaccgtag aagaggagga ggcgaggctg atccatcagc tgctgtgcat 180

agaggctggc aagccggtgg tggcaccggt ttgcctgatg aggtggtgtc taccgcagcc 240

gccttagaaa tgtttcatgc ttttgcttta atccatgatg atatcatgga tgatagtgca 300

actagaagag gctccccaac tgttcacaga gccctagctg atcgtttagg cgctgctctg 360

gacccagatc aggccggtca actaggagtt tctactgcta tcttggttgg agatctggct 420

ttgacatggt ccgatgaatt gttatacgct ccattgactc cacatagact ggcagcagta 480

ctaccattgg taacagctat gagagctgaa accgttcatg gccaatatct tgatataact 540

agtgctagaa gacctgggac cgatacttct cttgcattga gaatagccag atataagaca 600

gcagcttaca caatggaacg tccactgcac attggtgcag ccctggctgg ggcaagacca 660

gaactattag cagggctttc agcatacgcc ttgccagctg gagaagcctt ccaattggca 720

gatgacctgc taggcgtctt cggtgatcca agacgtacag ggaaacctga cctagatgat 780

cttagaggtg gaaagcatac tgtcttagtc gccttggcaa gagaacatgc cactccagaa 840

cagagacaca cattggatac attattgggt acaccaggtc ttgatagaca aggcgcttca 900

agactaagat gcgtattggt agcaactggt gcaagagccg aagccgaaag acttattaca 960

gagagaagag atcaagcatt aactgcattg aacgcattaa cactgccacc tcctttagct 1020

gaggcattag caagattgac attagggtct acagctcatc ctgcctaa 1068

<210> 28
<211> 355
<212> PRT
<213> Streptomyces clavuligerus

<400> 28

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Met His Leu Ala Pro Arg Arg Val Pro Arg Gly Arg Arg Ser Pro Pro
1               5                   10                  15


Asp Arg Val Pro Glu Arg Gln Gly Ala Leu Gly Arg Arg Arg Gly Ala
            20                  25                  30


Gly Ser Thr Gly Cys Ala Arg Ala Ala Ala Gly Val His Arg Arg Arg
        35                  40                  45


Gly Gly Gly Glu Ala Asp Pro Ser Ala Ala Val His Arg Gly Trp Gln
    50                  55                  60


Ala Gly Gly Gly Thr Gly Leu Pro Asp Glu Val Val Ser Thr Ala Ala
65                  70                  75                  80


Ala Leu Glu Met Phe His Ala Phe Ala Leu Ile His Asp Asp Ile Met
                85                  90                  95


Asp Asp Ser Ala Thr Arg Arg Gly Ser Pro Thr Val His Arg Ala Leu
            100                 105                 110


Ala Asp Arg Leu Gly Ala Ala Leu Asp Pro Asp Gln Ala Gly Gln Leu
        115                 120                 125


Gly Val Ser Thr Ala Ile Leu Val Gly Asp Leu Ala Leu Thr Trp Ser
    130                 135                 140


Asp Glu Leu Leu Tyr Ala Pro Leu Thr Pro His Arg Leu Ala Ala Val
145                 150                 155                 160


Leu Pro Leu Val Thr Ala Met Arg Ala Glu Thr Val His Gly Gln Tyr
                165                 170                 175
```

```
Leu Asp Ile Thr Ser Ala Arg Arg Pro Gly Thr Asp Thr Ser Leu Ala
            180                 185                 190

Leu Arg Ile Ala Arg Tyr Lys Thr Ala Ala Tyr Thr Met Glu Arg Pro
        195                 200                 205

Leu His Ile Gly Ala Ala Leu Ala Gly Ala Arg Pro Glu Leu Leu Ala
    210                 215                 220

Gly Leu Ser Ala Tyr Ala Leu Pro Ala Gly Glu Ala Phe Gln Leu Ala
225                 230                 235                 240

Asp Asp Leu Leu Gly Val Phe Gly Asp Pro Arg Arg Thr Gly Lys Pro
                245                 250                 255

Asp Leu Asp Asp Leu Arg Gly Gly Lys His Thr Val Leu Val Ala Leu
            260                 265                 270

Ala Arg Glu His Ala Thr Pro Glu Gln Arg His Thr Leu Asp Thr Leu
        275                 280                 285

Leu Gly Thr Pro Gly Leu Asp Arg Gln Gly Ala Ser Arg Leu Arg Cys
    290                 295                 300

Val Leu Val Ala Thr Gly Ala Arg Ala Glu Ala Glu Arg Leu Ile Thr
305                 310                 315                 320

Glu Arg Arg Asp Gln Ala Leu Thr Ala Leu Asn Ala Leu Thr Leu Pro
                325                 330                 335

Pro Pro Leu Ala Glu Ala Leu Ala Arg Leu Thr Leu Gly Ser Thr Ala
            340                 345                 350

His Pro Ala
        355
```

<210> 29
<211> 993
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized GGPPS

<400> 29
atgtcatatt tcgataacta cttcaatgag atagttaatt ccgtgaacga catcattaag 60

tcttacatct ctggcgacgt accaaaacta tacgaagcct cctaccattt gtttacatca 120

ggaggaaaga gactaagacc attgatcctt acaatttctt ctgatctttt cggtggacag 180

agagaaagag catactatgc tggcgcagca atcgaagttt tgcacacatt cactttggtt 240

cacgatgata tcatggatca agataacatt cgtagaggtc ttcctactgt acatgtcaag 300

tatggcctac ctttggccat tttagctggt gacttattgc atgcaaaagc ctttcaattg 360

ttgactcagg cattgagagg tctaccatct gaaactatca tcaaggcgtt tgatatcttt 420

acaagatcta tcattatcat atcagaaggt caagctgtcg atatggaatt cgaagataga 480

attgatatca aggaacaaga gtatttggat atgatatctc gtaaaaccgc tgccttattc 540

tcagcttctt cttccattgg ggcgttgata gctggagcta atgataacga tgtgagatta 600

atgtccgatt tcggtacaaa tcttgggatc gcatttcaaa ttgtagatga tatacttggt 660

ttaacagctg atgaaaaaga gctaggaaaa cctgttttca gtgatatcag agaaggtaaa 720

aagaccatat tagtcattaa gactttagaa ttgtgtaagg aagacgagaa aaagattgtg 780

ttaaaagcgc taggcaacaa gtcagcatca aaggaagagt tgatgagttc tgctgacata 840

atcaaaaagt actcattgga ttacgcctac aacttagctg agaaatacta caaaaacgcc 900

atcgattctc taaatcaagt ttcaagtaaa agtgatattc cagggaaggc attgaaatat 960

cttgctgaat tcaccatcag aagacgtaag taa 993

<210> 30
<211> 330
<212> PRT
<213> Sulfolobus acidocaldarius

<400> 30

```
Met Ser Tyr Phe Asp Asn Tyr Phe Asn Glu Ile Val Asn Ser Val Asn
1               5                  10                  15

Asp Ile Ile Lys Ser Tyr Ile Ser Gly Asp Val Pro Lys Leu Tyr Glu
            20                  25                  30

Ala Ser Tyr His Leu Phe Thr Ser Gly Gly Lys Arg Leu Arg Pro Leu
        35                  40                  45

Ile Leu Thr Ile Ser Ser Asp Leu Phe Gly Gly Gln Arg Glu Arg Ala
    50                  55                  60

Tyr Tyr Ala Gly Ala Ala Ile Glu Val Leu His Thr Phe Thr Leu Val
65                  70                  75                  80

His Asp Asp Ile Met Asp Gln Asp Asn Ile Arg Arg Gly Leu Pro Thr
                85                  90                  95

Val His Val Lys Tyr Gly Leu Pro Leu Ala Ile Leu Ala Gly Asp Leu
            100                 105                 110

Leu His Ala Lys Ala Phe Gln Leu Leu Thr Gln Ala Leu Arg Gly Leu
        115                 120                 125

Pro Ser Glu Thr Ile Ile Lys Ala Phe Asp Ile Phe Thr Arg Ser Ile
    130                 135                 140

Ile Ile Ile Ser Glu Gly Gln Ala Val Asp Met Glu Phe Glu Asp Arg
145                 150                 155                 160

Ile Asp Ile Lys Glu Gln Glu Tyr Leu Asp Met Ile Ser Arg Lys Thr
                165                 170                 175

Ala Ala Leu Phe Ser Ala Ser Ser Ser Ile Gly Ala Leu Ile Ala Gly
            180                 185                 190

Ala Asn Asp Asn Asp Val Arg Leu Met Ser Asp Phe Gly Thr Asn Leu
```

```
        195                 200                 205

Gly Ile Ala Phe Gln Ile Val Asp Asp Ile Leu Gly Leu Thr Ala Asp
    210                 215                 220

Glu Lys Glu Leu Gly Lys Pro Val Phe Ser Asp Ile Arg Glu Gly Lys
225                 230                 235                 240

Lys Thr Ile Leu Val Ile Lys Thr Leu Glu Leu Cys Lys Glu Asp Glu
                245                 250                 255

Lys Lys Ile Val Leu Lys Ala Leu Gly Asn Lys Ser Ala Ser Lys Glu
            260                 265                 270

Glu Leu Met Ser Ser Ala Asp Ile Ile Lys Lys Tyr Ser Leu Asp Tyr
        275                 280                 285

Ala Tyr Asn Leu Ala Glu Lys Tyr Tyr Lys Asn Ala Ile Asp Ser Leu
    290                 295                 300

Asn Gln Val Ser Ser Lys Ser Asp Ile Pro Gly Lys Ala Leu Lys Tyr
305                 310                 315                 320

Leu Ala Glu Phe Thr Ile Arg Arg Arg Lys
                325                 330
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<210> 31
<211> 894
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized GGPPS

<400> 31
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gaggccctaa gtgctgctct tgtgccagct tatcctgaga gaatatacga agctatgaga 120

tactccctcc tggcaggtgg caaaagatta agacctatct tatgtttagc tgcttgcgaa 180

ttggcaggtg gttctgttga acaagccatg ccaactgcgt gtgcacttga aatgatccat 240

acaatgtcac taattcatga tgacctgcca gccatggata acgatgattt cagaagagga 300

aagccaacta atcacaaggt gttcggggaa gatatagcca tcttagcggg tgatgcgctt 360

ttagcttacg cttttgaaca tattgcttct caaacaagag gagtaccacc tcaattggtg 420

ctacaagtta ttgctagaat cggacacgcc gttgctgcaa caggcctcgt tggaggccaa 480

gtcgtagacc ttgaatctga aggtaaagct atttccttag aaacattgga gtatattcac 540

tcacataaga ctggagcctt gctggaagca tcagttgtct caggcggtat tctcgcaggg 600

gcagatgaag agcttttggc cagattgtct cattacgcta gagatatagg cttggctttt 660

caaatcgtcg atgatatcct ggatgttact gctacatctg aacagttggg gaaaaccgct 720

ggtaaagacc aggcagccgc aaaggcaact tatccaagtc tattgggttt agaagcctct 780

agacagaaag cggaagagtt gattcaatct gctaaggaag ccttaagacc ttacggttca 840

caagcagagc cactcctagc gctggcagac ttcatcacac gtcgtcagca ttaa 894

<210> 32
<211> 297
<212> PRT
<213> Synechococcus sp.

<400> 32

Met Val Ala Gln Thr Phe Asn Leu Asp Thr Tyr Leu Ser Gln Arg Gln
1 5 10 15

Gln Gln Val Glu Glu Ala Leu Ser Ala Ala Leu Val Pro Ala Tyr Pro
20 25 30

Glu Arg Ile Tyr Glu Ala Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys
35 40 45

Arg Leu Arg Pro Ile Leu Cys Leu Ala Ala Cys Glu Leu Ala Gly Gly
50 55 60

Ser Val Glu Gln Ala Met Pro Thr Ala Cys Ala Leu Glu Met Ile His
65 70 75 80

```
Thr Met Ser Leu Ile His Asp Asp Leu Pro Ala Met Asp Asn Asp Asp
                85                  90                  95

Phe Arg Arg Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Ile
            100                 105                 110

Ala Ile Leu Ala Gly Asp Ala Leu Leu Ala Tyr Ala Phe Glu His Ile
        115                 120                 125

Ala Ser Gln Thr Arg Gly Val Pro Pro Gln Leu Val Leu Gln Val Ile
    130                 135                 140

Ala Arg Ile Gly His Ala Val Ala Ala Thr Gly Leu Val Gly Gly Gln
145                 150                 155                 160

Val Val Asp Leu Glu Ser Glu Gly Lys Ala Ile Ser Leu Glu Thr Leu
                165                 170                 175

Glu Tyr Ile His Ser His Lys Thr Gly Ala Leu Leu Glu Ala Ser Val
            180                 185                 190

Val Ser Gly Gly Ile Leu Ala Gly Ala Asp Glu Glu Leu Leu Ala Arg
        195                 200                 205

Leu Ser His Tyr Ala Arg Asp Ile Gly Leu Ala Phe Gln Ile Val Asp
    210                 215                 220

Asp Ile Leu Asp Val Thr Ala Thr Ser Glu Gln Leu Gly Lys Thr Ala
225                 230                 235                 240

Gly Lys Asp Gln Ala Ala Ala Lys Ala Thr Tyr Pro Ser Leu Leu Gly
                245                 250                 255

Leu Glu Ala Ser Arg Gln Lys Ala Glu Glu Leu Ile Gln Ser Ala Lys
            260                 265                 270
```

Glu Ala Leu Arg Pro Tyr Gly Ser Gln Ala Glu Pro Leu Leu Ala Leu
        275   280   285

Ala Asp Phe Ile Thr Arg Arg Gln His
    290   295

<210> 33
<211> 1680
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized CDPS

<400> 33
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actttcagac atcacttatc acctgctact acaaactcta caggcattgt cgccttaaga 120

gacatcaact tcagatgtaa agcagtttct aaagagtact ctgatctgtt gcagaaagat 180

gaggcttctt tcacaaaatg ggacgatgac aaggtgaaag atcatcttga taccaacaaa 240

aacttatacc caaatgatga gattaaggaa tttgttgaat cagtaaaggc tatgttcggt 300

agtatgaatg acggggagat aaacgtctct gcatacgata ctgcatgggt tgctttggtt 360

caagatgtcg atggatcagg tagtcctcag ttcccttctt ctttagaatg gattgccaac 420

aatcaattgt cagatggatc atggggagat catttgctgt tctcagctca cgatagaatc 480

atcaacacat tagcatgcgt tattgcactt acaagttgga atgttcatcc ttctaagtgt 540

gaaaaaggtt tgaattttct gagagaaaac atttgcaaat tagaagatga aaacgcagaa 600

catatgccaa ttggttttga agtaacattc ccatcactaa ttgatatcgc gaaaaagttg 660

aacattgaag tacctgagga tactccagca cttaaagaga tctacgcacg tagagatatc 720

aagttaacta agatcccaat ggaagttctt cacaaggtac ctactacttt gttacattct 780

ttggaaggaa tgcctgattt ggagtgggaa aaactgttaa agctacaatg taaagatggt 840

agtttcttgt tttccccatc tagtaccgca ttcgccctaa tgcaaacaaa agatgagaaa 900

tgcttacagt atctaacaaa tatcgtcact aagttcaacg gtggcgtgcc taatgtgtac 960

ccagtcgatt tgtttgaaca tatttgggtt gttgatagac tgcagagatt ggggattgcc 1020

agatacttca aatcagagat aaaagattgt gtagagtata tcaataagta ctggaccaaa 1080

aatggaattt gttgggctag aaatactcac gttcaagata tcgatgatac agccatggga 1140

ttcagagtgt tgagagcgca cggttatgac gtcactccag atgtttttag acaatttgaa 1200

aaagatggta aattcgtttg ctttgcaggg caatcaacac aagccgtgac aggaatgttt 1260

aacgtttaca gagcctctca aatgttgttc ccaggggaga gaattttgga agatgccaaa 1320

aagttctctt acaattactt aaaggaaaag caaagtacca acgaattgct ggataaatgg 1380

ataatcgcta aagatctacc tggtgaagtt ggttatgctc tggatatccc atggtatgct 1440

tccttaccaa gattggaaac tcgttattac cttgaacaat acggcggtga agatgatgtc 1500

tggataggca agacattata cagaatgggt tacgtgtcca ataacacata tctagaaatg 1560

gcaaagctgg attacaataa ctatgttgca gtccttcaat tagaatggta cacaatacaa 1620

caatggtacg tcgatattgg tatagagaag ttcgaatctg acaacatcaa gtcagtcctg 1680

<210> 34
<211> 787
<212> PRT
<213> Stevia rebaudiana

<400> 34

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

Ser Pro Ala Thr Thr Phe Arg His His Leu Ser Pro Ala Thr Thr Asn
20 25 30

Ser Thr Gly Ile Val Ala Leu Arg Asp Ile Asn Phe Arg Cys Lys Ala
35 40 45

Val Ser Lys Glu Tyr Ser Asp Leu Leu Gln Lys Asp Glu Ala Ser Phe
50 55 60

Thr Lys Trp Asp Asp Asp Lys Val Lys Asp His Leu Asp Thr Asn Lys
65 70 75 80

```
Asn Leu Tyr Pro Asn Asp Glu Ile Lys Glu Phe Val Glu Ser Val Lys
                85                  90                  95

Ala Met Phe Gly Ser Met Asn Asp Gly Glu Ile Asn Val Ser Ala Tyr
            100                 105                 110

Asp Thr Ala Trp Val Ala Leu Val Gln Asp Val Asp Gly Ser Gly Ser
        115                 120                 125

Pro Gln Phe Pro Ser Ser Leu Glu Trp Ile Ala Asn Asn Gln Leu Ser
    130                 135                 140

Asp Gly Ser Trp Gly Asp His Leu Leu Phe Ser Ala His Asp Arg Ile
145                 150                 155                 160

Ile Asn Thr Leu Ala Cys Val Ile Ala Leu Thr Ser Trp Asn Val His
                165                 170                 175

Pro Ser Lys Cys Glu Lys Gly Leu Asn Phe Leu Arg Glu Asn Ile Cys
            180                 185                 190

Lys Leu Glu Asp Glu Asn Ala Glu His Met Pro Ile Gly Phe Glu Val
        195                 200                 205

Thr Phe Pro Ser Leu Ile Asp Ile Ala Lys Lys Leu Asn Ile Glu Val
    210                 215                 220

Pro Glu Asp Thr Pro Ala Leu Lys Glu Ile Tyr Ala Arg Arg Asp Ile
225                 230                 235                 240

Lys Leu Thr Lys Ile Pro Met Glu Val Leu His Lys Val Pro Thr Thr
                245                 250                 255

Leu Leu His Ser Leu Glu Gly Met Pro Asp Leu Glu Trp Glu Lys Leu
            260                 265                 270

Leu Lys Leu Gln Cys Lys Asp Gly Ser Phe Leu Phe Ser Pro Ser Ser
```

```
        275                 280                 285

Thr Ala Phe Ala Leu Met Gln Thr Lys Asp Glu Lys Cys Leu Gln Tyr
    290                 295                 300

Leu Thr Asn Ile Val Thr Lys Phe Asn Gly Gly Val Pro Asn Val Tyr
305                 310                 315                 320

Pro Val Asp Leu Phe Glu His Ile Trp Val Val Asp Arg Leu Gln Arg
                325                 330                 335

Leu Gly Ile Ala Arg Tyr Phe Lys Ser Glu Ile Lys Asp Cys Val Glu
            340                 345                 350

Tyr Ile Asn Lys Tyr Trp Thr Lys Asn Gly Ile Cys Trp Ala Arg Asn
        355                 360                 365

Thr His Val Gln Asp Ile Asp Asp Thr Ala Met Gly Phe Arg Val Leu
    370                 375                 380

Arg Ala His Gly Tyr Asp Val Thr Pro Asp Val Phe Arg Gln Phe Glu
385                 390                 395                 400

Lys Asp Gly Lys Phe Val Cys Phe Ala Gly Gln Ser Thr Gln Ala Val
                405                 410                 415

Thr Gly Met Phe Asn Val Tyr Arg Ala Ser Gln Met Leu Phe Pro Gly
            420                 425                 430

Glu Arg Ile Leu Glu Asp Ala Lys Lys Phe Ser Tyr Asn Tyr Leu Lys
        435                 440                 445

Glu Lys Gln Ser Thr Asn Glu Leu Leu Asp Lys Trp Ile Ile Ala Lys
    450                 455                 460

Asp Leu Pro Gly Glu Val Gly Tyr Ala Leu Asp Ile Pro Trp Tyr Ala
465                 470                 475                 480
```

```
Ser Leu Pro Arg Leu Glu Thr Arg Tyr Tyr Leu Glu Gln Tyr Gly Gly
                485                 490                 495

Glu Asp Asp Val Trp Ile Gly Lys Thr Leu Tyr Arg Met Gly Tyr Val
            500                 505                 510

Ser Asn Asn Thr Tyr Leu Glu Met Ala Lys Leu Asp Tyr Asn Asn Tyr
        515                 520                 525

Val Ala Val Leu Gln Leu Glu Trp Tyr Thr Ile Gln Gln Trp Tyr Val
    530                 535                 540

Asp Ile Gly Ile Glu Lys Phe Glu Ser Asp Asn Ile Lys Ser Val Leu
545                 550                 555                 560

Val Ser Tyr Tyr Leu Ala Ala Ala Ser Ile Phe Glu Pro Glu Arg Ser
                565                 570                 575

Lys Glu Arg Ile Ala Trp Ala Lys Thr Thr Ile Leu Val Asp Lys Ile
            580                 585                 590

Thr Ser Ile Phe Asp Ser Ser Gln Ser Ser Lys Glu Asp Ile Thr Ala
        595                 600                 605

Phe Ile Asp Lys Phe Arg Asn Lys Ser Ser Ser Lys Lys His Ser Ile
    610                 615                 620

Asn Gly Glu Pro Trp His Glu Val Met Val Ala Leu Lys Lys Thr Leu
625                 630                 635                 640

His Gly Phe Ala Leu Asp Ala Leu Met Thr His Ser Gln Asp Ile His
                645                 650                 655

Pro Gln Leu His Gln Ala Trp Glu Met Trp Leu Thr Lys Leu Gln Asp
            660                 665                 670

Gly Val Asp Val Thr Ala Glu Leu Met Val Gln Met Ile Asn Met Thr
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675 680 685

Ala Gly Arg Trp Val Ser Lys Glu Leu Leu Thr His Pro Gln Tyr Gln
690 695 700

Arg Leu Ser Thr Val Thr Asn Ser Val Cys His Asp Ile Thr Lys Leu
705 710 715 720

His Asn Phe Lys Glu Asn Ser Thr Thr Val Asp Ser Lys Val Gln Glu
725 730 735

Leu Val Gln Leu Val Phe Ser Asp Thr Pro Asp Asp Leu Asp Gln Asp
740 745 750

Met Lys Gln Thr Phe Leu Thr Val Met Lys Thr Phe Tyr Tyr Lys Ala
755 760 765

Trp Cys Asp Pro Asn Thr Ile Asn Asp His Ile Ser Lys Val Phe Glu
770 775 780

Ile Val Ile
785

<210> 35
<211> 1584
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized CDPS

<400> 35
atgcctgatg cacacgatgc tccacctcca caaataagac agagaacact agtagatgag 60

gctacccaac tgctaactga gtccgcagaa gatgcatggg gtgaagtcag tgtgtcagaa 120

tacgaaacag caaggctagt tgcccatgct acatggttag gtggacacgc cacaagagtg 180

gccttccttc tggagagaca acacgaagac gggtcatggg gtccaccagg tggatatagg 240

ttagtcccta cattatctgc tgttcacgca ttattgacat gtcttgcctc tcctgctcag 300

gatcatggcg ttccacatga tagactttta agagctgttg acgcaggctt gactgccttg 360

agaagattgg ggacatctga ctccccacct gatactatag cagttgagct ggttatccca 420

tctttgctag agggcattca acacttactg gaccctgctc atcctcatag tagaccagcc 480

ttctctcaac atagaggctc tcttgtttgt cctggtggac tagatgggag aactctagga 540

gctttgagat cacacgccgc agcaggtaca ccagtaccag gaaaagtctg gcacgcttcc 600

gagactttgg gcttgagtac cgaagctgct tctcacttgc aaccagccca aggtataatc 660

ggtggctctg ctgctgccac agcaacatgg ctaaccaggg ttgcaccatc tcaacagtca 720

gattctgcca gaagatacct tgaggaatta caacacagat actctggccc agttccttcc 780

attaccccta tcacatactt cgaaagagca tggttattga acaattttgc agcagccggt 840

gttccttgtg aggctccagc tgctttgttg gattccttag aagcagcact tacaccacaa 900

ggtgctcctg ctggagcagg attgcctcca gatgctgatg atacagccgc tgtgttgctt 960

gcattggcaa cacatgggag aggtagaaga ccagaagtac tgatggatta caggactgac 1020

gggtatttcc aatgctttat tggggaaagg actccatcaa tttcaacaaa cgctcacgta 1080

ttggaaacat tagggcatca tgtggcccaa catccacaag atagagccag atacggatca 1140

gccatggata ccgcatcagc ttggctgctg gcagctcaaa agcaagatgg ctcttggtta 1200

gataaatggc atgcctcacc atactacgct actgtttgtt gcacacaagc cctagccgct 1260

catgcaagtc ctgcaactgc accagctaga cagagagctg tcagatgggt tttagccaca 1320

caaagatccg atggcggttg gggtctatgg cattcaactg ttgaagagac tgcttatgcc 1380

ttacagatct tggccccacc ttctggtggt ggcaatatcc cagtccaaca agcacttact 1440

agaggcagag caagattgtg tggagccttg ccactgactc ctttatggca tgataaggat 1500

ttgtatactc cagtaagagt agtcagagct gccagagctg ctgctctgta cactaccaga 1560

gatctattgt taccaccatt gtaa 1584

<210> 36
<211> 527
<212> PRT
<213> Streptomyces clavuligerus

<400> 36

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Met Pro Asp Ala His Asp Ala Pro Pro Pro Gln Ile Arg Gln Arg Thr
1               5                  10                  15

Leu Val Asp Glu Ala Thr Gln Leu Leu Thr Glu Ser Ala Glu Asp Ala
            20                  25                  30

Trp Gly Glu Val Ser Val Ser Glu Tyr Glu Thr Ala Arg Leu Val Ala
        35                  40                  45

His Ala Thr Trp Leu Gly Gly His Ala Thr Arg Val Ala Phe Leu Leu
    50                  55                  60

Glu Arg Gln His Glu Asp Gly Ser Trp Gly Pro Pro Gly Gly Tyr Arg
65                  70                  75                  80

Leu Val Pro Thr Leu Ser Ala Val His Ala Leu Leu Thr Cys Leu Ala
                85                  90                  95

Ser Pro Ala Gln Asp His Gly Val Pro His Asp Arg Leu Leu Arg Ala
            100                 105                 110

Val Asp Ala Gly Leu Thr Ala Leu Arg Arg Leu Gly Thr Ser Asp Ser
        115                 120                 125

Pro Pro Asp Thr Ile Ala Val Glu Leu Val Ile Pro Ser Leu Leu Glu
    130                 135                 140

Gly Ile Gln His Leu Leu Asp Pro Ala His Pro His Ser Arg Pro Ala
145                 150                 155                 160

Phe Ser Gln His Arg Gly Ser Leu Val Cys Pro Gly Gly Leu Asp Gly
                165                 170                 175

Arg Thr Leu Gly Ala Leu Arg Ser His Ala Ala Ala Gly Thr Pro Val
            180                 185                 190
```

```
Pro Gly Lys Val Trp His Ala Ser Glu Thr Leu Gly Leu Ser Thr Glu
        195                 200                 205

Ala Ala Ser His Leu Gln Pro Ala Gln Gly Ile Ile Gly Gly Ser Ala
    210                 215                 220

Ala Ala Thr Ala Thr Trp Leu Thr Arg Val Ala Pro Ser Gln Gln Ser
225                 230                 235                 240

Asp Ser Ala Arg Arg Tyr Leu Glu Glu Leu Gln His Arg Tyr Ser Gly
                245                 250                 255

Pro Val Pro Ser Ile Thr Pro Ile Thr Tyr Phe Glu Arg Ala Trp Leu
            260                 265                 270

Leu Asn Asn Phe Ala Ala Ala Gly Val Pro Cys Glu Ala Pro Ala Ala
        275                 280                 285

Leu Leu Asp Ser Leu Glu Ala Ala Leu Thr Pro Gln Gly Ala Pro Ala
    290                 295                 300

Gly Ala Gly Leu Pro Pro Asp Ala Asp Asp Thr Ala Ala Val Leu Leu
305                 310                 315                 320

Ala Leu Ala Thr His Gly Arg Gly Arg Arg Pro Glu Val Leu Met Asp
                325                 330                 335

Tyr Arg Thr Asp Gly Tyr Phe Gln Cys Phe Ile Gly Glu Arg Thr Pro
            340                 345                 350

Ser Ile Ser Thr Asn Ala His Val Leu Glu Thr Leu Gly His His Val
        355                 360                 365

Ala Gln His Pro Gln Asp Arg Ala Arg Tyr Gly Ser Ala Met Asp Thr
    370                 375                 380

Ala Ser Ala Trp Leu Leu Ala Ala Gln Lys Gln Asp Gly Ser Trp Leu
385                 390                 395                 400
```

```
Asp Lys Trp His Ala Ser Pro Tyr Tyr Ala Thr Val Cys Cys Thr Gln
                405                 410                 415

Ala Leu Ala Ala His Ala Ser Pro Ala Thr Ala Pro Ala Arg Gln Arg
            420                 425                 430

Ala Val Arg Trp Val Leu Ala Thr Gln Arg Ser Asp Gly Gly Trp Gly
        435                 440                 445

Leu Trp His Ser Thr Val Glu Glu Thr Ala Tyr Ala Leu Gln Ile Leu
    450                 455                 460

Ala Pro Pro Ser Gly Gly Gly Asn Ile Pro Val Gln Gln Ala Leu Thr
465                 470                 475                 480

Arg Gly Arg Ala Arg Leu Cys Gly Ala Leu Pro Leu Thr Pro Leu Trp
                485                 490                 495

His Asp Lys Asp Leu Tyr Thr Pro Val Arg Val Val Arg Ala Ala Arg
            500                 505                 510

Ala Ala Ala Leu Tyr Thr Thr Arg Asp Leu Leu Leu Pro Pro Leu
        515                 520                 525


<210>  37
<211>  1551
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Codon-optimized CDPS

<400>  37
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gatggcggat ctgttggtcc atctgtgtat gatacggccc aggccctaag attccacggt      120

aacgtaacag gtagacaaga tgcatatgct tggttgatcg cccagcaaca agcagatgga      180

ggttggggct ctgccgactt tccactcttt agacatgctc caacatgggc tgcacttctc      240
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gcattacaaa gagctgatcc acttcctggc gcagcagacg cagttcagac cgcaacaaga 300

ttcttgcaaa gacaaccaga tccatacgct catgccgttc ctgaggatgc ccctattggt 360

gctgaactga tcttgcctca gttttgtgga gaggctgctt ggttgttggg aggtgtggcc 420

ttccctagac acccagccct attaccatta agacaggctt gtttagtcaa actgggtgca 480

gtcgccatgt tgccttcagg acacccattg ctccactcct gggaggcatg gggtacttct 540

ccaacaacag cctgtccaga cgatgatggt tctataggta tctcaccagc agctacagcc 600

gcctggagag cccaggctgt gaccagaggc tcaactcctc aagtgggcag agctgacgca 660

tacttacaaa tggcttcaag agcaacgaga tcaggcatag aaggagtctt ccctaatgtt 720

tggcctataa acgtattcga accatgctgg tcactgtaca ctctccatct tgccggtctg 780

ttcgcccatc cagcactggc tgaggctgta agagttatcg ttgctcaact tgaagcaaga 840

ttgggagtgc atggcctcgg accagcttta cattttgctg ccgacgctga tgatactgca 900

gttgccttat gcgttctgca tttggctggc agagatcctg cagttgacgc attgagacat 960

tttgaaattg gtgagctctt tgttacattc ccaggagaga gaaatgctag tgtctctacg 1020

aacattcacg ctcttcatgc tttgagattg ttaggtaaac cagctgccgg agcaagtgca 1080

tacgtcgaag caaatagaaa tccacatggt ttgtgggaca acgaaaaatg gcacgtttca 1140

tggctttatc caactgcaca cgccgttgca gctctagctc aaggcaagcc tcaatggaga 1200

gatgaaagag cactagccgc tctactacaa gctcaaagag atgatggtgg ttggggagct 1260

ggtagaggat ccactttcga ggaaaccgcc tacgctcttt tcgctttaca cgttatggac 1320

ggatctgagg aagccacagg cagaagaaga atcgctcaag tcgtcgcaag agccttagaa 1380

tggatgctag ctagacatgc cgcacatgga ttaccacaaa caccactctg gattggtaag 1440

gaattgtact gtcctactag agtcgtaaga gtagctgagc tagctggcct gtggttagca 1500

ttaagatggg gtagaagagt attagctgaa ggtgctggtg ctgcacctta a 1551

<210> 38
<211> 516
<212> PRT
<213> Bradyrhizobium japonicum

<400> 38

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Met Asn Ala Leu Ser Glu His Ile Leu Ser Glu Leu Arg Arg Leu Leu
1               5                   10                  15

Ser Glu Met Ser Asp Gly Gly Ser Val Gly Pro Ser Val Tyr Asp Thr
            20                  25                  30

Ala Gln Ala Leu Arg Phe His Gly Asn Val Thr Gly Arg Gln Asp Ala
        35                  40                  45

Tyr Ala Trp Leu Ile Ala Gln Gln Gln Ala Asp Gly Gly Trp Gly Ser
    50                  55                  60

Ala Asp Phe Pro Leu Phe Arg His Ala Pro Thr Trp Ala Ala Leu Leu
65                  70                  75                  80

Ala Leu Gln Arg Ala Asp Pro Leu Pro Gly Ala Ala Asp Ala Val Gln
                85                  90                  95

Thr Ala Thr Arg Phe Leu Gln Arg Gln Pro Asp Pro Tyr Ala His Ala
            100                 105                 110

Val Pro Glu Asp Ala Pro Ile Gly Ala Glu Leu Ile Leu Pro Gln Phe
        115                 120                 125

Cys Gly Glu Ala Ala Trp Leu Leu Gly Gly Val Ala Phe Pro Arg His
    130                 135                 140

Pro Ala Leu Leu Pro Leu Arg Gln Ala Cys Leu Val Lys Leu Gly Ala
145                 150                 155                 160

Val Ala Met Leu Pro Ser Gly His Pro Leu Leu His Ser Trp Glu Ala
                165                 170                 175

Trp Gly Thr Ser Pro Thr Thr Ala Cys Pro Asp Asp Asp Gly Ser Ile
            180                 185                 190
```

```
Gly Ile Ser Pro Ala Ala Thr Ala Ala Trp Arg Ala Gln Ala Val Thr
        195                 200                 205

Arg Gly Ser Thr Pro Gln Val Gly Arg Ala Asp Ala Tyr Leu Gln Met
    210                 215                 220

Ala Ser Arg Ala Thr Arg Ser Gly Ile Glu Gly Val Phe Pro Asn Val
225                 230                 235                 240

Trp Pro Ile Asn Val Phe Glu Pro Cys Trp Ser Leu Tyr Thr Leu His
                245                 250                 255

Leu Ala Gly Leu Phe Ala His Pro Ala Leu Ala Glu Ala Val Arg Val
            260                 265                 270

Ile Val Ala Gln Leu Glu Ala Arg Leu Gly Val His Gly Leu Gly Pro
        275                 280                 285

Ala Leu His Phe Ala Ala Asp Ala Asp Asp Thr Ala Val Ala Leu Cys
    290                 295                 300

Val Leu His Leu Ala Gly Arg Asp Pro Ala Val Asp Ala Leu Arg His
305                 310                 315                 320

Phe Glu Ile Gly Glu Leu Phe Val Thr Phe Pro Gly Glu Arg Asn Ala
                325                 330                 335

Ser Val Ser Thr Asn Ile His Ala Leu His Ala Leu Arg Leu Leu Gly
            340                 345                 350

Lys Pro Ala Ala Gly Ala Ser Ala Tyr Val Glu Ala Asn Arg Asn Pro
        355                 360                 365

His Gly Leu Trp Asp Asn Glu Lys Trp His Val Ser Trp Leu Tyr Pro
    370                 375                 380

Thr Ala His Ala Val Ala Ala Leu Ala Gln Gly Lys Pro Gln Trp Arg
```

385 390 395 400

Asp Glu Arg Ala Leu Ala Ala Leu Leu Gln Ala Gln Arg Asp Asp Gly
405 410 415

Gly Trp Gly Ala Gly Arg Gly Ser Thr Phe Glu Glu Thr Ala Tyr Ala
420 425 430

Leu Phe Ala Leu His Val Met Asp Gly Ser Glu Glu Ala Thr Gly Arg
435 440 445

Arg Arg Ile Ala Gln Val Val Ala Arg Ala Leu Glu Trp Met Leu Ala
450 455 460

Arg His Ala Ala His Gly Leu Pro Gln Thr Pro Leu Trp Ile Gly Lys
465 470 475 480

Glu Leu Tyr Cys Pro Thr Arg Val Val Arg Val Ala Glu Leu Ala Gly
485 490 495

Leu Trp Leu Ala Leu Arg Trp Gly Arg Arg Val Leu Ala Glu Gly Ala
500 505 510

Gly Ala Ala Pro
515

<210> 39
<211> 2490
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized CDPS

<400> 39
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gcaggaaggt ggagaagggc cttggctaga gcacagcaca catcagaatc cgcagctgtc 180

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ccaagattag acggcggtga aggtcctcaa tttccagcag ctgtgagatg gataagaaat 420

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<213> Zea mays

<400> 40

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20 25 30

Asp Thr Val Ala Val Pro Ala Ala Ala Gly Arg Trp Arg Arg Ala Leu
35 40 45

Ala Arg Ala Gln His Thr Ser Glu Ser Ala Ala Val Ala Lys Gly Ser
50 55 60

```
Ser Leu Thr Pro Ile Val Arg Thr Asp Ala Glu Ser Arg Arg Thr Arg
65                  70                  75                  80

Trp Pro Thr Asp Asp Asp Asp Ala Glu Pro Leu Val Asp Glu Ile Arg
                85                  90                  95

Ala Met Leu Thr Ser Met Ser Asp Gly Asp Ile Ser Val Ser Ala Tyr
            100                 105                 110

Asp Thr Ala Trp Val Gly Leu Val Pro Arg Leu Asp Gly Gly Glu Gly
        115                 120                 125

Pro Gln Phe Pro Ala Ala Val Arg Trp Ile Arg Asn Asn Gln Leu Pro
    130                 135                 140

Asp Gly Ser Trp Gly Asp Ala Ala Leu Phe Ser Ala Tyr Asp Arg Leu
145                 150                 155                 160

Ile Asn Thr Leu Ala Cys Val Val Thr Leu Thr Arg Trp Ser Leu Glu
                165                 170                 175

Pro Glu Met Arg Gly Arg Gly Leu Ser Phe Leu Gly Arg Asn Met Trp
            180                 185                 190

Lys Leu Ala Thr Glu Asp Glu Glu Ser Met Pro Ile Gly Phe Glu Leu
        195                 200                 205

Ala Phe Pro Ser Leu Ile Glu Leu Ala Lys Ser Leu Gly Val His Asp
    210                 215                 220

Phe Pro Tyr Asp His Gln Ala Leu Gln Gly Ile Tyr Ser Ser Arg Glu
225                 230                 235                 240

Ile Lys Met Lys Arg Ile Pro Lys Glu Val Met His Thr Val Pro Thr
                245                 250                 255
```

```
Ser Ile Leu His Ser Leu Glu Gly Met Pro Gly Leu Asp Trp Ala Lys
            260                 265                 270

Leu Leu Lys Leu Gln Ser Ser Asp Gly Ser Phe Leu Phe Ser Pro Ala
        275                 280                 285

Ala Thr Ala Tyr Ala Leu Met Asn Thr Gly Asp Asp Arg Cys Phe Ser
    290                 295                 300

Tyr Ile Asp Arg Thr Val Lys Lys Phe Asn Gly Gly Val Pro Asn Val
305                 310                 315                 320

Tyr Pro Val Asp Leu Phe Glu His Ile Trp Ala Val Asp Arg Leu Glu
                325                 330                 335

Arg Leu Gly Ile Ser Arg Tyr Phe Gln Lys Glu Ile Glu Gln Cys Met
            340                 345                 350

Asp Tyr Val Asn Arg His Trp Thr Glu Asp Gly Ile Cys Trp Ala Arg
        355                 360                 365

Asn Ser Asp Val Lys Glu Val Asp Asp Thr Ala Met Ala Phe Arg Leu
    370                 375                 380

Leu Arg Leu His Gly Tyr Ser Val Ser Pro Asp Val Phe Lys Asn Phe
385                 390                 395                 400

Glu Lys Asp Gly Glu Phe Phe Ala Phe Val Gly Gln Ser Asn Gln Ala
                405                 410                 415

Val Thr Gly Met Tyr Asn Leu Asn Arg Ala Ser Gln Ile Ser Phe Pro
            420                 425                 430

Gly Glu Asp Val Leu His Arg Ala Gly Ala Phe Ser Tyr Glu Phe Leu
        435                 440                 445

Arg Arg Lys Glu Ala Glu Gly Ala Leu Arg Asp Lys Trp Ile Ile Ser
    450                 455                 460
```

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Lys Asp Leu Pro Gly Glu Val Val Tyr Thr Leu Asp Phe Pro Trp Tyr
465                 470                 475                 480

Gly Asn Leu Pro Arg Val Glu Ala Arg Asp Tyr Leu Glu Gln Tyr Gly
                485                 490                 495

Gly Gly Asp Asp Val Trp Ile Gly Lys Thr Leu Tyr Arg Met Pro Leu
            500                 505                 510

Val Asn Asn Asp Val Tyr Leu Glu Leu Ala Arg Met Asp Phe Asn His
        515                 520                 525

Cys Gln Ala Leu His Gln Leu Glu Trp Gln Gly Leu Lys Arg Trp Tyr
    530                 535                 540

Thr Glu Asn Arg Leu Met Asp Phe Gly Val Ala Gln Glu Asp Ala Leu
545                 550                 555                 560

Arg Ala Tyr Phe Leu Ala Ala Ala Ser Val Tyr Glu Pro Cys Arg Ala
                565                 570                 575

Ala Glu Arg Leu Ala Trp Ala Arg Ala Ala Ile Leu Ala Asn Ala Val
            580                 585                 590

Ser Thr His Leu Arg Asn Ser Pro Ser Phe Arg Glu Arg Leu Glu His
        595                 600                 605

Ser Leu Arg Cys Arg Pro Ser Glu Glu Thr Asp Gly Ser Trp Phe Asn
    610                 615                 620

Ser Ser Ser Gly Ser Asp Ala Val Leu Val Lys Ala Val Leu Arg Leu
625                 630                 635                 640

Thr Asp Ser Leu Ala Arg Glu Ala Gln Pro Ile His Gly Gly Asp Pro
                645                 650                 655
```

```
Glu Asp Ile Ile His Lys Leu Leu Arg Ser Ala Trp Ala Glu Trp Val
            660                 665                 670

Arg Glu Lys Ala Asp Ala Ala Asp Ser Val Cys Asn Gly Ser Ser Ala
        675                 680                 685

Val Glu Gln Glu Gly Ser Arg Met Val His Asp Lys Gln Thr Cys Leu
    690                 695                 700

Leu Leu Ala Arg Met Ile Glu Ile Ser Ala Gly Arg Ala Ala Gly Glu
705                 710                 715                 720

Ala Ala Ser Glu Asp Gly Asp Arg Arg Ile Ile Gln Leu Thr Gly Ser
                725                 730                 735

Ile Cys Asp Ser Leu Lys Gln Lys Met Leu Val Ser Gln Asp Pro Glu
            740                 745                 750

Lys Asn Glu Glu Met Met Ser His Val Asp Asp Glu Leu Lys Leu Arg
        755                 760                 765

Ile Arg Glu Phe Val Gln Tyr Leu Leu Arg Leu Gly Glu Lys Lys Thr
    770                 775                 780

Gly Ser Ser Glu Thr Arg Gln Thr Phe Leu Ser Ile Val Lys Ser Cys
785                 790                 795                 800

Tyr Tyr Ala Ala His Cys Pro Pro His Val Val Asp Arg His Ile Ser
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Arg Val Ile Phe Glu Pro Val Ser Ala Ala Lys
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<212> DNA
<213> Artificial Sequence

<220>

<223> Codon-optimized CDPS

<400> 41

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gcggttccat acattgttca aagcttcgaa ctcaagaata cattaattct caagaggttc 240

aacatgattt gcctctaata catgagtggc aacagcttca aggagaagat gctcctcaga 300

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accaactttc cgatggttct tggggagatg cgtatctctt ctcttatcat gatcgtctca 540

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atatgccaat cggattcgaa gtagcattcc catcgttgct tgagatagct cgaggaataa 720

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ccgtggatct tttcgagcac atatggatag tggatcggtt acaacgttta gggatatcga 1080

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<213> Arabidopsis thaliana

<400> 42

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Leu Ser Ser Thr Lys Thr Thr Ile Ser Ser Ser Phe Leu Thr Ile Ser
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Gly Ser Pro Leu Asn Val Ala Arg Asp Lys Ser Arg Ser Gly Ser Ile
        35                  40                  45

His Cys Ser Lys Leu Arg Thr Gln Glu Tyr Ile Asn Ser Gln Glu Val
    50                  55                  60

Gln His Asp Leu Pro Leu Ile His Glu Trp Gln Gln Leu Gln Gly Glu
65                  70                  75                  80

Asp Ala Pro Gln Ile Ser Val Gly Ser Asn Ser Asn Ala Phe Lys Glu
                85                  90                  95

Ala Val Lys Ser Val Lys Thr Ile Leu Arg Asn Leu Thr Asp Gly Glu
            100                 105                 110

Ile Thr Ile Ser Ala Tyr Asp Thr Ala Trp Val Ala Leu Ile Asp Ala
        115                 120                 125

Gly Asp Lys Thr Pro Ala Phe Pro Ser Ala Val Lys Trp Ile Ala Glu
    130                 135                 140

Asn Gln Leu Ser Asp Gly Ser Trp Gly Asp Ala Tyr Leu Phe Ser Tyr
145                 150                 155                 160

His Asp Arg Leu Ile Asn Thr Leu Ala Cys Val Val Ala Leu Arg Ser
                165                 170                 175

Trp Asn Leu Phe Pro His Gln Cys Asn Lys Gly Ile Thr Phe Phe Arg
            180                 185                 190

Glu Asn Ile Gly Lys Leu Glu Asp Glu Asn Asp Glu His Met Pro Ile
        195                 200                 205

Gly Phe Glu Val Ala Phe Pro Ser Leu Leu Glu Ile Ala Arg Gly Ile
```

```
    210                 215                 220

Asn Ile Asp Val Pro Tyr Asp Ser Pro Val Leu Lys Asp Ile Tyr Ala
225                 230                 235                 240

Lys Lys Glu Leu Lys Leu Thr Arg Ile Pro Lys Glu Ile Met His Lys
                245                 250                 255

Ile Pro Thr Thr Leu Leu His Ser Leu Glu Gly Met Arg Asp Leu Asp
            260                 265                 270

Trp Glu Lys Leu Leu Lys Leu Gln Ser Gln Asp Gly Ser Phe Leu Phe
        275                 280                 285

Ser Pro Ser Ser Thr Ala Phe Ala Phe Met Gln Thr Arg Asp Ser Asn
    290                 295                 300

Cys Leu Glu Tyr Leu Arg Asn Ala Val Lys Arg Phe Asn Gly Gly Val
305                 310                 315                 320

Pro Asn Val Phe Pro Val Asp Leu Phe Glu His Ile Trp Ile Val Asp
                325                 330                 335

Arg Leu Gln Arg Leu Gly Ile Ser Arg Tyr Phe Glu Glu Glu Ile Lys
            340                 345                 350

Glu Cys Leu Asp Tyr Val His Arg Tyr Trp Thr Asp Asn Gly Ile Cys
        355                 360                 365

Trp Ala Arg Cys Ser His Val Gln Asp Ile Asp Asp Thr Ala Met Ala
    370                 375                 380

Phe Arg Leu Leu Arg Gln His Gly Tyr Gln Val Ser Ala Asp Val Phe
385                 390                 395                 400

Lys Asn Phe Glu Lys Glu Gly Glu Phe Phe Cys Phe Val Gly Gln Ser
                405                 410                 415
```

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Asn Gln Ala Val Thr Gly Met Phe Asn Leu Tyr Arg Ala Ser Gln Leu
            420                 425                 430

Ala Phe Pro Arg Glu Glu Ile Leu Lys Asn Ala Lys Glu Phe Ser Tyr
        435                 440                 445

Asn Tyr Leu Leu Glu Lys Arg Glu Arg Glu Glu Leu Ile Asp Lys Trp
    450                 455                 460

Ile Ile Met Lys Asp Leu Pro Gly Glu Ile Gly Phe Ala Leu Glu Ile
465                 470                 475                 480

Pro Trp Tyr Ala Ser Leu Pro Arg Val Glu Thr Arg Phe Tyr Ile Asp
                485                 490                 495

Gln Tyr Gly Gly Glu Asn Asp Val Trp Ile Gly Lys Thr Leu Tyr Arg
            500                 505                 510

Met Pro Tyr Val Asn Asn Asn Gly Tyr Leu Glu Leu Ala Lys Gln Asp
        515                 520                 525

Tyr Asn Asn Cys Gln Ala Gln His Gln Leu Glu Trp Asp Ile Phe Gln
    530                 535                 540

Lys Trp Tyr Glu Glu Asn Arg Leu Ser Glu Trp Gly Val Arg Arg Ser
545                 550                 555                 560

Glu Leu Leu Glu Cys Tyr Tyr Leu Ala Ala Ala Thr Ile Phe Glu Ser
                565                 570                 575

Glu Arg Ser His Glu Arg Met Val Trp Ala Lys Ser Ser Val Leu Val
            580                 585                 590

Lys Ala Ile Ser Ser Ser Phe Gly Glu Ser Ser Asp Ser Arg Arg Ser
        595                 600                 605

Phe Ser Asp Gln Phe His Glu Tyr Ile Ala Asn Ala Arg Arg Ser Asp
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    610                 615                 620

His His Phe Asn Asp Arg Asn Met Arg Leu Asp Arg Pro Gly Ser Val
625                 630                 635                 640

Gln Ala Ser Arg Leu Ala Gly Val Leu Ile Gly Thr Leu Asn Gln Met
                645                 650                 655

Ser Phe Asp Leu Phe Met Ser His Gly Arg Asp Val Asn Asn Leu Leu
            660                 665                 670

Tyr Leu Ser Trp Gly Asp Trp Met Glu Lys Trp Lys Leu Tyr Gly Asp
        675                 680                 685

Glu Gly Glu Gly Glu Leu Met Val Lys Met Ile Ile Leu Met Lys Asn
    690                 695                 700

Asn Asp Leu Thr Asn Phe Phe Thr His Thr His Phe Val Arg Leu Ala
705                 710                 715                 720

Glu Ile Ile Asn Arg Ile Cys Leu Pro Arg Gln Tyr Leu Lys Ala Arg
                725                 730                 735

Arg Asn Asp Glu Lys Glu Lys Thr Ile Lys Ser Met Glu Lys Glu Met
            740                 745                 750

Gly Lys Met Val Glu Leu Ala Leu Ser Glu Ser Asp Thr Phe Arg Asp
        755                 760                 765

Val Ser Ile Thr Phe Leu Asp Val Ala Lys Ala Phe Tyr Tyr Phe Ala
    770                 775                 780

Leu Cys Gly Asp His Leu Gln Thr His Ile Ser Lys Val Leu Phe Gln
785                 790                 795                 800

Lys Val
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<212> DNA
<213> Artificial Sequence

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<223> Codon-optimized KS

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ataatcgata cgaccaagga gagaatacaa aaacaattca aaaatgttga aatttcagtt 180

tcttcttatg atactgcgtg ggttgccatg gttccatcac ctaattctcc aaagtctcca 240

tgtttcccag aatgtttgaa ttggctgatt aacaaccagt tgaatgatgg atcttggggt 300

ttagtcaatc acacgcacaa tcacaaccat ccacttttga aagattcttt atcctcaact 360

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cttagtttca ttgaatctaa cttggcttcc gcgactgaaa aatctcaacc atctccaata 480

ggattcgata tcatctttcc aggtctgtta gagtacgcca aaaatctaga tatcaactta 540

ctgtctaagc aaactgattt ctcactaatg ttacacaaga gagaattaga acaaaagaga 600

tgtcattcaa acgaaatgga tggttaccta gcttatatct ctgaaggtct tggtaatctt 660

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ttcaagttaa tgtccacaca aggcagatta cttaatgata ttcattcttt caaaagagag 2040

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<211> 784
<212> PRT
<213> Stevia rebaudiana

<400> 44

Met Asn Leu Ser Leu Cys Ile Ala Ser Pro Leu Leu Thr Lys Ser Asn
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Arg Pro Ala Ala Leu Ser Ala Ile His Thr Ala Ser Thr Ser His Gly
            20                  25                  30

Gly Gln Thr Asn Pro Thr Asn Leu Ile Ile Asp Thr Thr Lys Glu Arg
        35                  40                  45

Ile Gln Lys Gln Phe Lys Asn Val Glu Ile Ser Val Ser Ser Tyr Asp
    50                  55                  60

Thr Ala Trp Val Ala Met Val Pro Ser Pro Asn Ser Pro Lys Ser Pro
65                  70                  75                  80

Cys Phe Pro Glu Cys Leu Asn Trp Leu Ile Asn Asn Gln Leu Asn Asp
                85                  90                  95

Gly Ser Trp Gly Leu Val Asn His Thr His Asn His Asn His Pro Leu
            100                 105                 110

Leu Lys Asp Ser Leu Ser Ser Thr Leu Ala Cys Ile Val Ala Leu Lys
        115                 120                 125

Arg Trp Asn Val Gly Glu Asp Gln Ile Asn Lys Gly Leu Ser Phe Ile
    130                 135                 140

Glu Ser Asn Leu Ala Ser Ala Thr Glu Lys Ser Gln Pro Ser Pro Ile
145                 150                 155                 160

Gly Phe Asp Ile Ile Phe Pro Gly Leu Leu Glu Tyr Ala Lys Asn Leu
                165                 170                 175

Asp Ile Asn Leu Leu Ser Lys Gln Thr Asp Phe Ser Leu Met Leu His
            180                 185                 190

Lys Arg Glu Leu Glu Gln Lys Arg Cys His Ser Asn Glu Met Asp Gly
        195                 200                 205
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```
Tyr Leu Ala Tyr Ile Ser Glu Gly Leu Gly Asn Leu Tyr Asp Trp Asn
    210                 215                 220

Met Val Lys Lys Tyr Gln Met Lys Asn Gly Ser Val Phe Asn Ser Pro
225                 230                 235                 240

Ser Ala Thr Ala Ala Ala Phe Ile Asn His Gln Asn Pro Gly Cys Leu
                245                 250                 255

Asn Tyr Leu Asn Ser Leu Leu Asp Lys Phe Gly Asn Ala Val Pro Thr
            260                 265                 270

Val Tyr Pro His Asp Leu Phe Ile Arg Leu Ser Met Val Asp Thr Ile
        275                 280                 285

Glu Arg Leu Gly Ile Ser His His Phe Arg Val Glu Ile Lys Asn Val
    290                 295                 300

Leu Asp Glu Thr Tyr Arg Cys Trp Val Glu Arg Asp Glu Gln Ile Phe
305                 310                 315                 320

Met Asp Val Val Thr Cys Ala Leu Ala Phe Arg Leu Leu Arg Ile Asn
                325                 330                 335

Gly Tyr Glu Val Ser Pro Asp Pro Leu Ala Glu Ile Thr Asn Glu Leu
            340                 345                 350

Ala Leu Lys Asp Glu Tyr Ala Ala Leu Glu Thr Tyr His Ala Ser His
        355                 360                 365

Ile Leu Tyr Gln Glu Asp Leu Ser Ser Gly Lys Gln Ile Leu Lys Ser
    370                 375                 380

Ala Asp Phe Leu Lys Glu Ile Ile Ser Thr Asp Ser Asn Arg Leu Ser
385                 390                 395                 400

Lys Leu Ile His Lys Glu Val Glu Asn Ala Leu Lys Phe Pro Ile Asn
                405                 410                 415
```

```
Thr Gly Leu Glu Arg Ile Asn Thr Arg Arg Asn Ile Gln Leu Tyr Asn
            420                 425                 430

Val Asp Asn Thr Arg Ile Leu Lys Thr Thr Tyr His Ser Ser Asn Ile
        435                 440                 445

Ser Asn Thr Asp Tyr Leu Arg Leu Ala Val Glu Asp Phe Tyr Thr Cys
    450                 455                 460

Gln Ser Ile Tyr Arg Glu Glu Leu Lys Gly Leu Glu Arg Trp Val Val
465                 470                 475                 480

Glu Asn Lys Leu Asp Gln Leu Lys Phe Ala Arg Gln Lys Thr Ala Tyr
                485                 490                 495

Cys Tyr Phe Ser Val Ala Ala Thr Leu Ser Ser Pro Glu Leu Ser Asp
            500                 505                 510

Ala Arg Ile Ser Trp Ala Lys Asn Gly Ile Leu Thr Thr Val Val Asp
        515                 520                 525

Asp Phe Phe Asp Ile Gly Gly Thr Ile Asp Glu Leu Thr Asn Leu Ile
    530                 535                 540

Gln Cys Val Glu Lys Trp Asn Val Asp Val Asp Lys Asp Cys Cys Ser
545                 550                 555                 560

Glu His Val Arg Ile Leu Phe Leu Ala Leu Lys Asp Ala Ile Cys Trp
                565                 570                 575

Ile Gly Asp Glu Ala Phe Lys Trp Gln Ala Arg Asp Val Thr Ser His
            580                 585                 590

Val Ile Gln Thr Trp Leu Glu Leu Met Asn Ser Met Leu Arg Glu Ala
        595                 600                 605
```

```
Ile Trp Thr Arg Asp Ala Tyr Val Pro Thr Leu Asn Glu Tyr Met Glu
    610                 615                 620

Asn Ala Tyr Val Ser Phe Ala Leu Gly Pro Ile Val Lys Pro Ala Ile
625                 630                 635                 640

Tyr Phe Val Gly Pro Lys Leu Ser Glu Glu Ile Val Glu Ser Ser Glu
                645                 650                 655

Tyr His Asn Leu Phe Lys Leu Met Ser Thr Gln Gly Arg Leu Leu Asn
            660                 665                 670

Asp Ile His Ser Phe Lys Arg Glu Phe Lys Glu Gly Lys Leu Asn Ala
        675                 680                 685

Val Ala Leu His Leu Ser Asn Gly Glu Ser Gly Lys Val Glu Glu Glu
    690                 695                 700

Val Val Glu Glu Met Met Met Met Ile Lys Asn Lys Arg Lys Glu Leu
705                 710                 715                 720

Met Lys Leu Ile Phe Glu Glu Asn Gly Ser Ile Val Pro Arg Ala Cys
                725                 730                 735

Lys Asp Ala Phe Trp Asn Met Cys His Val Leu Asn Phe Phe Tyr Ala
            740                 745                 750

Asn Asp Asp Gly Phe Thr Gly Asn Thr Ile Leu Asp Thr Val Lys Asp
        755                 760                 765

Ile Ile Tyr Asn Pro Leu Val Leu Val Asn Glu Asn Glu Glu Gln Arg
    770                 775                 780
```

<210> 45
<211> 2355
<212> DNA
<213> Artificial Sequence

<220>

<223> Codon-optimized KS

<400> 45
atgaatctgt ccctttgtat agctagtcca ctgttgacaa aatcttctag accaactgct 60

ctttctgcaa ttcatactgc cagtactagt catggaggtc aaacaaaccc aacaaatttg 120

ataatcgata ctactaagga gagaatccaa aagctattca aaaatgttga aatctcagta 180

tcatcttatg acaccgcatg ggttgcaatg gtgccatcac ctaattcccc aaaaagtcca 240

tgttttccag agtgcttgaa ttggttaatc aataatcagt taaacgatgg ttcttggggt 300

ttagtcaacc acactcataa ccacaatcat ccattattga aggactcttt atcatcaaca 360

ttagcctgta ttgttgcatt gaaaagatgg aatgtaggtg aagatcaaat caacaagggt 420

ttatcattca tagaatccaa tctagcttct gctaccgaca aatcacaacc atctccaatc 480

gggttcgaca taatcttccc tggtttgctg gagtatgcca aaaaccttga tatcaactta 540

ctgtctaaac aaacagattt ctctttgatg ctacacaaaa gagagttaga gcagaaaaga 600

tgccattcta acgaaattga cgggtactta gcatatatct cagaaggttt gggtaatttg 660

tatgactgga acatggtcaa aaagtatcag atgaaaaatg gatccgtatt caattctcct 720

tctgcaactg ccgcagcatt cattaatcat caaaaccctg ggtgtcttaa ctacttgaac 780

tcactattag ataagtttgg aaatgcagtt ccaacagtct atcctttgga cttgtacatc 840

agattatcta tggttgacac tatagagaga ttaggtattt ctcatcattt cagagttgag 900

atcaaaaatg ttttggacga gacatacaga tgttgggtcg aaagagatga gcaaatcttt 960

atggatgtcg tgacctgcgc tctggctttt agattgctaa ggatacacgg atacaaagta 1020

tctcctgatc aactggctga gattacaaac gaactggctt tcaaagacga atacgccgca 1080

ttagaaacat accatgcatc ccaaatactt taccaggaag acctaagttc aggaaaacaa 1140

atcttgaagt ctgcagattt cctgaaaggc attctgtcta cagatagtaa taggttgtct 1200

aaattgatac acaaggaagt agaaaacgca ctaaagtttc ctattaacac tggtttagag 1260

agaatcaata ctaggagaaa cattcagctg tacaacgtag ataatacaag gattcttaag 1320

accacctacc atagttcaaa catttccaac acctattact taagattagc tgtcgaagac 1380

ttttacactt gtcaatcaat ctacagagag gagttaaagg gcctagaaag atgggtagtt 1440

caaaacaagt tggatcaact gaagtttgct agacagaaga cagcatactg ttatttctct 1500

gttgctgcta ccctttcatc cccagaattg tctgatgcca gaataagttg ggccaaaaat 1560

ggtattctta caactgtagt cgatgatttc tttgatattg gaggtactat tgatgaactg 1620

acaaatctta ttcaatgtgt tgaaaagtgg aacgtggatg tagataagga ttgctgcagt 1680

gaacatgtga gaatactttt cctggctcta aaagatgcaa tatgttggat tggcgacgag 1740

gccttcaagt ggcaagctag agatgttaca tctcatgtca tccaaacttg gcttgaactg 1800

atgaactcaa tgctaagaga agcaatctgg acaagagatg catacgttcc aacattgaac 1860

gaatacatgg aaaacgctta cgtctcattt gccttgggtc ctattgttaa gccagccata 1920

tactttgttg ggccaaagtt atccgaagag attgttgagt cttccgaata tcataaccta 1980

ttcaagttaa tgtcaacaca aggcagactt ctgaacgata tccactcctt caaaagagaa 2040

ttcaaggaag gtaagctaaa cgctgttgct ttgcacttgt ctaatggtga atctggcaaa 2100

gtggaagagg aagtcgttga ggaaatgatg atgatgatca aaaacaagag aaaggaattg 2160

atgaaattga ttttcgagga aaatggttca atcgtaccta gagcttgtaa agatgctttt 2220

tggaatatgt gccatgttct taacttcttt tacgctaatg atgatggctt cactggaaat 2280

acaatattgg atacagttaa agatatcatc tacaacccac ttgttttggt caatgagaac 2340

gaggaacaaa gataa 2355

<210> 46
<211> 784
<212> PRT
<213> Stevia rebaudiana

<400> 46

Met Asn Leu Ser Leu Cys Ile Ala Ser Pro Leu Leu Thr Lys Ser Ser
1 5 10 15

Arg Pro Thr Ala Leu Ser Ala Ile His Thr Ala Ser Thr Ser His Gly
20 25 30

Gly Gln Thr Asn Pro Thr Asn Leu Ile Ile Asp Thr Thr Lys Glu Arg

```
        35                  40                  45

Ile Gln Lys Leu Phe Lys Asn Val Glu Ile Ser Val Ser Ser Tyr Asp
    50                  55                  60

Thr Ala Trp Val Ala Met Val Pro Ser Pro Asn Ser Pro Lys Ser Pro
65                  70                  75                  80

Cys Phe Pro Glu Cys Leu Asn Trp Leu Ile Asn Asn Gln Leu Asn Asp
                85                  90                  95

Gly Ser Trp Gly Leu Val Asn His Thr His Asn His Asn His Pro Leu
            100                 105                 110

Leu Lys Asp Ser Leu Ser Ser Thr Leu Ala Cys Ile Val Ala Leu Lys
        115                 120                 125

Arg Trp Asn Val Gly Glu Asp Gln Ile Asn Lys Gly Leu Ser Phe Ile
    130                 135                 140

Glu Ser Asn Leu Ala Ser Ala Thr Asp Lys Ser Gln Pro Ser Pro Ile
145                 150                 155                 160

Gly Phe Asp Ile Ile Phe Pro Gly Leu Leu Glu Tyr Ala Lys Asn Leu
                165                 170                 175

Asp Ile Asn Leu Leu Ser Lys Gln Thr Asp Phe Ser Leu Met Leu His
            180                 185                 190

Lys Arg Glu Leu Glu Gln Lys Arg Cys His Ser Asn Glu Ile Asp Gly
        195                 200                 205

Tyr Leu Ala Tyr Ile Ser Glu Gly Leu Gly Asn Leu Tyr Asp Trp Asn
    210                 215                 220

Met Val Lys Lys Tyr Gln Met Lys Asn Gly Ser Val Phe Asn Ser Pro
225                 230                 235                 240
```

```
Ser Ala Thr Ala Ala Ala Phe Ile Asn His Gln Asn Pro Gly Cys Leu
                245                 250                 255

Asn Tyr Leu Asn Ser Leu Leu Asp Lys Phe Gly Asn Ala Val Pro Thr
            260                 265                 270

Val Tyr Pro Leu Asp Leu Tyr Ile Arg Leu Ser Met Val Asp Thr Ile
        275                 280                 285

Glu Arg Leu Gly Ile Ser His His Phe Arg Val Glu Ile Lys Asn Val
    290                 295                 300

Leu Asp Glu Thr Tyr Arg Cys Trp Val Glu Arg Asp Glu Gln Ile Phe
305                 310                 315                 320

Met Asp Val Val Thr Cys Ala Leu Ala Phe Arg Leu Leu Arg Ile His
                325                 330                 335

Gly Tyr Lys Val Ser Pro Asp Gln Leu Ala Glu Ile Thr Asn Glu Leu
            340                 345                 350

Ala Phe Lys Asp Glu Tyr Ala Ala Leu Glu Thr Tyr His Ala Ser Gln
        355                 360                 365

Ile Leu Tyr Gln Glu Asp Leu Ser Ser Gly Lys Gln Ile Leu Lys Ser
    370                 375                 380

Ala Asp Phe Leu Lys Gly Ile Leu Ser Thr Asp Ser Asn Arg Leu Ser
385                 390                 395                 400

Lys Leu Ile His Lys Glu Val Glu Asn Ala Leu Lys Phe Pro Ile Asn
                405                 410                 415

Thr Gly Leu Glu Arg Ile Asn Thr Arg Arg Asn Ile Gln Leu Tyr Asn
            420                 425                 430

Val Asp Asn Thr Arg Ile Leu Lys Thr Thr Tyr His Ser Ser Asn Ile
```

```
        435                 440                 445

Ser Asn Thr Tyr Tyr Leu Arg Leu Ala Val Glu Asp Phe Tyr Thr Cys
    450                 455                 460

Gln Ser Ile Tyr Arg Glu Glu Leu Lys Gly Leu Glu Arg Trp Val Val
465                 470                 475                 480

Gln Asn Lys Leu Asp Gln Leu Lys Phe Ala Arg Gln Lys Thr Ala Tyr
                485                 490                 495

Cys Tyr Phe Ser Val Ala Ala Thr Leu Ser Ser Pro Glu Leu Ser Asp
            500                 505                 510

Ala Arg Ile Ser Trp Ala Lys Asn Gly Ile Leu Thr Thr Val Val Asp
        515                 520                 525

Asp Phe Phe Asp Ile Gly Gly Thr Ile Asp Glu Leu Thr Asn Leu Ile
    530                 535                 540

Gln Cys Val Glu Lys Trp Asn Val Asp Val Asp Lys Asp Cys Cys Ser
545                 550                 555                 560

Glu His Val Arg Ile Leu Phe Leu Ala Leu Lys Asp Ala Ile Cys Trp
                565                 570                 575

Ile Gly Asp Glu Ala Phe Lys Trp Gln Ala Arg Asp Val Thr Ser His
            580                 585                 590

Val Ile Gln Thr Trp Leu Glu Leu Met Asn Ser Met Leu Arg Glu Ala
        595                 600                 605

Ile Trp Thr Arg Asp Ala Tyr Val Pro Thr Leu Asn Glu Tyr Met Glu
    610                 615                 620

Asn Ala Tyr Val Ser Phe Ala Leu Gly Pro Ile Val Lys Pro Ala Ile
625                 630                 635                 640
```

Tyr Phe Val Gly Pro Lys Leu Ser Glu Glu Ile Val Glu Ser Ser Glu
645 650 655

Tyr His Asn Leu Phe Lys Leu Met Ser Thr Gln Gly Arg Leu Leu Asn
660 665 670

Asp Ile His Ser Phe Lys Arg Glu Phe Lys Glu Gly Lys Leu Asn Ala
675 680 685

Val Ala Leu His Leu Ser Asn Gly Glu Ser Gly Lys Val Glu Glu Glu
690 695 700

Val Val Glu Glu Met Met Met Met Ile Lys Asn Lys Arg Lys Glu Leu
705 710 715 720

Met Lys Leu Ile Phe Glu Glu Asn Gly Ser Ile Val Pro Arg Ala Cys
725 730 735

Lys Asp Ala Phe Trp Asn Met Cys His Val Leu Asn Phe Phe Tyr Ala
740 745 750

Asn Asp Asp Gly Phe Thr Gly Asn Thr Ile Leu Asp Thr Val Lys Asp
755 760 765

Ile Ile Tyr Asn Pro Leu Val Leu Val Asn Glu Asn Glu Glu Gln Arg
770 775 780

<210> 47
<211> 1773
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized KS

<400> 47
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ttctcatccg gtggccatgc tttgagattc gggagtagtc tgccatgttg gagaaggacc 120

cctacccaaa gatctacttc ttcctctact actagaccag ctgccgaagt gtcatcaggt 180

aagagtaaac aacatgatca ggaagctagt gaagcgacta tcagacaaca attacaactt 240

gtggatgtcc tggagaatat gggaatatcc agacattttg ctgcagagat aaagtgcata 300

ctagacagaa cttacagatc ttggttacaa agacacgagg aaatcatgct ggacactatg 360

acatgtgcta tggcttttag aatcctaaga ttgaacggat acaacgtttc atcagatgaa 420

ctataccacg ttgtagaggc atctggtctg cataattctt tgggtgggta tcttaacgat 480

accagaacac tacttgaatt acacaaggct tcaacagtta gtatctctga ggatgaatct 540

atcttagatt caattggctc tagatccaga acattgctta gagaacaatt ggagtctggt 600

ggcgcactga gaaagccttc tttattcaaa gaggttgaac atgcactgga tggacctttt 660

tacaccacac ttgatagact tcatcatagg tggaatattg aaaacttcaa cattattgag 720

caacacatgt tggagactcc atacttatct aaccagcata catcaaggga tatcctagca 780

ttgtcaatta gagatttttc ctcctcacaa ttcacttatc aacaagagct acagcatctg 840

gagagttggg ttaaggaatg tagattagat caactacagt tcgcaagaca gaaattagcg 900

tacttttacc tatcagccgc aggcaccatg ttttctcctg agctttctga tgcgagaaca 960

ttatgggcca aaaacggggt gttgacaact attgttgatg atttctttga tgttgccggt 1020

tctaaagagg aattggaaaa cttagtcatg ctggtcgaaa tgtgggatga acatcacaaa 1080

gttgaattct attctgagca ggtcgaaatc atcttctctt ccatctacga ttctgtcaac 1140

caattgggtg agaaggcctc tttggttcaa gacagatcaa ttacaaaaca ccttgttgaa 1200

atatggttag acttgttaaa gtccatgatg acggaagttg aatggagact gtcaaaatac 1260

gtgcctacag aaaaggaata catgattaat gcctctctta tcttcggcct aggtccaatc 1320

gttttaccag ctttgtattt cgttggtcca aagatttcag aaagtatagt aaaggaccca 1380

gaatatgatg aattgttcaa actaatgtca acatgtggta gattgttgaa tgacgtgcaa 1440

acgttcgaaa gagaatacaa tgagggtaaa ctgaattctg tcagtctatt ggttcttcac 1500

ggaggcccaa tgtctatttc agacgcaaag aggaaattac aaaagcctat tgatacgtgt 1560

agaagagatc ttctttcttt ggtccttaga gaagagtctg tagtaccaag accatgtaag 1620

gaactattct ggaaaatgtg taaagtgtgc tatttctttt actcaacaac tgatgggttt 1680

tctagtcaag tcgaaagagc aaaagaggta gacgctgtca taaatgagcc actgaagttg 1740

caaggttctc atacactggt atctgatgtt taa 1773

<210> 48
<211> 590
<212> PRT
<213> Zea mays

<400> 48

Met Ala Met Pro Val Lys Leu Thr Pro Ala Ser Leu Ser Leu Lys Ala
1 5 10 15

Val Cys Cys Arg Phe Ser Ser Gly Gly His Ala Leu Arg Phe Gly Ser
20 25 30

Ser Leu Pro Cys Trp Arg Arg Thr Pro Thr Gln Arg Ser Thr Ser Ser
35 40 45

Ser Thr Thr Arg Pro Ala Ala Glu Val Ser Ser Gly Lys Ser Lys Gln
50 55 60

His Asp Gln Glu Ala Ser Glu Ala Thr Ile Arg Gln Gln Leu Gln Leu
65 70 75 80

Val Asp Val Leu Glu Asn Met Gly Ile Ser Arg His Phe Ala Ala Glu
85 90 95

Ile Lys Cys Ile Leu Asp Arg Thr Tyr Arg Ser Trp Leu Gln Arg His
100 105 110

Glu Glu Ile Met Leu Asp Thr Met Thr Cys Ala Met Ala Phe Arg Ile
115 120 125

Leu Arg Leu Asn Gly Tyr Asn Val Ser Ser Asp Glu Leu Tyr His Val
130 135 140

```
Val Glu Ala Ser Gly Leu His Asn Ser Leu Gly Gly Tyr Leu Asn Asp
145                 150                 155                 160

Thr Arg Thr Leu Leu Glu Leu His Lys Ala Ser Thr Val Ser Ile Ser
                165                 170                 175

Glu Asp Glu Ser Ile Leu Asp Ser Ile Gly Ser Arg Ser Arg Thr Leu
            180                 185                 190

Leu Arg Glu Gln Leu Glu Ser Gly Gly Ala Leu Arg Lys Pro Ser Leu
        195                 200                 205

Phe Lys Glu Val Glu His Ala Leu Asp Gly Pro Phe Tyr Thr Thr Leu
    210                 215                 220

Asp Arg Leu His His Arg Trp Asn Ile Glu Asn Phe Asn Ile Ile Glu
225                 230                 235                 240

Gln His Met Leu Glu Thr Pro Tyr Leu Ser Asn Gln His Thr Ser Arg
                245                 250                 255

Asp Ile Leu Ala Leu Ser Ile Arg Asp Phe Ser Ser Ser Gln Phe Thr
            260                 265                 270

Tyr Gln Gln Glu Leu Gln His Leu Glu Ser Trp Val Lys Glu Cys Arg
        275                 280                 285

Leu Asp Gln Leu Gln Phe Ala Arg Gln Lys Leu Ala Tyr Phe Tyr Leu
    290                 295                 300

Ser Ala Ala Gly Thr Met Phe Ser Pro Glu Leu Ser Asp Ala Arg Thr
305                 310                 315                 320

Leu Trp Ala Lys Asn Gly Val Leu Thr Thr Ile Val Asp Asp Phe Phe
                325                 330                 335

Asp Val Ala Gly Ser Lys Glu Glu Leu Glu Asn Leu Val Met Leu Val
            340                 345                 350
```

```
Glu Met Trp Asp Glu His His Lys Val Glu Phe Tyr Ser Glu Gln Val
        355                 360                 365

Glu Ile Ile Phe Ser Ser Ile Tyr Asp Ser Val Asn Gln Leu Gly Glu
    370                 375                 380

Lys Ala Ser Leu Val Gln Asp Arg Ser Ile Thr Lys His Leu Val Glu
385                 390                 395                 400

Ile Trp Leu Asp Leu Leu Lys Ser Met Met Thr Glu Val Glu Trp Arg
                405                 410                 415

Leu Ser Lys Tyr Val Pro Thr Glu Lys Glu Tyr Met Ile Asn Ala Ser
            420                 425                 430

Leu Ile Phe Gly Leu Gly Pro Ile Val Leu Pro Ala Leu Tyr Phe Val
        435                 440                 445

Gly Pro Lys Ile Ser Glu Ser Ile Val Lys Asp Pro Glu Tyr Asp Glu
    450                 455                 460

Leu Phe Lys Leu Met Ser Thr Cys Gly Arg Leu Leu Asn Asp Val Gln
465                 470                 475                 480

Thr Phe Glu Arg Glu Tyr Asn Glu Gly Lys Leu Asn Ser Val Ser Leu
                485                 490                 495

Leu Val Leu His Gly Gly Pro Met Ser Ile Ser Asp Ala Lys Arg Lys
            500                 505                 510

Leu Gln Lys Pro Ile Asp Thr Cys Arg Arg Asp Leu Leu Ser Leu Val
        515                 520                 525

Leu Arg Glu Glu Ser Val Val Pro Arg Pro Cys Lys Glu Leu Phe Trp
    530                 535                 540
```

```
Lys Met Cys Lys Val Cys Tyr Phe Phe Tyr Ser Thr Thr Asp Gly Phe
545                 550                 555                 560


Ser Ser Gln Val Glu Arg Ala Lys Glu Val Asp Ala Val Ile Asn Glu
                565                 570                 575


Pro Leu Lys Leu Gln Gly Ser His Thr Leu Val Ser Asp Val
            580                 585                 590
```

<210> 49
<211> 2232
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized KS

<400> 49

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acaccttgtt ttccagaatg tactaaatgg atcctagaaa atcagttggg tgatggtagt      180

tggtcacttc ctcatggcaa tccacttcta gttaaagatg cattatcttc cactcttgct      240

tgtattctgg ctcttaaaag atggggaatc ggtgaggaac agattaacaa aggactgaga      300

ttcatagaac tcaactctgc tagtgtaacc gataacgaac aacacaaacc aattggattt      360

gacattatct ttccaggtat gattgaatac gctatagact tagacctgaa tctaccacta      420

aaaccaactg acattaactc catgttgcat cgtagagccc ttgaattgac atcaggtgga      480

ggcaaaaatc tagaaggtag aagagcttac ttggcctacg tctctgaagg aatcggtaag      540

ctgcaagatt gggaaatggc tatgaaatac caacgtaaaa acggatctct gttcaatagt      600

ccatcaacaa ctgcagctgc attcatccat atacaagatg ctgaatgcct ccactatatt      660

cgttctcttc tccagaaatt tggaaacgca gtccctacaa tataccctct cgatatctat      720

gccagacttt caatggtaga tgccctggaa cgtcttggta ttgatagaca tttcagaaag      780

gagagaaagt tcgttctgga tgaaacatac agattttggt tgcaaggaga agaggagatt      840

ttctccgata acgcaacctg tgctttggcc ttcagaatat tgagacttaa tggttacgat      900
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gtctctcttg aagatcactt ctctaactct ctgggcggtt acttaaagga ctcaggagca 960

gctttagaac tgtacagagc cctccaattg tcttacccag acgagtccct cctggaaaag 1020

caaaattcta gaacttctta cttcttaaaa caaggtttat ccaatgtctc cctctgtggt 1080

gacagattgc gtaaaaacat aattggagag gtgcatgatg ctttaaactt ttccgaccac 1140

gctaacttac aaagattagc tattcgtaga aggattaagc attacgctac tgacgataca 1200

aggattctaa aaacttccta cagatgctca acaatcggta accaagattt tctaaaactt 1260

gcagtggaag atttcaatat ctgtcaatca atacaaagag aggaattcaa gcatattgaa 1320

agatgggtcg ttgaaagacg tctagacaag ttaaagttcg ctagacaaaa agaggcctat 1380

tgctatttct cagccgcagc aacattgttt gcccctgaat tgtctgatgc tagaatgtct 1440

tgggccaaaa atggtgtatt gacaactgtg gttgatgatt tcttcgatgt cggaggctct 1500

gaagaggaat tagttaactt gatagaattg atcgagcgtt gggatgtgaa tggcagtgca 1560

gatttttgta gtgaggaagt tgagattatc tattctgcta tccactcaac tatctctgaa 1620

ataggtgata agtcatttgg ctggcaaggt agagatgtaa agtctcaagt tatcaagatc 1680

tggctggact tattgaaatc aatgttaact gaagctcaat ggtcttcaaa caagtctgtt 1740

cctaccctag atgagtatat gacaaccgcc catgtttcat tcgcacttgg tccaattgta 1800

cttccagcct tatacttcgt tggcccaaag ttgtcagaag aggttgcagg tcatcctgaa 1860

ctactaaacc tctacaaagt cacatctact tgtggcagac tactgaatga ttggagaagt 1920

tttaagagag aatccgagga aggtaagctc aacgctatta gtttatacat gatccactcc 1980

ggtggtgctt ctacagaaga ggaaacaatc gaacatttca aaggtttgat tgattctcag 2040

agaaggcaac tgttacaatt ggtgttgcaa gagaaggata gtatcatacc tagaccatgt 2100

aaagatctat tttggaatat gattaagtta ttacacactt tctacatgaa agatgatggc 2160

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gatgaattat ga 2232

<210> 50
<211> 775

<212> PRT
<213> Populus trichocarpa

<400> 50

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Met Ser Cys Ile Arg Pro Trp Phe Cys Pro Ser Ser Ile Ser Ala Thr
1               5                   10                  15


Leu Thr Asp Pro Ala Ser Lys Leu Val Thr Gly Glu Phe Lys Thr Thr
            20                  25                  30


Ser Leu Asn Phe His Gly Thr Lys Glu Arg Ile Lys Lys Met Phe Asp
        35                  40                  45


Lys Ile Glu Leu Ser Val Ser Ser Tyr Asp Thr Ala Trp Val Ala Met
    50                  55                  60


Val Pro Ser Pro Asp Cys Pro Glu Thr Pro Cys Phe Pro Glu Cys Thr
65                  70                  75                  80


Lys Trp Ile Leu Glu Asn Gln Leu Gly Asp Gly Ser Trp Ser Leu Pro
                85                  90                  95


His Gly Asn Pro Leu Leu Val Lys Asp Ala Leu Ser Ser Thr Leu Ala
            100                 105                 110


Cys Ile Leu Ala Leu Lys Arg Trp Gly Ile Gly Glu Glu Gln Ile Asn
        115                 120                 125


Lys Gly Leu Arg Phe Ile Glu Leu Asn Ser Ala Ser Val Thr Asp Asn
    130                 135                 140


Glu Gln His Lys Pro Ile Gly Phe Asp Ile Ile Phe Pro Gly Met Ile
145                 150                 155                 160


Glu Tyr Ala Lys Asp Leu Asp Leu Asn Leu Pro Leu Lys Pro Thr Asp
                165                 170                 175


Ile Asn Ser Met Leu His Arg Arg Ala Leu Glu Leu Thr Ser Gly Gly
```

```
            180                 185                 190

Gly Lys Asn Leu Glu Gly Arg Arg Ala Tyr Leu Ala Tyr Val Ser Glu
        195                 200                 205

Gly Ile Gly Lys Leu Gln Asp Trp Glu Met Ala Met Lys Tyr Gln Arg
    210                 215                 220

Lys Asn Gly Ser Leu Phe Asn Ser Pro Ser Thr Thr Ala Ala Ala Phe
225                 230                 235                 240

Ile His Ile Gln Asp Ala Glu Cys Leu His Tyr Ile Arg Ser Leu Leu
                245                 250                 255

Gln Lys Phe Gly Asn Ala Val Pro Thr Ile Tyr Pro Leu Asp Ile Tyr
            260                 265                 270

Ala Arg Leu Ser Met Val Asp Ala Leu Glu Arg Leu Gly Ile Asp Arg
        275                 280                 285

His Phe Arg Lys Glu Arg Lys Phe Val Leu Asp Glu Thr Tyr Arg Phe
    290                 295                 300

Trp Leu Gln Gly Glu Glu Glu Ile Phe Ser Asp Asn Ala Thr Cys Ala
305                 310                 315                 320

Leu Ala Phe Arg Ile Leu Arg Leu Asn Gly Tyr Asp Val Ser Leu Glu
                325                 330                 335

Asp His Phe Ser Asn Ser Leu Gly Gly Tyr Leu Lys Asp Ser Gly Ala
            340                 345                 350

Ala Leu Glu Leu Tyr Arg Ala Leu Gln Leu Ser Tyr Pro Asp Glu Ser
        355                 360                 365

Leu Leu Glu Lys Gln Asn Ser Arg Thr Ser Tyr Phe Leu Lys Gln Gly
    370                 375                 380
```

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Leu Ser Asn Val Ser Leu Cys Gly Asp Arg Leu Arg Lys Asn Ile Ile
385                 390                 395                 400


Gly Glu Val His Asp Ala Leu Asn Phe Pro Asp His Ala Asn Leu Gln
                405                 410                 415


Arg Leu Ala Ile Arg Arg Arg Ile Lys His Tyr Ala Thr Asp Asp Thr
            420                 425                 430


Arg Ile Leu Lys Thr Ser Tyr Arg Cys Ser Thr Ile Gly Asn Gln Asp
        435                 440                 445


Phe Leu Lys Leu Ala Val Glu Asp Phe Asn Ile Cys Gln Ser Ile Gln
    450                 455                 460


Arg Glu Glu Phe Lys His Ile Glu Arg Trp Val Val Glu Arg Arg Leu
465                 470                 475                 480


Asp Lys Leu Lys Phe Ala Arg Gln Lys Glu Ala Tyr Cys Tyr Phe Ser
                485                 490                 495


Ala Ala Ala Thr Leu Phe Ala Pro Glu Leu Ser Asp Ala Arg Met Ser
            500                 505                 510


Trp Ala Lys Asn Gly Val Leu Thr Thr Val Val Asp Asp Phe Phe Asp
        515                 520                 525


Val Gly Gly Ser Glu Glu Glu Leu Val Asn Leu Ile Glu Leu Ile Glu
    530                 535                 540


Arg Trp Asp Val Asn Gly Ser Ala Asp Phe Cys Ser Glu Glu Val Glu
545                 550                 555                 560


Ile Ile Tyr Ser Ala Ile His Ser Thr Ile Ser Glu Ile Gly Asp Lys
                565                 570                 575


Ser Phe Gly Trp Gln Gly Arg Asp Val Lys Ser His Val Ile Lys Ile
```

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            580                 585                 590

Trp Leu Asp Leu Leu Lys Ser Met Leu Thr Glu Ala Gln Trp Ser Ser
        595                 600                 605

Asn Lys Ser Val Pro Thr Leu Asp Glu Tyr Met Thr Thr Ala His Val
    610                 615                 620

Ser Phe Ala Leu Gly Pro Ile Val Leu Pro Ala Leu Tyr Phe Val Gly
625                 630                 635                 640

Pro Lys Leu Ser Glu Glu Val Ala Gly His Pro Glu Leu Leu Asn Leu
                645                 650                 655

Tyr Lys Val Met Ser Thr Cys Gly Arg Leu Leu Asn Asp Trp Arg Ser
            660                 665                 670

Phe Lys Arg Glu Ser Glu Glu Gly Lys Leu Asn Ala Ile Ser Leu Tyr
        675                 680                 685

Met Ile His Ser Gly Gly Ala Ser Thr Glu Glu Glu Thr Ile Glu His
    690                 695                 700

Phe Lys Gly Leu Ile Asp Ser Gln Arg Arg Gln Leu Leu Gln Leu Val
705                 710                 715                 720

Leu Gln Glu Lys Asp Ser Ile Ile Pro Arg Pro Cys Lys Asp Leu Phe
                725                 730                 735

Trp Asn Met Ile Lys Leu Leu His Thr Phe Tyr Met Lys Asp Asp Gly
            740                 745                 750

Phe Thr Ser Asn Glu Met Arg Asn Val Val Lys Ala Ile Ile Asn Glu
        755                 760                 765

Pro Ile Ser Leu Asp Glu Leu
    770                 775
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<210> 51
<211> 2358
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized KS

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aagattagga agatgttgga gaaagtggag ctttctgttt cggcctacga tactagttgg 180

gtagcaatgg ttccatcacc gagctcccaa aatgctccac ttttcccaca gtgtgtgaaa 240

tggttattgg ataatcaaca tgaagatgga tcttggggac ttgataacca tgaccatcaa 300

tctcttaaga aggatgtgtt atcatctaca ctggctagta tcctcgcgtt aaagaagtgg 360

ggaattggtg aaagacaaat aaacaagggt ctccagttta ttgagctgaa ttctgcatta 420

gtcactgatg aaaccataca gaaaccaaca gggtttgata ttatatttcc tgggatgatt 480

aaatatgcta gagatttgaa tctgacgatt ccattgggct cagaagtggt ggatgacatg 540

atacgaaaaa gagatctgga tcttaaatgt gatagtgaaa agttttcaaa gggaagagaa 600

gcatatctgg cctatgtttt agaggggaca agaaacctaa aagattggga tttgatagtc 660

aaatatcaaa ggaaaaatgg gtcactgttt gattctccag ccacaacagc agctgctttt 720

actcagtttg ggaatgatgg ttgtctccgt tatctctgtt ctctccttca gaaattcgag 780

gctgcagttc cttcagttta tccatttgat caatatgcac gccttagtat aattgtcact 840

cttgaaagct taggaattga tagagatttc aaaaccgaaa tcaaaagcat attggatgaa 900

acctatagat attggcttcg tggggatgaa gaaatatgtt tggacttggc cacttgtgct 960

ttggctttcc gattattgct tgctcatggc tatgatgtgt cttacgatcc gctaaaacca 1020

tttgcagaag aatctggttt ctctgatact ttggaaggat atgttaagaa tacgttttct 1080

gtgttagaat tatttaaggc tgctcaaagt tatccacatg aatcagcttt gaagaagcag 1140

tgttgttgga ctaaacaata tctggagatg gaattgtcca gctgggttaa gacctctgtt 1200

cgagataaat acctcaagaa agaggtcgag gatgctcttg cttttccctc ctatgcaagc 1260

ctagaaagat cagatcacag gagaaaaata ctcaatggtt ctgctgtgga aaacaccaga 1320

gttacaaaaa cctcatatcg tttgcacaat atttgcacct ctgatatcct gaagttagct 1380

gtggatgact tcaatttctg ccagtccata caccgtgaag aaatggaacg tcttgatagg 1440

tggattgtgg agaatagatt gcaggaactg aaatttgcca gacagaagct ggcttactgt 1500

tatttctctg gggctgcaac tttattttct ccagaactat ctgatgctcg tatatcgtgg 1560

gccaaaggtg gagtacttac aacggttgta gacgacttct ttgatgttgg agggtccaaa 1620

gaagaactgg aaaacctcat acacttggtc gaaaagtggg atttgaacgg tgttcctgag 1680

tacagctcag aacatgttga gatcatattc tcagttctaa gggacaccat tctcgaaaca 1740

ggagacaaag cattcaccta tcaaggacgc aatgtgacac accacattgt gaaaatttgg 1800

ttggatctgc tcaagtctat gttgagagaa gccgagtggt ccagtgacaa gtcaacacca 1860

agcttggagg attacatgga aaatgcgtac atatcatttg cattaggacc aattgtcctc 1920

ccagctacct atctgatcgg acctccactt ccagagaaga cagtcgatag ccaccaatat 1980

aatcagctct acaagctcgt gagcactatg ggtcgtcttc taaatgacat acaaggtttt 2040

aagagagaaa gcgcggaagg gaagctgaat gcggtttcat tgcacatgaa acacgagaga 2100

gacaatcgca gcaaagaagt gatcatagaa tcgatgaaag gtttagcaga gagaaagagg 2160

gaagaattgc ataagctagt tttggaggag aaaggaagtg tggttccaag ggaatgcaaa 2220

gaagcgttct tgaaaatgag caaagtgttg aacttatttt acaggaagga cgatggattc 2280

acatcaaatg atctgatgag tcttgttaaa tcagtgatct acgagcctgt tagcttacag 2340

aaagaatctt taacttga 2358

<210> 52
<211> 785
<212> PRT
<213> Arabidopsis thaliana

<400> 52

Met Ser Ile Asn Leu Arg Ser Ser Gly Cys Ser Ser Pro Ile Ser Ala
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Thr Leu Glu Arg Gly Leu Asp Ser Glu Val Gln Thr Arg Ala Asn Asn
            20                  25                  30

Val Ser Phe Glu Gln Thr Lys Glu Lys Ile Arg Lys Met Leu Glu Lys
        35                  40                  45

Val Glu Leu Ser Val Ser Ala Tyr Asp Thr Ser Trp Val Ala Met Val
    50                  55                  60

Pro Ser Pro Ser Ser Gln Asn Ala Pro Leu Phe Pro Gln Cys Val Lys
65                  70                  75                  80

Trp Leu Leu Asp Asn Gln His Glu Asp Gly Ser Trp Gly Leu Asp Asn
                85                  90                  95

His Asp His Gln Ser Leu Lys Lys Asp Val Leu Ser Ser Thr Leu Ala
            100                 105                 110

Ser Ile Leu Ala Leu Lys Lys Trp Gly Ile Gly Glu Arg Gln Ile Asn
        115                 120                 125

Lys Gly Leu Gln Phe Ile Glu Leu Asn Ser Ala Leu Val Thr Asp Glu
    130                 135                 140

Thr Ile Gln Lys Pro Thr Gly Phe Asp Ile Ile Phe Pro Gly Met Ile
145                 150                 155                 160

Lys Tyr Ala Arg Asp Leu Asn Leu Thr Ile Pro Leu Gly Ser Glu Val
                165                 170                 175

Val Asp Asp Met Ile Arg Lys Arg Asp Leu Asp Leu Lys Cys Asp Ser
            180                 185                 190

Glu Lys Phe Ser Lys Gly Arg Glu Ala Tyr Leu Ala Tyr Val Leu Glu
        195                 200                 205
```

```
Gly Thr Arg Asn Leu Lys Asp Trp Asp Leu Ile Val Lys Tyr Gln Arg
    210                 215                 220

Lys Asn Gly Ser Leu Phe Asp Ser Pro Ala Thr Thr Ala Ala Ala Phe
225                 230                 235                 240

Thr Gln Phe Gly Asn Asp Gly Cys Leu Arg Tyr Leu Cys Ser Leu Leu
                245                 250                 255

Gln Lys Phe Glu Ala Ala Val Pro Ser Val Tyr Pro Phe Asp Gln Tyr
            260                 265                 270

Ala Arg Leu Ser Ile Ile Val Thr Leu Glu Ser Leu Gly Ile Asp Arg
        275                 280                 285

Asp Phe Lys Thr Glu Ile Lys Ser Ile Leu Asp Glu Thr Tyr Arg Tyr
    290                 295                 300

Trp Leu Arg Gly Asp Glu Glu Ile Cys Leu Asp Leu Ala Thr Cys Ala
305                 310                 315                 320

Leu Ala Phe Arg Leu Leu Leu Ala His Gly Tyr Asp Val Ser Tyr Asp
                325                 330                 335

Pro Leu Lys Pro Phe Ala Glu Glu Ser Gly Phe Ser Asp Thr Leu Glu
            340                 345                 350

Gly Tyr Val Lys Asn Thr Phe Ser Val Leu Glu Leu Phe Lys Ala Ala
        355                 360                 365

Gln Ser Tyr Pro His Glu Ser Ala Leu Lys Lys Gln Cys Cys Trp Thr
    370                 375                 380

Lys Gln Tyr Leu Glu Met Glu Leu Ser Ser Trp Val Lys Thr Ser Val
385                 390                 395                 400

Arg Asp Lys Tyr Leu Lys Lys Glu Val Glu Asp Ala Leu Ala Phe Pro
                405                 410                 415
```

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Ser Tyr Ala Ser Leu Glu Arg Ser Asp His Arg Arg Lys Ile Leu Asn
            420                 425                 430

Gly Ser Ala Val Glu Asn Thr Arg Val Thr Lys Thr Ser Tyr Arg Leu
        435                 440                 445

His Asn Ile Cys Thr Ser Asp Ile Leu Lys Leu Ala Val Asp Asp Phe
    450                 455                 460

Asn Phe Cys Gln Ser Ile His Arg Glu Glu Met Glu Arg Leu Asp Arg
465                 470                 475                 480

Trp Ile Val Glu Asn Arg Leu Gln Glu Leu Lys Phe Ala Arg Gln Lys
                485                 490                 495

Leu Ala Tyr Cys Tyr Phe Ser Gly Ala Ala Thr Leu Phe Ser Pro Glu
            500                 505                 510

Leu Ser Asp Ala Arg Ile Ser Trp Ala Lys Gly Gly Val Leu Thr Thr
        515                 520                 525

Val Val Asp Asp Phe Phe Asp Val Gly Gly Ser Lys Glu Glu Leu Glu
    530                 535                 540

Asn Leu Ile His Leu Val Glu Lys Trp Asp Leu Asn Gly Val Pro Glu
545                 550                 555                 560

Tyr Ser Ser Glu His Val Glu Ile Ile Phe Ser Val Leu Arg Asp Thr
                565                 570                 575

Ile Leu Glu Thr Gly Asp Lys Ala Phe Thr Tyr Gln Gly Arg Asn Val
            580                 585                 590

Thr His His Ile Val Lys Ile Trp Leu Asp Leu Leu Lys Ser Met Leu
        595                 600                 605
```

```
Arg Glu Ala Glu Trp Ser Ser Asp Lys Ser Thr Pro Ser Leu Glu Asp
    610                 615                 620

Tyr Met Glu Asn Ala Tyr Ile Ser Phe Ala Leu Gly Pro Ile Val Leu
625                 630                 635                 640

Pro Ala Thr Tyr Leu Ile Gly Pro Pro Leu Pro Glu Lys Thr Val Asp
                645                 650                 655

Ser His Gln Tyr Asn Gln Leu Tyr Lys Leu Val Ser Thr Met Gly Arg
            660                 665                 670

Leu Leu Asn Asp Ile Gln Gly Phe Lys Arg Glu Ser Ala Glu Gly Lys
        675                 680                 685

Leu Asn Ala Val Ser Leu His Met Lys His Glu Arg Asp Asn Arg Ser
    690                 695                 700

Lys Glu Val Ile Ile Glu Ser Met Lys Gly Leu Ala Glu Arg Lys Arg
705                 710                 715                 720

Glu Glu Leu His Lys Leu Val Leu Glu Glu Lys Gly Ser Val Val Pro
                725                 730                 735

Arg Glu Cys Lys Glu Ala Phe Leu Lys Met Ser Lys Val Leu Asn Leu
            740                 745                 750

Phe Tyr Arg Lys Asp Asp Gly Phe Thr Ser Asn Asp Leu Met Ser Leu
        755                 760                 765

Val Lys Ser Val Ile Tyr Glu Pro Val Ser Leu Gln Lys Glu Ser Leu
    770                 775                 780

Thr
785
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<211> 2952

<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized CDPS-KS

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gattatgatg acagatacgg cttcggtact atgtcatgtg ctgcttatga tacagcctgg 120

gtgtctttag ttacaaaaac agtcgatggg agaaaacaat ggcttttccc agagtgtttt 180

gaatttctac tagaaacaca atctgatgcc ggaggatggg aaatcgggaa ttcagcacca 240

atcgacggta tattgaatac agctgcatcc ttacttgctc taaaacgtca cgttcaaact 300

gagcaaatca tccaacctca acatgaccat aaggatctag caggtagagc tgaacgtgcc 360

gctgcatctt tgagagcaca attggctgca ttggatgtgt ctacaactga acacgtcggt 420

tttgagataa ttgttcctgc aatgctagac ccattagaag ccgaagatcc atctctagtt 480

ttcgattttc cagctaggaa acctttgatg aagattcatg atgctaagat gagtagattc 540

aggccagaat acttgtatgg caaacaacca atgaccgcct tacattcatt agaggctttc 600

ataggcaaaa tcgacttcga taaggtaaga caccaccgta cccatgggtc tatgatgggt 660

tctccttcat ctaccgcagc ctacttaatg cacgcttcac aatgggatgg tgactcagag 720

gcttacctta gacacgtgat taaacacgca gcagggcagg gaactggtgc tgtaccatct 780

gctttcccat caacacattt tgagtcatct tggattctta ccacattgtt tagagctgga 840

ttttcagctt ctcatcttgc ctgtgatgag ttgaacaagt tggtcgagat acttgagggc 900

tcattcgaga aggaaggtgg ggcaatcggt tacgctccag ggtttcaagc agatgttgat 960

gatactgcta aaacaataag tacattagca gtccttggaa gagatgctac accaagacaa 1020

atgatcaagg tatttgaagc taatacacat tttagaacat accctggtga aagagatcct 1080

tctttgacag ctaattgtaa tgctctatca gccttactac accaaccaga tgcagcaatg 1140

tatggatctc aaattcaaaa gattaccaaa tttgtctgtg actattggtg gaagtctgat 1200

ggtaagatta aagataagtg gaacacttgc tacttgtacc catctgtctt attagttgag 1260

gttttggttg atcttgttag tttattggag cagggtaaat tgcctgatgt tttggatcaa 1320

gagcttcaat acagagtcgc catcacattg ttccaagcat gtttaaggcc attactagac 1380

caagatgccg aaggatcatg gaacaagtct atcgaagcca cagcctacgg catccttatc 1440

ctaactgaag ctaggagagt ttgtttcttc gacagattgt ctgagccatt gaatgaggca 1500

atccgtagag gtatcgcttt cgccgactct atgtctggaa ctgaagctca gttgaactac 1560

atttggatcg aaaaggttag ttacgcacct gcattattga ctaaatccta tttgttagca 1620

gcaagatggg ctgctaagtc tcctttaggc gcttccgtag gctcttcttt gtggactcca 1680

ccaagagaag gattggataa gcatgtcaga ttattccatc aagctgagtt attcagatcc 1740

cttccagaat gggaattaag agcctccatg attgaagcag ctttgttcac accacttcta 1800

agagcacata gactagacgt tttccctaga caagatgtag gtgaagacaa atatcttgat 1860

gtagttccat tcttttggac tgccgctaac aacagagata gaacttacgc ttccactcta 1920

ttcctttacg atatgtgttt tatcgcaatg ttaaacttcc agttagacga attcatggag 1980

gccacagccg gtatcttatt cagagatcat atggatgatt tgaggcaatt gattcatgat 2040

cttttggcag agaaaacttc cccaaagagt tctggtagaa gtagtcaggg cacaaaagat 2100

gctgactcag gtatagagga agacgtgtca atgtccgatt cagcttcaga ttcccaggat 2160

agaagtccag aatacgactt ggttttcagt gcattgagta cctttacaaa acatgtcttg 2220

caacacccat ctatacaaag tgcctctgta tgggatagaa aactacttgc tagagagatg 2280

aaggcttact tacttgctca tatccaacaa gcagaagatt caactccatt gtctgaattg 2340

aaagatgtgc ctcaaaagac tgatgtaaca agagtttcta catctactac taccttcttt 2400

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agggatattt ccgctcgtat tcctaaaaac gaggttgaga aaaagagaaa attggatgat 2940

gctttcaatt ga 2952

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<211> 983
<212> PRT
<213> Phomopsis amygdali

<400> 54

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Arg Thr Leu Gln Asp Tyr Asp Asp Arg Tyr Gly Phe Gly Thr Met Ser
20 25 30

Cys Ala Ala Tyr Asp Thr Ala Trp Val Ser Leu Val Thr Lys Thr Val
35 40 45

Asp Gly Arg Lys Gln Trp Leu Phe Pro Glu Cys Phe Glu Phe Leu Leu
50 55 60

Glu Thr Gln Ser Asp Ala Gly Gly Trp Glu Ile Gly Asn Ser Ala Pro
65 70 75 80

Ile Asp Gly Ile Leu Asn Thr Ala Ala Ser Leu Leu Ala Leu Lys Arg
85 90 95

His Val Gln Thr Glu Gln Ile Ile Gln Pro Gln His Asp His Lys Asp
100 105 110

Leu Ala Gly Arg Ala Glu Arg Ala Ala Ala Ser Leu Arg Ala Gln Leu
115 120 125

Ala Ala Leu Asp Val Ser Thr Thr Glu His Val Gly Phe Glu Ile Ile
130 135 140

```
Val Pro Ala Met Leu Asp Pro Leu Glu Ala Glu Asp Pro Ser Leu Val
145                 150                 155                 160

Phe Asp Phe Pro Ala Arg Lys Pro Leu Met Lys Ile His Asp Ala Lys
                165                 170                 175

Met Ser Arg Phe Arg Pro Glu Tyr Leu Tyr Gly Lys Gln Pro Met Thr
            180                 185                 190

Ala Leu His Ser Leu Glu Ala Phe Ile Gly Lys Ile Asp Phe Asp Lys
        195                 200                 205

Val Arg His His Arg Thr His Gly Ser Met Met Gly Ser Pro Ser Ser
    210                 215                 220

Thr Ala Ala Tyr Leu Met His Ala Ser Gln Trp Asp Gly Asp Ser Glu
225                 230                 235                 240

Ala Tyr Leu Arg His Val Ile Lys His Ala Ala Gly Gln Gly Thr Gly
                245                 250                 255

Ala Val Pro Ser Ala Phe Pro Ser Thr His Phe Glu Ser Ser Trp Ile
            260                 265                 270

Leu Thr Thr Leu Phe Arg Ala Gly Phe Ser Ala Ser His Leu Ala Cys
        275                 280                 285

Asp Glu Leu Asn Lys Leu Val Glu Ile Leu Glu Gly Ser Phe Glu Lys
    290                 295                 300

Glu Gly Gly Ala Ile Gly Tyr Ala Pro Gly Phe Gln Ala Asp Val Asp
305                 310                 315                 320

Asp Thr Ala Lys Thr Ile Ser Thr Leu Ala Val Leu Gly Arg Asp Ala
                325                 330                 335

Thr Pro Arg Gln Met Ile Lys Val Phe Glu Ala Asn Thr His Phe Arg
```

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            340                 345                 350

Thr Tyr Pro Gly Glu Arg Asp Pro Ser Leu Thr Ala Asn Cys Asn Ala
        355                 360                 365

Leu Ser Ala Leu Leu His Gln Pro Asp Ala Ala Met Tyr Gly Ser Gln
    370                 375                 380

Ile Gln Lys Ile Thr Lys Phe Val Cys Asp Tyr Trp Trp Lys Ser Asp
385                 390                 395                 400

Gly Lys Ile Lys Asp Lys Trp Asn Thr Cys Tyr Leu Tyr Pro Ser Val
                405                 410                 415

Leu Leu Val Glu Val Leu Val Asp Leu Val Ser Leu Leu Glu Gln Gly
            420                 425                 430

Lys Leu Pro Asp Val Leu Asp Gln Glu Leu Gln Tyr Arg Val Ala Ile
        435                 440                 445

Thr Leu Phe Gln Ala Cys Leu Arg Pro Leu Leu Asp Gln Asp Ala Glu
    450                 455                 460

Gly Ser Trp Asn Lys Ser Ile Glu Ala Thr Ala Tyr Gly Ile Leu Ile
465                 470                 475                 480

Leu Thr Glu Ala Arg Arg Val Cys Phe Phe Asp Arg Leu Ser Glu Pro
                485                 490                 495

Leu Asn Glu Ala Ile Arg Arg Gly Ile Ala Phe Ala Asp Ser Met Ser
            500                 505                 510

Gly Thr Glu Ala Gln Leu Asn Tyr Ile Trp Ile Glu Lys Val Ser Tyr
        515                 520                 525

Ala Pro Ala Leu Leu Thr Lys Ser Tyr Leu Leu Ala Ala Arg Trp Ala
    530                 535                 540
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```
Ala Lys Ser Pro Leu Gly Ala Ser Val Gly Ser Ser Leu Trp Thr Pro
545                 550                 555                 560

Pro Arg Glu Gly Leu Asp Lys His Val Arg Leu Phe His Gln Ala Glu
                565                 570                 575

Leu Phe Arg Ser Leu Pro Glu Trp Glu Leu Arg Ala Ser Met Ile Glu
            580                 585                 590

Ala Ala Leu Phe Thr Pro Leu Leu Arg Ala His Arg Leu Asp Val Phe
        595                 600                 605

Pro Arg Gln Asp Val Gly Glu Asp Lys Tyr Leu Asp Val Val Pro Phe
    610                 615                 620

Phe Trp Thr Ala Ala Asn Asn Arg Asp Arg Thr Tyr Ala Ser Thr Leu
625                 630                 635                 640

Phe Leu Tyr Asp Met Cys Phe Ile Ala Met Leu Asn Phe Gln Leu Asp
                645                 650                 655

Glu Phe Met Glu Ala Thr Ala Gly Ile Leu Phe Arg Asp His Met Asp
            660                 665                 670

Asp Leu Arg Gln Leu Ile His Asp Leu Leu Ala Glu Lys Thr Ser Pro
        675                 680                 685

Lys Ser Ser Gly Arg Ser Ser Gln Gly Thr Lys Asp Ala Asp Ser Gly
    690                 695                 700

Ile Glu Glu Asp Val Ser Met Ser Asp Ser Ala Ser Asp Ser Gln Asp
705                 710                 715                 720

Arg Ser Pro Glu Tyr Asp Leu Val Phe Ser Ala Leu Ser Thr Phe Thr
                725                 730                 735

Lys His Val Leu Gln His Pro Ser Ile Gln Ser Ala Ser Val Trp Asp
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            740                 745                 750

Arg Lys Leu Leu Ala Arg Glu Met Lys Ala Tyr Leu Leu Ala His Ile
        755                 760                 765

Gln Gln Ala Glu Asp Ser Thr Pro Leu Ser Glu Leu Lys Asp Val Pro
    770                 775                 780

Gln Lys Thr Asp Val Thr Arg Val Ser Thr Ser Thr Thr Thr Phe Phe
785                 790                 795                 800

Asn Trp Val Arg Thr Thr Ser Ala Asp His Ile Ser Cys Pro Tyr Ser
                805                 810                 815

Phe His Phe Val Ala Cys His Leu Gly Ala Ala Leu Ser Pro Lys Gly
            820                 825                 830

Ser Asn Gly Asp Cys Tyr Pro Ser Ala Gly Glu Lys Phe Leu Ala Ala
        835                 840                 845

Ala Val Cys Arg His Leu Ala Thr Met Cys Arg Met Tyr Asn Asp Leu
    850                 855                 860

Gly Ser Ala Glu Arg Asp Ser Asp Glu Gly Asn Leu Asn Ser Leu Asp
865                 870                 875                 880

Phe Pro Glu Phe Ala Asp Ser Ala Gly Asn Gly Gly Ile Glu Ile Gln
                885                 890                 895

Lys Ala Ala Leu Leu Arg Leu Ala Glu Phe Glu Arg Asp Ser Tyr Leu
            900                 905                 910

Glu Ala Phe Arg Arg Leu Gln Asp Glu Ser Asn Arg Val His Gly Pro
        915                 920                 925

Ala Gly Gly Asp Glu Ala Arg Leu Ser Arg Arg Arg Met Ala Ile Leu
    930                 935                 940
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Glu Phe Phe Ala Gln Gln Val Asp Leu Tyr Gly Gln Val Tyr Val Ile
945 950 955 960

Arg Asp Ile Ser Ala Arg Ile Pro Lys Asn Glu Val Glu Lys Lys Arg
965 970 975

Lys Leu Asp Asp Ala Phe Asn
980

<210> 55
<211> 2646
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized CDPS-KS

<400> 55
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caatgcttga aaaagaggag atgccttagg ccaaccgaat ccgtactaga atcatctcct 180

ggctctggtt catatagaat agtaactggc ccttctggaa ttaaccctag ttctaacggg 240

cacttgcaag agggttcctt gactcacagg ttaccaatac caatggaaaa atctatcgat 300

aacttccaat ctactctata tgtgtcagat atttggtctg aaacactaca gagaactgaa 360

tgtttgctac aagtaactga aaacgtccag atgaatgagt ggattgagga aattagaatg 420

tactttagaa atatgacttt aggtgaaatt tccatgtccc cttacgacac tgcttgggtg 480

gctagagttc cagcgttgga cggttctcat gggcctcaat tccacagatc tttgcaatgg 540

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gatagagttt gtaatacttt agcctgtgtg attgcgttga aaacatgggg tgttggggca 660

caaaacgttg aaagaggaat tcagttccta caatctaaca tatacaagat ggaggaagat 720

gacgctaatc atatgccaat aggattcgaa atcgtattcc ctgctatgat ggaagatgcc 780

aaagcattag gtttggattt gccatacgat gctactattt tgcaacagat ttcagccgaa 840

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cttcactcct tagaaggctt gcatagagaa gttgattgga ataagttgtt acaattacaa 960

tctgaaaatg gtagttttct ttattcacct gcttcaaccg catgcgcctt aatgtacact 1020

aaggacgtta aatgttttga ttacttaaac cagttgttga tcaagttcga ccacgcatgc 1080

ccaaatgtat atccagtcga tctattcgaa agattatgga tggttgacag attgcagaga 1140

ttagggatct ccagatactt tgaaagagag attagagatt gtttacaata cgtctacaga 1200

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aaaaaggcta gaaccttctc tagaaacttc ttgagaacaa agcatgagaa caacgaatgt 1500

ttcgataaat ggatcattac taaagatttg gctggtgaag tcgagtataa cttgaccttc 1560

ccatggtatg cctctttgcc tagattagaa cataggacat acttagatca atatggaatc 1620

gatgatatct ggataggcaa atctttatac aaaatgcctg ctgttaccaa cgaagttttc 1680

ctaaagttgg caaaggcaga ctttaacatg tgtcaagctc tacacaaaaa ggaattggaa 1740

caagtgataa agtggaacgc gtcctgtcaa ttcagagatc ttgaattcgc cagacaaaaa 1800

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agattagtct gggcaagatg ttgtgtattg acaactgtct tagacgatta ctttgaccac 1920

gggacacctg ttgaggaact tagagtgttt gttcaagctg tcagaacatg gaatccagag 1980

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cactattggg acaagttgat aacaagtgcc ctaaaggagg ccgaatgggc agagtcaggt 2160

tacgtcccaa catttgatga atacatggaa gtagctgaaa tttctgttgc tctagaacca 2220

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tacgattacc atctagttat gcatttggta aacagagtcg gtagaatctt gaatgatata 2340

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gaacatccat ctgttccatc tgaggccatg gcgatcgctc atcttcaaga gttagttgat 2460

aattcaatgc agcaattgac atacgaagtt cttaggttca ctgcggttcc aaaaagttgt 2520

aagagaatcc acttgaatat ggctaaaatc atgcatgcct tctacaagga tactgatgga 2580

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<211> 881
<212> PRT
<213> Physcomitrella patens

<400> 56

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20 25 30

Gly Thr Arg Thr Pro Ala Ala Val Gln Cys Leu Lys Lys Arg Arg Cys
35 40 45

Leu Arg Pro Thr Glu Ser Val Leu Glu Ser Ser Pro Gly Ser Gly Ser
50 55 60

Tyr Arg Ile Val Thr Gly Pro Ser Gly Ile Asn Pro Ser Ser Asn Gly
65 70 75 80

His Leu Gln Glu Gly Ser Leu Thr His Arg Leu Pro Ile Pro Met Glu
85 90 95

Lys Ser Ile Asp Asn Phe Gln Ser Thr Leu Tyr Val Ser Asp Ile Trp
100 105 110

Ser Glu Thr Leu Gln Arg Thr Glu Cys Leu Leu Gln Val Thr Glu Asn
115 120 125

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Val Gln Met Asn Glu Trp Ile Glu Glu Ile Arg Met Tyr Phe Arg Asn
    130                 135                 140

Met Thr Leu Gly Glu Ile Ser Met Ser Pro Tyr Asp Thr Ala Trp Val
145                 150                 155                 160

Ala Arg Val Pro Ala Leu Asp Gly Ser His Gly Pro Gln Phe His Arg
                165                 170                 175

Ser Leu Gln Trp Ile Ile Asp Asn Gln Leu Pro Asp Gly Asp Trp Gly
            180                 185                 190

Glu Pro Ser Leu Phe Leu Gly Tyr Asp Arg Val Cys Asn Thr Leu Ala
        195                 200                 205

Cys Val Ile Ala Leu Lys Thr Trp Gly Val Gly Ala Gln Asn Val Glu
    210                 215                 220

Arg Gly Ile Gln Phe Leu Gln Ser Asn Ile Tyr Lys Met Glu Glu Asp
225                 230                 235                 240

Asp Ala Asn His Met Pro Ile Gly Phe Glu Ile Val Phe Pro Ala Met
                245                 250                 255

Met Glu Asp Ala Lys Ala Leu Gly Leu Asp Leu Pro Tyr Asp Ala Thr
            260                 265                 270

Ile Leu Gln Gln Ile Ser Ala Glu Arg Glu Lys Lys Met Lys Lys Ile
        275                 280                 285

Pro Met Ala Met Val Tyr Lys Tyr Pro Thr Thr Leu Leu His Ser Leu
    290                 295                 300

Glu Gly Leu His Arg Glu Val Asp Trp Asn Lys Leu Leu Gln Leu Gln
305                 310                 315                 320
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Ser Glu Asn Gly Ser Phe Leu Tyr Ser Pro Ala Ser Thr Ala Cys Ala
                325                 330                 335

Leu Met Tyr Thr Lys Asp Val Lys Cys Phe Asp Tyr Leu Asn Gln Leu
            340                 345                 350

Leu Ile Lys Phe Asp His Ala Cys Pro Asn Val Tyr Pro Val Asp Leu
        355                 360                 365

Phe Glu Arg Leu Trp Met Val Asp Arg Leu Gln Arg Leu Gly Ile Ser
    370                 375                 380

Arg Tyr Phe Glu Arg Glu Ile Arg Asp Cys Leu Gln Tyr Val Tyr Arg
385                 390                 395                 400

Tyr Trp Lys Asp Cys Gly Ile Gly Trp Ala Ser Asn Ser Ser Val Gln
                405                 410                 415

Asp Val Asp Asp Thr Ala Met Ala Phe Arg Leu Leu Arg Thr His Gly
            420                 425                 430

Phe Asp Val Lys Glu Asp Cys Phe Arg Gln Phe Phe Lys Asp Gly Glu
        435                 440                 445

Phe Phe Cys Phe Ala Gly Gln Ser Ser Gln Ala Val Thr Gly Met Phe
    450                 455                 460

Asn Leu Ser Arg Ala Ser Gln Thr Leu Phe Pro Gly Glu Ser Leu Leu
465                 470                 475                 480

Lys Lys Ala Arg Thr Phe Ser Arg Asn Phe Leu Arg Thr Lys His Glu
                485                 490                 495

Asn Asn Glu Cys Phe Asp Lys Trp Ile Ile Thr Lys Asp Leu Ala Gly
            500                 505                 510

Glu Val Glu Tyr Asn Leu Thr Phe Pro Trp Tyr Ala Ser Leu Pro Arg
        515                 520                 525
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Leu Glu His Arg Thr Tyr Leu Asp Gln Tyr Gly Ile Asp Asp Ile Trp
    530                 535                 540

Ile Gly Lys Ser Leu Tyr Lys Met Pro Ala Val Thr Asn Glu Val Phe
545                 550                 555                 560

Leu Lys Leu Ala Lys Ala Asp Phe Asn Met Cys Gln Ala Leu His Lys
                565                 570                 575

Lys Glu Leu Glu Gln Val Ile Lys Trp Asn Ala Ser Cys Gln Phe Arg
            580                 585                 590

Asp Leu Glu Phe Ala Arg Gln Lys Ser Val Glu Cys Tyr Phe Ala Gly
        595                 600                 605

Ala Ala Thr Met Phe Glu Pro Glu Met Val Gln Ala Arg Leu Val Trp
    610                 615                 620

Ala Arg Cys Cys Val Leu Thr Thr Val Leu Asp Asp Tyr Phe Asp His
625                 630                 635                 640

Gly Thr Pro Val Glu Glu Leu Arg Val Phe Val Gln Ala Val Arg Thr
                645                 650                 655

Trp Asn Pro Glu Leu Ile Asn Gly Leu Pro Glu Gln Ala Lys Ile Leu
            660                 665                 670

Phe Met Gly Leu Tyr Lys Thr Val Asn Thr Ile Ala Glu Glu Ala Phe
        675                 680                 685

Met Ala Gln Lys Arg Asp Val His His His Leu Lys His Tyr Trp Asp
    690                 695                 700

Lys Leu Ile Thr Ser Ala Leu Lys Glu Ala Glu Trp Ala Glu Ser Gly
705                 710                 715                 720
```

```
Tyr Val Pro Thr Phe Asp Glu Tyr Met Glu Val Ala Glu Ile Ser Val
                725                 730                 735

Ala Leu Glu Pro Ile Val Cys Ser Thr Leu Phe Phe Ala Gly His Arg
            740                 745                 750

Leu Asp Glu Asp Val Leu Asp Ser Tyr Asp Tyr His Leu Val Met His
        755                 760                 765

Leu Val Asn Arg Val Gly Arg Ile Leu Asn Asp Ile Gln Gly Met Lys
    770                 775                 780

Arg Glu Ala Ser Gln Gly Lys Ile Ser Ser Val Gln Ile Tyr Met Glu
785                 790                 795                 800

Glu His Pro Ser Val Pro Ser Glu Ala Met Ala Ile Ala His Leu Gln
                805                 810                 815

Glu Leu Val Asp Asn Ser Met Gln Gln Leu Thr Tyr Glu Val Leu Arg
            820                 825                 830

Phe Thr Ala Val Pro Lys Ser Cys Lys Arg Ile His Leu Asn Met Ala
        835                 840                 845

Lys Ile Met His Ala Phe Tyr Lys Asp Thr Asp Gly Phe Ser Ser Leu
    850                 855                 860

Thr Ala Met Thr Gly Phe Val Lys Lys Val Leu Phe Glu Pro Val Pro
865                 870                 875                 880

Glu
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<211> 2859
<212> DNA
<213> Artificial Sequence

<220>

<223> Codon-optimized CDPS-KS

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tctgctgcta agagtttact agatcgagct ttcaaaagtc atcattccta ctacggatta 120

tgctcaactt catgtcaagt ttatgataca gcttgggttg caatgattcc aaaaacaaga 180

gataatgtaa aacagtggtt gtttccagaa tgtttccatt acctcttaaa aacacaagcc 240

gcagatggct catggggttc attgcctaca acacagacag cgggtatcct agatacagcc 300

tcagctgtgc tggcattatt gtgccacgca caagagcctt tacaaatatt ggatgtatct 360

ccagatgaaa tggggttgag aatagaacac ggtgtcacat ccttgaaacg tcaattagca 420

gtttggaatg atgtggagga caccaaccat attggcgtcg agtttatcat accagcctta 480

ctttccatgc tagaaaagga attagatgtt ccatcttttg aatttccatg taggtccatc 540

ttagagagaa tgcacgggga gaaattaggt catttcgacc tggaacaagt ttacggcaag 600

ccaagctcat tgttgcactc attggaagca tttctcggta agctagattt tgatcgacta 660

tcacatcacc tataccacgg cagtatgatg gcatctccat cttcaacggc tgcttatctt 720

attggggcta caaaatggga tgacgaagcc gaagattacc taagacatgt aatgcgtaat 780

ggtgcaggac atgggaatgg aggtatttct ggtacatttc caactactca tttcgaatgt 840

agctggatta tagcaacgtt gttaaaggtt ggctttactt tgaagcaaat tgacggcgat 900

ggcttaagag gtttatcaac catcttactt gaggcgcttc gtgatgagaa tggtgtcata 960

ggctttgccc ctagaacagc agatgtagat gacacagcca aagctctatt ggccttgtca 1020

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tttaccactt ttggttcaga aagagatcca tcattgactt ccaacctgca cgtcctttta 1140

tctttactta aacaatctaa cttgtctcaa taccatcctc aaatcctcaa aacaacatta 1200

ttcacttgta gatggtggtg gggttccgat cattgtgtca aagacaaatg gaatttgagt 1260

cacctatatc caactatgtt gttggttgaa gccttcactg aagtgctcca tctcattgac 1320

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agagaacaga cgtgttacgc aatattggct ttagttcaag cgagacatgt atgctttttc 1500

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gataatatca aggtggacga agataagtac ttgtctatta tcccattcac atgggtcgga 1920

tgcaataata ggtctagaac tttcgcaagt aacagatggc tatacgatat gatgtacctt 1980

tcattactcg gctatcaaac cgacgagtac atggaagctg tagctgggcc agtgtttggg 2040

gatgtttcct tgttacatca aacaattgat aaggtgattg ataatacaat gggtaacctt 2100

gcgagagcca atggaacagt acacagtggt aatggacatc agcacgaatc tcctaatata 2160

ggtcaagtcg aggacacctt gactcgtttc acaaattcag tcttgaatca caaagacgtc 2220

cttaactcta gctcatctga tcaagatact ttgagaagag agtttagaac attcatgcac 2280

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aatgttaata gtattcattt tcctgagttt actctctgta acggaacttc tcaaaaccta 2640

gatgaaagga aggaaagact tctgaaaatc gcaacttacg aacaagggta tttggataga 2700

gcactagagg ccttggaaag acagagtaga gatgatgccg gagacagagc tggatctaaa 2760

gatatgagaa agttgaaaat cgttaagtta ttctgtgatg ttacggactt atacgatcag 2820

ctctacgtta tcaaagattt gtcatcctct atgaagtaa 2859

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<211> 952
<212> PRT
<213> Gibberella fujikuroi

<400> 58

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Asn Asp Phe Val Ser Ala Ala Lys Ser Leu Leu Asp Arg Ala Phe Lys
            20                  25                  30


Ser His His Ser Tyr Tyr Gly Leu Cys Ser Thr Ser Cys Gln Val Tyr
        35                  40                  45


Asp Thr Ala Trp Val Ala Met Ile Pro Lys Thr Arg Asp Asn Val Lys
    50                  55                  60


Gln Trp Leu Phe Pro Glu Cys Phe His Tyr Leu Leu Lys Thr Gln Ala
65                  70                  75                  80


Ala Asp Gly Ser Trp Gly Ser Leu Pro Thr Thr Gln Thr Ala Gly Ile
                85                  90                  95


Leu Asp Thr Ala Ser Ala Val Leu Ala Leu Leu Cys His Ala Gln Glu
            100                 105                 110


Pro Leu Gln Ile Leu Asp Val Ser Pro Asp Glu Met Gly Leu Arg Ile
        115                 120                 125


Glu His Gly Val Thr Ser Leu Lys Arg Gln Leu Ala Val Trp Asn Asp
    130                 135                 140


Val Glu Asp Thr Asn His Ile Gly Val Glu Phe Ile Ile Pro Ala Leu
145                 150                 155                 160


Leu Ser Met Leu Glu Lys Glu Leu Asp Val Pro Ser Phe Glu Phe Pro
                165                 170                 175
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Cys Arg Ser Ile Leu Glu Arg Met His Gly Glu Lys Leu Gly His Phe
            180                 185                 190

Asp Leu Glu Gln Val Tyr Gly Lys Pro Ser Ser Leu Leu His Ser Leu
        195                 200                 205

Glu Ala Phe Leu Gly Lys Leu Asp Phe Asp Arg Leu Ser His His Leu
    210                 215                 220

Tyr His Gly Ser Met Met Ala Ser Pro Ser Ser Thr Ala Ala Tyr Leu
225                 230                 235                 240

Ile Gly Ala Thr Lys Trp Asp Asp Glu Ala Glu Asp Tyr Leu Arg His
                245                 250                 255

Val Met Arg Asn Gly Ala Gly His Gly Asn Gly Gly Ile Ser Gly Thr
            260                 265                 270

Phe Pro Thr Thr His Phe Glu Cys Ser Trp Ile Ile Ala Thr Leu Leu
        275                 280                 285

Lys Val Gly Phe Thr Leu Lys Gln Ile Asp Gly Asp Gly Leu Arg Gly
    290                 295                 300

Leu Ser Thr Ile Leu Leu Glu Ala Leu Arg Asp Glu Asn Gly Val Ile
305                 310                 315                 320

Gly Phe Ala Pro Arg Thr Ala Asp Val Asp Asp Thr Ala Lys Ala Leu
                325                 330                 335

Leu Ala Leu Ser Leu Val Asn Gln Pro Val Ser Pro Asp Ile Met Ile
            340                 345                 350

Lys Val Phe Glu Gly Lys Asp His Phe Thr Thr Phe Gly Ser Glu Arg
        355                 360                 365

Asp Pro Ser Leu Thr Ser Asn Leu His Val Leu Leu Ser Leu Leu Lys
```

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    370                 375                 380

Gln Ser Asn Leu Ser Gln Tyr His Pro Gln Ile Leu Lys Thr Thr Leu
385                 390                 395                 400

Phe Thr Cys Arg Trp Trp Trp Gly Ser Asp His Cys Val Lys Asp Lys
                405                 410                 415

Trp Asn Leu Ser His Leu Tyr Pro Thr Met Leu Leu Val Glu Ala Phe
            420                 425                 430

Thr Glu Val Leu His Leu Ile Asp Gly Gly Glu Leu Ser Ser Leu Phe
        435                 440                 445

Asp Glu Ser Phe Lys Cys Lys Ile Gly Leu Ser Ile Phe Gln Ala Val
    450                 455                 460

Leu Arg Ile Ile Leu Thr Gln Asp Asn Asp Gly Ser Trp Arg Gly Tyr
465                 470                 475                 480

Arg Glu Gln Thr Cys Tyr Ala Ile Leu Ala Leu Val Gln Ala Arg His
                485                 490                 495

Val Cys Phe Phe Thr His Met Val Asp Arg Leu Gln Ser Cys Val Asp
            500                 505                 510

Arg Gly Phe Ser Trp Leu Lys Ser Cys Ser Phe His Ser Gln Asp Leu
        515                 520                 525

Thr Trp Thr Ser Lys Thr Ala Tyr Glu Val Gly Phe Val Ala Glu Ala
    530                 535                 540

Tyr Lys Leu Ala Ala Leu Gln Ser Ala Ser Leu Glu Val Pro Ala Ala
545                 550                 555                 560

Thr Ile Gly His Ser Val Thr Ser Ala Val Pro Ser Ser Asp Leu Glu
                565                 570                 575
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Lys Tyr Met Arg Leu Val Arg Lys Thr Ala Leu Phe Ser Pro Leu Asp
            580                 585                 590

Glu Trp Gly Leu Met Ala Ser Ile Ile Glu Ser Ser Phe Phe Val Pro
        595                 600                 605

Leu Leu Gln Ala Gln Arg Val Glu Ile Tyr Pro Arg Asp Asn Ile Lys
    610                 615                 620

Val Asp Glu Asp Lys Tyr Leu Ser Ile Ile Pro Phe Thr Trp Val Gly
625                 630                 635                 640

Cys Asn Asn Arg Ser Arg Thr Phe Ala Ser Asn Arg Trp Leu Tyr Asp
                645                 650                 655

Met Met Tyr Leu Ser Leu Leu Gly Tyr Gln Thr Asp Glu Tyr Met Glu
            660                 665                 670

Ala Val Ala Gly Pro Val Phe Gly Asp Val Ser Leu Leu His Gln Thr
        675                 680                 685

Ile Asp Lys Val Ile Asp Asn Thr Met Gly Asn Leu Ala Arg Ala Asn
    690                 695                 700

Gly Thr Val His Ser Gly Asn Gly His Gln His Glu Ser Pro Asn Ile
705                 710                 715                 720

Gly Gln Val Glu Asp Thr Leu Thr Arg Phe Thr Asn Ser Val Leu Asn
                725                 730                 735

His Lys Asp Val Leu Asn Ser Ser Ser Ser Asp Gln Asp Thr Leu Arg
            740                 745                 750

Arg Glu Phe Arg Thr Phe Met His Ala His Ile Thr Gln Ile Glu Asp
        755                 760                 765

Asn Ser Arg Phe Ser Lys Gln Ala Ser Ser Asp Ala Phe Ser Ser Pro
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    770                 775                 780

Glu Gln Ser Tyr Phe Gln Trp Val Asn Ser Thr Gly Gly Ser His Val
785                 790                 795                 800

Ala Cys Ala Tyr Ser Phe Ala Phe Ser Asn Cys Leu Met Ser Ala Asn
                805                 810                 815

Leu Leu Gln Gly Lys Asp Ala Phe Pro Ser Gly Thr Gln Lys Tyr Leu
            820                 825                 830

Ile Ser Ser Val Met Arg His Ala Thr Asn Met Cys Arg Met Tyr Asn
        835                 840                 845

Asp Phe Gly Ser Ile Ala Arg Asp Asn Ala Glu Arg Asn Val Asn Ser
    850                 855                 860

Ile His Phe Pro Glu Phe Thr Leu Cys Asn Gly Thr Ser Gln Asn Leu
865                 870                 875                 880

Asp Glu Arg Lys Glu Arg Leu Leu Lys Ile Ala Thr Tyr Glu Gln Gly
                885                 890                 895

Tyr Leu Asp Arg Ala Leu Glu Ala Leu Glu Arg Gln Ser Arg Asp Asp
            900                 905                 910

Ala Gly Asp Arg Ala Gly Ser Lys Asp Met Arg Lys Leu Lys Ile Val
        915                 920                 925

Lys Leu Phe Cys Asp Val Thr Asp Leu Tyr Asp Gln Leu Tyr Val Ile
    930                 935                 940

Lys Asp Leu Ser Ser Ser Met Lys
945                 950
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<211> 1542
<212> DNA

<213> Artificial Sequence

<220>
<223> Codon-optimized KO

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agatcccaat caaatcatct tccaagagtg cctgaagtcc caggtgttcc attgttagga 180

aatctgttac aattgaagga gaaaaagcca tacatgactt ttacgagatg ggcagcgaca 240

tatggaccta tctatagtat caaaactggg gctacaagta tggttgtggt atcatctaat 300

gagatagcca aggaggcatt ggtgaccaga ttccaatcca tatctacaag gaacttatct 360

aaagccctga aagtacttac agcagataag acaatggtcg caatgtcaga ttatgatgat 420

tatcataaaa cagttaagag acacatactg accgccgtct tgggtcctaa tgcacagaaa 480

aagcatagaa ttcacagaga tatcatgatg gataacatat ctactcaact tcatgaattc 540

gtgaaaaaca acccagaaca ggaagaggta gaccttagaa aaatctttca atctgagtta 600

ttcggcttag ctatgagaca agccttagga aaggatgttg aaagtttgta cgttgaagac 660

ctgaaaatca ctatgaatag agacgaaatc tttcaagtcc ttgttgttga tccaatgatg 720

ggagcaatcg atgttgattg gagagacttc tttccatacc taaagtgggt cccaaacaaa 780

aagttcgaaa atactattca acaaatgtac atcagaagag aagctgttat gaaatcttta 840

atcaaagagc acaaaaagag aatagcgtca ggcgaaaagc taaatagtta tatcgattac 900

cttttatctg aagctcaaac tttaaccgat cagcaactat tgatgtcctt gtgggaacca 960

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aaaaacccta aattgcaaga taggttgtac agagacatta agtccgtctg tggatctgaa 1080

aagataaccg aagagcatct atcacagctg ccttacatta cagctatttt ccacgaaaca 1140

ctgagaagac actcaccagt tcctatcatt cctctaagac atgtacatga agataccgtt 1200

ctaggcggct accatgttcc tgctggcaca gaacttgccg ttaacatcta cggttgcaac 1260

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aatgagacaa ttgattttca aaagacgatg gccttcggtg gtggtaagag agtttgtgct 1380

ggttccttgc aagccctttt aactgcatct attgggattg ggagaatggt tcaagagttc 1440

gaatggaaac tgaaggatat gactcaagag gaagtgaaca cgataggcct aactacacaa 1500

atgttaagac cattgagagc tattatcaaa cctaggatct aa 1542

<210> 60
<211> 513
<212> PRT
<213> Stevia rebaudiana

<400> 60

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1 5 10 15

Ile Gly Gly Thr Ala Val Ala Leu Ala Val Ala Leu Ile Phe Trp Tyr
20 25 30

Leu Lys Ser Tyr Thr Ser Ala Arg Arg Ser Gln Ser Asn His Leu Pro
35 40 45

Arg Val Pro Glu Val Pro Gly Val Pro Leu Leu Gly Asn Leu Leu Gln
50 55 60

Leu Lys Glu Lys Lys Pro Tyr Met Thr Phe Thr Arg Trp Ala Ala Thr
65 70 75 80

Tyr Gly Pro Ile Tyr Ser Ile Lys Thr Gly Ala Thr Ser Met Val Val
85 90 95

Val Ser Ser Asn Glu Ile Ala Lys Glu Ala Leu Val Thr Arg Phe Gln
100 105 110

Ser Ile Ser Thr Arg Asn Leu Ser Lys Ala Leu Lys Val Leu Thr Ala
115 120 125

Asp Lys Thr Met Val Ala Met Ser Asp Tyr Asp Asp Tyr His Lys Thr
130 135 140

```
Val Lys Arg His Ile Leu Thr Ala Val Leu Gly Pro Asn Ala Gln Lys
145                 150                 155                 160

Lys His Arg Ile His Arg Asp Ile Met Met Asp Asn Ile Ser Thr Gln
                165                 170                 175

Leu His Glu Phe Val Lys Asn Asn Pro Glu Gln Glu Glu Val Asp Leu
            180                 185                 190

Arg Lys Ile Phe Gln Ser Glu Leu Phe Gly Leu Ala Met Arg Gln Ala
        195                 200                 205

Leu Gly Lys Asp Val Glu Ser Leu Tyr Val Glu Asp Leu Lys Ile Thr
    210                 215                 220

Met Asn Arg Asp Glu Ile Phe Gln Val Leu Val Val Asp Pro Met Met
225                 230                 235                 240

Gly Ala Ile Asp Val Asp Trp Arg Asp Phe Phe Pro Tyr Leu Lys Trp
                245                 250                 255

Val Pro Asn Lys Lys Phe Glu Asn Thr Ile Gln Gln Met Tyr Ile Arg
            260                 265                 270

Arg Glu Ala Val Met Lys Ser Leu Ile Lys Glu His Lys Lys Arg Ile
        275                 280                 285

Ala Ser Gly Glu Lys Leu Asn Ser Tyr Ile Asp Tyr Leu Leu Ser Glu
    290                 295                 300

Ala Gln Thr Leu Thr Asp Gln Gln Leu Leu Met Ser Leu Trp Glu Pro
305                 310                 315                 320

Ile Ile Glu Ser Ser Asp Thr Thr Met Val Thr Thr Glu Trp Ala Met
                325                 330                 335
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Tyr Glu Leu Ala Lys Asn Pro Lys Leu Gln Asp Arg Leu Tyr Arg Asp
            340                 345                 350

Ile Lys Ser Val Cys Gly Ser Glu Lys Ile Thr Glu Glu His Leu Ser
        355                 360                 365

Gln Leu Pro Tyr Ile Thr Ala Ile Phe His Glu Thr Leu Arg Arg His
    370                 375                 380

Ser Pro Val Pro Ile Ile Pro Leu Arg His Val His Glu Asp Thr Val
385                 390                 395                 400

Leu Gly Gly Tyr His Val Pro Ala Gly Thr Glu Leu Ala Val Asn Ile
                405                 410                 415

Tyr Gly Cys Asn Met Asp Lys Asn Val Trp Glu Asn Pro Glu Glu Trp
            420                 425                 430

Asn Pro Glu Arg Phe Met Lys Glu Asn Glu Thr Ile Asp Phe Gln Lys
        435                 440                 445

Thr Met Ala Phe Gly Gly Gly Lys Arg Val Cys Ala Gly Ser Leu Gln
    450                 455                 460

Ala Leu Leu Thr Ala Ser Ile Gly Ile Gly Arg Met Val Gln Glu Phe
465                 470                 475                 480

Glu Trp Lys Leu Lys Asp Met Thr Gln Glu Glu Val Asn Thr Ile Gly
                485                 490                 495

Leu Thr Thr Gln Met Leu Arg Pro Leu Arg Ala Ile Ile Lys Pro Arg
            500                 505                 510

Ile
```

<210> 61
<211> 1566

<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized KO

<400> 61
aagcttacta gtaaaatgga cggtgtcatc gatatgcaaa ccattccatt gagaaccgct 60

attgctattg gtggtactgc tgttgctttg gttgttgcat tatacttttg gttcttgaga 120

tcctacgctt ccccatctca tcattctaat catttgccac cagtacctga agttccaggt 180

gttccagttt tgggtaattt gttgcaattg aaagaaaaaa agccttacat gaccttcacc 240

aagtgggctg aaatgtatgg tccaatctac tctattagaa ctggtgctac ttccatggtt 300

gttgtctctt ctaacgaaat cgccaaagaa gttgttgtta ccagattccc atctatctct 360

accagaaaat tgtcttacgc cttgaaggtt ttgaccgaag ataagtctat ggttgccatg 420

tctgattatc acgattacca taagaccgtc aagagacata ttttgactgc tgttttgggt 480

ccaaacgccc aaaaaaagtt tagagcacat agagacacca tgatggaaaa cgtttccaat 540

gaattgcatg ccttcttcga aaagaaccca aatcaagaag tcaacttgag aaagatcttc 600

caatcccaat tattcggttt ggctatgaag caagccttgg gtaaagatgt tgaatccatc 660

tacgttaagg atttggaaac caccatgaag agagaagaaa tcttcgaagt tttggttgtc 720

gatccaatga tgggtgctat tgaagttgat tggagagact ttttcccata cttgaaatgg 780

gttccaaaca agtccttcga aaacatcatc catagaatgt acactagaag agaagctgtt 840

atgaaggcct tgatccaaga acacaagaaa agaattgcct ccggtgaaaa cttgaactcc 900

tacattgatt acttgttgtc tgaagcccaa accttgaccg ataagcaatt attgatgtct 960

ttgtgggaac ctattatcga atcttctgat accactatgg ttactactga atgggctatg 1020

tacgaattgg ctaagaatcc aaacatgcaa gacagattat acgaagaaat ccaatccgtt 1080

tgcggttccg aaaagattac tgaagaaaac ttgtcccaat tgccatactt gtacgctgtt 1140

ttccaagaaa ctttgagaaa gcactgtcca gttcctatta tgccattgag atatgttcac 1200

gaaaacaccg ttttgggtgg ttatcatgtt ccagctggta ctgaagttgc tattaacatc 1260

tacggttgca acatggataa gaaggtctgg gaaaatccag aagaatggaa tccagaaaga 1320

ttcttgtccg aaaaagaatc catggacttg tacaaaacta tggcttttgg tggtggtaaa 1380

agagtttgcg ctggttcttt acaagccatg gttatttctt gcattggtat cggtagattg 1440

gtccaagatt ttgaatggaa gttgaaggat gatgccgaag aagatgttaa cactttgggt 1500

ttgactaccc aaaagttgca tccattattg gccttgatta acccaagaaa gtaactcgag 1560

ccgcgg 1566

<210> 62
<211> 512
<212> PRT
<213> Lactuca sativa

<400> 62

Met Asp Gly Val Ile Asp Met Gln Thr Ile Pro Leu Arg Thr Ala Ile
1 5 10 15

Ala Ile Gly Gly Thr Ala Val Ala Leu Val Val Ala Leu Tyr Phe Trp
20 25 30

Phe Leu Arg Ser Tyr Ala Ser Pro Ser His His Ser Asn His Leu Pro
35 40 45

Pro Val Pro Glu Val Pro Gly Val Pro Val Leu Gly Asn Leu Leu Gln
50 55 60

Leu Lys Glu Lys Lys Pro Tyr Met Thr Phe Thr Lys Trp Ala Glu Met
65 70 75 80

Tyr Gly Pro Ile Tyr Ser Ile Arg Thr Gly Ala Thr Ser Met Val Val
85 90 95

Val Ser Ser Asn Glu Ile Ala Lys Glu Val Val Val Thr Arg Phe Pro
100 105 110

Ser Ile Ser Thr Arg Lys Leu Ser Tyr Ala Leu Lys Val Leu Thr Glu
115 120 125

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Asp Lys Ser Met Val Ala Met Ser Asp Tyr His Asp Tyr His Lys Thr
    130                 135                 140

Val Lys Arg His Ile Leu Thr Ala Val Leu Gly Pro Asn Ala Gln Lys
145                 150                 155                 160

Lys Phe Arg Ala His Arg Asp Thr Met Met Glu Asn Val Ser Asn Glu
                165                 170                 175

Leu His Ala Phe Phe Glu Lys Asn Pro Asn Gln Glu Val Asn Leu Arg
            180                 185                 190

Lys Ile Phe Gln Ser Gln Leu Phe Gly Leu Ala Met Lys Gln Ala Leu
        195                 200                 205

Gly Lys Asp Val Glu Ser Ile Tyr Val Lys Asp Leu Glu Thr Thr Met
    210                 215                 220

Lys Arg Glu Glu Ile Phe Glu Val Leu Val Val Asp Pro Met Met Gly
225                 230                 235                 240

Ala Ile Glu Val Asp Trp Arg Asp Phe Phe Pro Tyr Leu Lys Trp Val
                245                 250                 255

Pro Asn Lys Ser Phe Glu Asn Ile Ile His Arg Met Tyr Thr Arg Arg
            260                 265                 270

Glu Ala Val Met Lys Ala Leu Ile Gln Glu His Lys Lys Arg Ile Ala
        275                 280                 285

Ser Gly Glu Asn Leu Asn Ser Tyr Ile Asp Tyr Leu Leu Ser Glu Ala
    290                 295                 300

Gln Thr Leu Thr Asp Lys Gln Leu Leu Met Ser Leu Trp Glu Pro Ile
305                 310                 315                 320

Ile Glu Ser Ser Asp Thr Thr Met Val Thr Thr Glu Trp Ala Met Tyr
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                325                 330                 335

Glu Leu Ala Lys Asn Pro Asn Met Gln Asp Arg Leu Tyr Glu Glu Ile
            340                 345                 350

Gln Ser Val Cys Gly Ser Glu Lys Ile Thr Glu Glu Asn Leu Ser Gln
        355                 360                 365

Leu Pro Tyr Leu Tyr Ala Val Phe Gln Glu Thr Leu Arg Lys His Cys
    370                 375                 380

Pro Val Pro Ile Met Pro Leu Arg Tyr Val His Glu Asn Thr Val Leu
385                 390                 395                 400

Gly Gly Tyr His Val Pro Ala Gly Thr Glu Val Ala Ile Asn Ile Tyr
                405                 410                 415

Gly Cys Asn Met Asp Lys Lys Val Trp Glu Asn Pro Glu Glu Trp Asn
            420                 425                 430

Pro Glu Arg Phe Leu Ser Glu Lys Glu Ser Met Asp Leu Tyr Lys Thr
        435                 440                 445

Met Ala Phe Gly Gly Gly Lys Arg Val Cys Ala Gly Ser Leu Gln Ala
    450                 455                 460

Met Val Ile Ser Cys Ile Gly Ile Gly Arg Leu Val Gln Asp Phe Glu
465                 470                 475                 480

Trp Lys Leu Lys Asp Asp Ala Glu Glu Asp Val Asn Thr Leu Gly Leu
                485                 490                 495

Thr Thr Gln Lys Leu His Pro Leu Leu Ala Leu Ile Asn Pro Arg Lys
            500                 505                 510
```

<210> 63
<211> 1535
<212> DNA

<213> Rubus suavissimus

<400> 63
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gctctgtctt ggctgttcct cttttacatc aaagtttcat tcttttccaa caagagtgct 120

caggctaagc tccctcctgt gccagtggtt cctgggctgc cggtgattgg gaatttactg 180

caactcaagg agaagaaacc ctaccagact tttacaaggt gggctgagga gtatggacca 240

atctattcta tcaggactgg tgcttccacc atggtcgttc tcaataccac ccaagttgca 300

aaagaggcca tggtgaccag atatttatcc atctcaacca gaaagctatc aaacgcacta 360

aagattctta ctgctgataa atgtatggtt gcaataagtg actacaacga ttttcacaag 420

atgataaagc gatacatact ctcaaatgtt cttggaccta gtgctcagaa gcgtcaccgg 480

agcaacagag ataccttgag agctaatgtc tgcagccgat tgcattctca agtaaagaac 540

tctcctcgag aagctgtgaa tttcagaaga gtttttgagt gggaactctt tggaattgca 600

ttgaagcaag cctttggaaa ggacatagaa aagcccattt atgtggagga acttggcact 660

acactgtcaa gagatgagat ctttaaggtt ctagtgcttg acataatgga gggtgcaatt 720

gaggttgatt ggagagattt cttcccttac ctgagatgga ttccgaatac gcgcatggaa 780

acaaaaattc agcgactcta tttccgcagg aaagcagtga tgactgccct gatcaacgag 840

cagaagaagc gaattgcttc aggagaggaa atcaactgtt atatcgactt cttgcttaag 900

gaagggaaga cactgacaat ggaccaaata agtatgttgc tttgggagac ggttattgaa 960

acagcagata ctacaatggt aacgacagaa tgggctatgt atgaagttgc taaagactca 1020

aagcgtcagg atcgtctcta tcaggaaatc caaaaggttt gtggatcgga gatggttaca 1080

gaggaatact tgtcccaact gccgtacctg aatgcagttt tccatgaaac gctaaggaag 1140

cacagtccgg ctgcgttagt tcctttaaga tatgcacatg aagataccca actaggaggt 1200

tactacattc cagctggaac tgagattgct ataaacatat acgggtgtaa catggacaag 1260

catcaatggg aaagccctga ggaatggaaa ccggagagat ttttggaccc gaaatttgat 1320

cctatggatt tgtacaagac catggctttt ggggctggaa agagggtatg tgctggttct 1380

cttcaggcaa tgttaatagc gtgcccgacg attggtaggc tggtgcagga gtttgagtgg 1440

aagctgagag atggagaaga agaaaatgta gatactgttg ggctcaccac tcacaaacgc 1500

tatccaatgc atgcaatcct gaagccaaga agtta 1535

<210> 64
<211> 1536
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized KO

<400> 64
atggctacct tgttggaaca ttttcaagct atgccattcg ctattccaat tgctttggct 60

gctttgtctt ggttgttttt gttctacatc aaggtttctt tcttctccaa caaatccgct 120

caagctaaat tgccaccagt tccagttgtt ccaggtttgc cagttattgg taatttgttg 180

caattgaaag aaaagaagcc ataccaaacc ttcactagat gggctgaaga atatggtcca 240

atctactcta ttagaactgg tgcttctact atggttgtct tgaacactac tcaagttgcc 300

aaagaagcta tggttaccag atacttgtct atctctacca gaaagttgtc caacgccttg 360

aaaattttga ccgctgataa gtgcatggtt gccatttctg attacaacga tttccacaag 420

atgatcaaga gatatatctt gtctaacgtt ttgggtccat ctgcccaaaa aagacataga 480

tctaacagag ataccttgag agccaacgtt tgttctagat tgcattccca agttaagaac 540

tctccaagag aagctgtcaa ctttagaaga gttttcgaat gggaattatt cggtatcgct 600

ttgaaacaag ccttcggtaa ggatattgaa aagccaatct acgtcgaaga attgggtact 660

actttgtcca gagatgaaat cttcaaggtt ttggtcttgg acattatgga aggtgccatt 720

gaagttgatt ggagagattt tttcccatac ttgcgttgga ttccaaacac cagaatggaa 780

actaagatcc aaagattata ctttagaaga aaggccgtta tgaccgcctt gattaacgaa 840

caaaagaaaa gaattgcctc cggtgaagaa atcaactgct acatcgattt cttgttgaaa 900

gaaggtaaga ccttgaccat ggaccaaatc tctatgttgt tgtgggaaac cgttattgaa 960

actgctgata ccacaatggt tactactgaa tgggctatgt acgaagttgc taaggattct 1020

aaaagacaag acagattata ccaagaaatc caaaaggtct gcggttctga aatggttaca 1080

gaagaatact tgtcccaatt gccatacttg aatgctgttt tccacgaaac tttgagaaaa 1140

cattctccag ctgctttggt tccattgaga tatgctcatg aagatactca attgggtggt 1200

tattacattc cagccggtac tgaaattgcc attaacatct acggttgcaa catggacaaa 1260

caccaatggg aatctccaga agaatggaag ccagaaagat ttttggatcc taagtttgac 1320

ccaatggact tgtacaaaac tatggctttt ggtgctggta aaagagtttg cgctggttct 1380

ttacaagcta tgttgattgc ttgtccaacc atcggtagat tggttcaaga atttgaatgg 1440

aagttgagag atggtgaaga agaaaacgtt gatactgttg gtttgaccac ccataagaga 1500

tatccaatgc atgctatttt gaagccaaga tcttaa 1536

<210> 65
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized KO

<400> 65
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ttcgctactg cttttgctgt tggtggtgtt tctttgttga tattcttctt cttcatccgt 120

ggtttccact ctactaagaa aaacgaatat tacaagttgc caccagttcc agttgttcca 180

ggtttgccag ttgttggtaa tttgttgcaa ttgaaagaaa agaagccata caagactttc 240

ttgagatggg ctgaaattca tggtccaatc tactctatta gaactggtgc ttctaccatg 300

gttgttgtta actctactca tgttgccaaa gaagctatgg ttaccagatt ctcttcaatc 360

tctaccagaa agttgtccaa ggctttggaa ttattgacct ccaacaaatc tatggttgcc 420

acctctgatt acaacgaatt tcacaagatg gtcaagaagt acatcttggc cgaattattg 480

ggtgctaatg ctcaaaagag acacagaatt catagagaca ccttgatcga aaacgtcttg 540

aacaaattgc atgcccatac caagaattct ccattgcaag ctgttaactt cagaaagatc 600

ttcgaatctg aattattcgg tttggctatg aagcaagcct tgggttatga tgttgattcc 660

ttgttcgttg aagaattggg tactaccttg tccagagaag aaatctacaa cgttttggtc 720

agtgacatgt tgaagggtgc tattgaagtt gattggagag acttttccc atacttgaaa 780

tggatcccaa acaagtcctt cgaaatgaag attcaaagat tggcctctag aagacaagcc 840

gttatgaact ctattgtcaa agaacaaaag aagtccattg cctctggtaa gggtgaaaac 900

tgttacttga attacttgtt gtccgaagct aagactttga ccgaaaagca aatttccatt 960

ttggcctggg aaaccattat tgaaactgct gatacaactg ttgttaccac tgaatgggct 1020

atgtacgaat tggctaaaaa cccaaagcaa caagacagat tatacaacga aatccaaaac 1080

gtctgcggta ctgataagat taccgaagaa catttgtcca agttgcctta cttgtctgct 1140

gtttttcacg aaaccttgag aaagtattct ccatctccat tggttccatt gagatacgct 1200

catgaagata ctcaattggg tggttattat gttccagccg gtactgaaat tgctgttaat 1260

atctacggtt gcaacatgga caagaatcaa tgggaaactc cagaagaatg gaagccagaa 1320

agatttttgg acgaaaagta cgatccaatg gacatgtaca agactatgtc ttttggttcc 1380

ggtaaaagag tttgcgctgg ttctttacaa gctagtttga ttgcttgtac ctccatcggt 1440

agattggttc aagaatttga atggagattg aaagacggtg aagttgaaaa cgttgatacc 1500

ttgggtttga ctacccataa gttgtatcca atgcaagcta tcttgcaacc tagaaactga 1560

ctcgagccgc gg 1572

<210> 66
<211> 514
<212> PRT
<213> Castanea mollissima

<400> 66

Met Ala Ser Ile Thr His Phe Leu Gln Asp Phe Gln Ala Thr Pro Phe
1 5 10 15

Ala Thr Ala Phe Ala Val Gly Gly Val Ser Leu Leu Ile Phe Phe Phe
20 25 30

Phe Ile Arg Gly Phe His Ser Thr Lys Lys Asn Glu Tyr Tyr Lys Leu
35 40 45

```
Pro Pro Val Pro Val Val Pro Gly Leu Pro Val Val Gly Asn Leu Leu
    50                  55                  60

Gln Leu Lys Glu Lys Lys Pro Tyr Lys Thr Phe Leu Arg Trp Ala Glu
65                  70                  75                  80

Ile His Gly Pro Ile Tyr Ser Ile Arg Thr Gly Ala Ser Thr Met Val
                85                  90                  95

Val Val Asn Ser Thr His Val Ala Lys Glu Ala Met Val Thr Arg Phe
            100                 105                 110

Ser Ser Ile Ser Thr Arg Lys Leu Ser Lys Ala Leu Glu Leu Leu Thr
        115                 120                 125

Ser Asn Lys Ser Met Val Ala Thr Ser Asp Tyr Asn Glu Phe His Lys
    130                 135                 140

Met Val Lys Lys Tyr Ile Leu Ala Glu Leu Leu Gly Ala Asn Ala Gln
145                 150                 155                 160

Lys Arg His Arg Ile His Arg Asp Thr Leu Ile Glu Asn Val Leu Asn
                165                 170                 175

Lys Leu His Ala His Thr Lys Asn Ser Pro Leu Gln Ala Val Asn Phe
            180                 185                 190

Arg Lys Ile Phe Glu Ser Glu Leu Phe Gly Leu Ala Met Lys Gln Ala
        195                 200                 205

Leu Gly Tyr Asp Val Asp Ser Leu Phe Val Glu Glu Leu Gly Thr Thr
    210                 215                 220

Leu Ser Arg Glu Glu Ile Tyr Asn Val Leu Val Ser Asp Met Leu Lys
225                 230                 235                 240

Gly Ala Ile Glu Val Asp Trp Arg Asp Phe Phe Pro Tyr Leu Lys Trp
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                245                 250                 255

Ile Pro Asn Lys Ser Phe Glu Met Lys Ile Gln Arg Leu Ala Ser Arg
            260                 265                 270

Arg Gln Ala Val Met Asn Ser Ile Val Lys Glu Gln Lys Lys Ser Ile
        275                 280                 285

Ala Ser Gly Lys Gly Glu Asn Cys Tyr Leu Asn Tyr Leu Leu Ser Glu
    290                 295                 300

Ala Lys Thr Leu Thr Glu Lys Gln Ile Ser Ile Leu Ala Trp Glu Thr
305                 310                 315                 320

Ile Ile Glu Thr Ala Asp Thr Thr Val Val Thr Thr Glu Trp Ala Met
                325                 330                 335

Tyr Glu Leu Ala Lys Asn Pro Lys Gln Gln Asp Arg Leu Tyr Asn Glu
            340                 345                 350

Ile Gln Asn Val Cys Gly Thr Asp Lys Ile Thr Glu Glu His Leu Ser
        355                 360                 365

Lys Leu Pro Tyr Leu Ser Ala Val Phe His Glu Thr Leu Arg Lys Tyr
    370                 375                 380

Ser Pro Ser Pro Leu Val Pro Leu Arg Tyr Ala His Glu Asp Thr Gln
385                 390                 395                 400

Leu Gly Gly Tyr Tyr Val Pro Ala Gly Thr Glu Ile Ala Val Asn Ile
                405                 410                 415

Tyr Gly Cys Asn Met Asp Lys Asn Gln Trp Glu Thr Pro Glu Glu Trp
            420                 425                 430

Lys Pro Glu Arg Phe Leu Asp Glu Lys Tyr Asp Pro Met Asp Met Tyr
        435                 440                 445
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Lys Thr Met Ser Phe Gly Ser Gly Lys Arg Val Cys Ala Gly Ser Leu
    450                 455                 460

Gln Ala Ser Leu Ile Ala Cys Thr Ser Ile Gly Arg Leu Val Gln Glu
465                 470                 475                 480

Phe Glu Trp Arg Leu Lys Asp Gly Glu Val Glu Asn Val Asp Thr Leu
                485                 490                 495

Gly Leu Thr Thr His Lys Leu Tyr Pro Met Gln Ala Ile Leu Gln Pro
            500                 505                 510

Arg Asn
```

<210> 67
<211> 1512
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized KO

<400> 67

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aaattgttgt tcttcttcag tcgtcacaaa atgtccgaag tttctagatt gccatctgtt      120

ccagttccag gttttccatt gattggtaac ttgttgcaat tgaaagaaaa gaagccacac      180

aagactttca ccaagtggtc tgaattatat ggtccaatct actctatcaa gatgggttcc      240

tcttctttga tcgtcttgaa ctctattgaa accgccaaag aagctatggt cagtagattc      300

tcttcaatct ctaccagaaa gttgtctaac gctttgactg ttttgacctg caacaaatct      360

atggttgcta cctctgatta cgatgacttt cataagttcg tcaagagatg cttgttgaac      420

ggtttgttgg gtgctaatgc tcaagaaaga aaaagacatt acagagatgc cttgatcgaa      480

aacgttacct ctaaattgca tgcccatacc agaaatcatc cacaagaacc agttaacttc      540

agagccattt tcgaacacga attattcggt gttgctttga aacaagcctt cggtaaagat      600
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gtcgaatcca tctatgtaaa agaattgggt gtcaccttgt ccagagatga aattttcaag 660

gttttggtcc acgacatgat ggaaggtgct attgatgttg attggagaga tttcttccca 720

tacttgaaat ggatcccaaa caactctttc gaagccagaa ttcaacaaaa gcacaagaga 780

agattggctg ttatgaacgc cttgatccaa gacagattga atcaaaacga ttccgaatcc 840

gatgatgact gctacttgaa tttcttgatg tctgaagcta agaccttgac catggaacaa 900

attgctattt tggtttggga aaccattatc gaaactgctg ataccacttt ggttactact 960

gaatgggcta tgtacgaatt ggccaaacat caatctgttc aagatagatt attcaaagaa 1020

atccaatccg tctgcggtgg tgaaaagatc aaagaagaac aattgccaag attgccttac 1080

gtcaatggtg tttttcacga aaccttgaga aagtattctc agctccatt ggttccaatt 1140

agatacgctc atgaagatac ccaaattggt ggttatcata ttccagccgg ttctgaaatt 1200

gccattaaca tctacggttg caacatggat aagaagagat gggaaagacc tgaagaatgg 1260

tggccagaaa gatttttgga agatagatac gaatcctccg acttgcataa gactatggct 1320

tttggtgctg gtaaaagagt ttgtgctggt gctttacaag ctagtttgat ggctggtatt 1380

gctatcggta gattggttca agaattcgaa tggaagttga gagatggtga agaagaaaac 1440

gttgatactt acggtttgac ctcccaaaag ttgtatccat tgatggccat tatcaaccca 1500

agaagatctt aa 1512

<210> 68
<211> 506
<212> PRT
<213> Thellungiella halophila

<400> 68

Met Ala Ser Met Ile Ser Leu Leu Leu Gly Phe Val Val Ser Ser Phe
1 5 10 15

Leu Phe Ile Phe Phe Leu Lys Lys Leu Leu Phe Phe Phe Ser Arg His
20 25 30

Lys Met Ser Glu Val Ser Arg Leu Pro Ser Val Pro Val Pro Gly Phe
35 40 45

```
Pro Leu Ile Gly Asn Leu Leu Gln Leu Lys Glu Lys Lys Pro His Lys
    50                  55                  60

Thr Phe Thr Lys Trp Ser Glu Leu Tyr Gly Pro Ile Tyr Ser Ile Lys
65                  70                  75                  80

Met Gly Ser Ser Ser Leu Ile Val Leu Asn Ser Ile Glu Thr Ala Lys
                85                  90                  95

Glu Ala Met Val Ser Arg Phe Ser Ser Ile Ser Thr Arg Lys Leu Ser
            100                 105                 110

Asn Ala Leu Thr Val Leu Thr Cys Asn Lys Ser Met Val Ala Thr Ser
        115                 120                 125

Asp Tyr Asp Asp Phe His Lys Phe Val Lys Arg Cys Leu Leu Asn Gly
    130                 135                 140

Leu Leu Gly Ala Asn Ala Gln Glu Arg Lys Arg His Tyr Arg Asp Ala
145                 150                 155                 160

Leu Ile Glu Asn Val Thr Ser Lys Leu His Ala His Thr Arg Asn His
                165                 170                 175

Pro Gln Glu Pro Val Asn Phe Arg Ala Ile Phe Glu His Glu Leu Phe
            180                 185                 190

Gly Val Ala Leu Lys Gln Ala Phe Gly Lys Asp Val Glu Ser Ile Tyr
        195                 200                 205

Val Lys Glu Leu Gly Val Thr Leu Ser Arg Asp Glu Ile Phe Lys Val
    210                 215                 220

Leu Val His Asp Met Met Glu Gly Ala Ile Asp Val Asp Trp Arg Asp
225                 230                 235                 240
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```
Phe Phe Pro Tyr Leu Lys Trp Ile Pro Asn Asn Ser Phe Glu Ala Arg
                245                 250                 255

Ile Gln Gln Lys His Lys Arg Arg Leu Ala Val Met Asn Ala Leu Ile
            260                 265                 270

Gln Asp Arg Leu Asn Gln Asn Asp Ser Glu Ser Asp Asp Asp Cys Tyr
        275                 280                 285

Leu Asn Phe Leu Met Ser Glu Ala Lys Thr Leu Thr Met Glu Gln Ile
    290                 295                 300

Ala Ile Leu Val Trp Glu Thr Ile Ile Glu Thr Ala Asp Thr Thr Leu
305                 310                 315                 320

Val Thr Thr Glu Trp Ala Met Tyr Glu Leu Ala Lys His Gln Ser Val
                325                 330                 335

Gln Asp Arg Leu Phe Lys Glu Ile Gln Ser Val Cys Gly Gly Glu Lys
            340                 345                 350

Ile Lys Glu Glu Gln Leu Pro Arg Leu Pro Tyr Val Asn Gly Val Phe
        355                 360                 365

His Glu Thr Leu Arg Lys Tyr Ser Pro Ala Pro Leu Val Pro Ile Arg
    370                 375                 380

Tyr Ala His Glu Asp Thr Gln Ile Gly Gly Tyr His Ile Pro Ala Gly
385                 390                 395                 400

Ser Glu Ile Ala Ile Asn Ile Tyr Gly Cys Asn Met Asp Lys Lys Arg
                405                 410                 415

Trp Glu Arg Pro Glu Glu Trp Trp Pro Glu Arg Phe Leu Glu Asp Arg
            420                 425                 430

Tyr Glu Ser Ser Asp Leu His Lys Thr Met Ala Phe Gly Ala Gly Lys
        435                 440                 445
```

Arg Val Cys Ala Gly Ala Leu Gln Ala Ser Leu Met Ala Gly Ile Ala
    450   455   460

Ile Gly Arg Leu Val Gln Glu Phe Glu Trp Lys Leu Arg Asp Gly Glu
465   470   475   480

Glu Glu Asn Val Asp Thr Tyr Gly Leu Thr Ser Gln Lys Leu Tyr Pro
                485   490   495

Leu Met Ala Ile Ile Asn Pro Arg Arg Ser
            500   505

<210> 69
<211> 1554
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized KO

<400> 69
aagcttacta gtaaaatgga catgatgggt attgaagctg ttccatttgc tactgctgtt   60

gttttgggtg gtatttcctt ggttgttttg atcttcatca gaagattcgt ttccaacaga   120

aagagatccg ttgaaggttt gccaccagtt ccagatattc caggtttacc attgattggt   180

aacttgttgc aattgaaaga aaagaagcca cataagacct ttgctagatg ggctgaaact   240

tacggtccaa ttttctctat tagaactggt gcttctacca tgatcgtctt gaattcttct   300

gaagttgcca aagaagctat ggtcactaga ttctcttcaa tctctaccag aaagttgtcc   360

aacgccttga agattttgac cttcgataag tgtatggttg ccacctctga ttacaacgat   420

tttcacaaaa tggtcaaggg tttcatcttg agaaacgttt taggtgctcc agcccaaaaa   480

agacatagat gtcatagaga taccttgatc gaaaacatct ctaagtactt gcatgcccat   540

gttaagactt ctccattgga accagttgtc ttgaagaaga ttttcgaatc cgaaattttc   600

ggtttggctt tgaaacaagc cttgggtaag gatatcgaat ccatctatgt tgaagaattg   660

ggtactacct tgtccagaga agaaattttt gccgttttgg ttgttgatcc aatggctggt   720

gctattgaag ttgattggag agatttttc ccatacttgt cctggattcc aaacaagtct 780

atggaaatga agatccaaag aatggatttt agaagaggtg ctttgatgaa ggccttgatt 840

ggtgaacaaa agaaaagaat cggttccggt gaagaaaaga actcctacat tgatttcttg 900

ttgtctgaag ctaccacttt gaccgaaaag caaattgcta tgttgatctg ggaaaccatc 960

atcgaaattt ccgatacaac tttggttacc tctgaatggg ctatgtacga attggctaaa 1020

gacccaaata gacaagaaat cttgtacaga gaaatccaca aggtttgcgg ttctaacaag 1080

ttgactgaag aaaacttgtc caagttgcca tacttgaact ctgttttcca cgaaaccttg 1140

agaaagtatt ctccagctcc aatggttcca gttagatatg ctcatgaaga tactcaattg 1200

ggtggttacc atattccagc tggttctcaa attgccatta acatctacgg ttgcaacatg 1260

aacaaaaagc aatgggaaaa tcctgaagaa tggaagccag aaagattctt ggacgaaaag 1320

tatgacttga tggacttgca taagactatg gcttttggtg gtggtaaaag agtttgtgct 1380

ggtgctttac aagcaatgtt gattgcttgc acttccatcg gtagattcgt tcaagaattt 1440

gaatggaagt tgatgggtgg tgaagaagaa aacgttgata ctgttgcttt gacctcccaa 1500

aaattgcatc caatgcaagc cattattaag gccagagaat gactcgagcc gcgg 1554

<210> 70
<211> 508
<212> PRT
<213> Vitis vinifera

<400> 70

Met Asp Met Met Gly Ile Glu Ala Val Pro Phe Ala Thr Ala Val Val
1 5 10 15

Leu Gly Gly Ile Ser Leu Val Val Leu Ile Phe Ile Arg Arg Phe Val
20 25 30

Ser Asn Arg Lys Arg Ser Val Glu Gly Leu Pro Pro Val Pro Asp Ile
35 40 45

Pro Gly Leu Pro Leu Ile Gly Asn Leu Leu Gln Leu Lys Glu Lys Lys

```
    50                  55                  60

Pro His Lys Thr Phe Ala Arg Trp Ala Glu Thr Tyr Gly Pro Ile Phe
65                  70                  75                  80

Ser Ile Arg Thr Gly Ala Ser Thr Met Ile Val Leu Asn Ser Ser Glu
                85                  90                  95

Val Ala Lys Glu Ala Met Val Thr Arg Phe Ser Ser Ile Ser Thr Arg
            100                 105                 110

Lys Leu Ser Asn Ala Leu Lys Ile Leu Thr Phe Asp Lys Cys Met Val
        115                 120                 125

Ala Thr Ser Asp Tyr Asn Asp Phe His Lys Met Val Lys Gly Phe Ile
    130                 135                 140

Leu Arg Asn Val Leu Gly Ala Pro Ala Gln Lys Arg His Arg Cys His
145                 150                 155                 160

Arg Asp Thr Leu Ile Glu Asn Ile Ser Lys Tyr Leu His Ala His Val
                165                 170                 175

Lys Thr Ser Pro Leu Glu Pro Val Val Leu Lys Lys Ile Phe Glu Ser
            180                 185                 190

Glu Ile Phe Gly Leu Ala Leu Lys Gln Ala Leu Gly Lys Asp Ile Glu
        195                 200                 205

Ser Ile Tyr Val Glu Glu Leu Gly Thr Thr Leu Ser Arg Glu Glu Ile
    210                 215                 220

Phe Ala Val Leu Val Val Asp Pro Met Ala Gly Ala Ile Glu Val Asp
225                 230                 235                 240

Trp Arg Asp Phe Phe Pro Tyr Leu Ser Trp Ile Pro Asn Lys Ser Met
                245                 250                 255
```

```
Glu Met Lys Ile Gln Arg Met Asp Phe Arg Arg Gly Ala Leu Met Lys
            260                 265                 270

Ala Leu Ile Gly Glu Gln Lys Lys Arg Ile Gly Ser Gly Glu Glu Lys
        275                 280                 285

Asn Ser Tyr Ile Asp Phe Leu Leu Ser Glu Ala Thr Thr Leu Thr Glu
    290                 295                 300

Lys Gln Ile Ala Met Leu Ile Trp Glu Thr Ile Ile Glu Ile Ser Asp
305                 310                 315                 320

Thr Thr Leu Val Thr Ser Glu Trp Ala Met Tyr Glu Leu Ala Lys Asp
                325                 330                 335

Pro Asn Arg Gln Glu Ile Leu Tyr Arg Glu Ile His Lys Val Cys Gly
            340                 345                 350

Ser Asn Lys Leu Thr Glu Glu Asn Leu Ser Lys Leu Pro Tyr Leu Asn
        355                 360                 365

Ser Val Phe His Glu Thr Leu Arg Lys Tyr Ser Pro Ala Pro Met Val
    370                 375                 380

Pro Val Arg Tyr Ala His Glu Asp Thr Gln Leu Gly Gly Tyr His Ile
385                 390                 395                 400

Pro Ala Gly Ser Gln Ile Ala Ile Asn Ile Tyr Gly Cys Asn Met Asn
                405                 410                 415

Lys Lys Gln Trp Glu Asn Pro Glu Glu Trp Lys Pro Glu Arg Phe Leu
            420                 425                 430

Asp Glu Lys Tyr Asp Leu Met Asp Leu His Lys Thr Met Ala Phe Gly
        435                 440                 445

Gly Gly Lys Arg Val Cys Ala Gly Ala Leu Gln Ala Met Leu Ile Ala
```

```
    450                 455                 460

Cys Thr Ser Ile Gly Arg Phe Val Gln Glu Phe Glu Trp Lys Leu Met
465                 470                 475                 480

Gly Gly Glu Glu Glu Asn Val Asp Thr Val Ala Leu Thr Ser Gln Lys
                485                 490                 495

Leu His Pro Met Gln Ala Ile Ile Lys Ala Arg Glu
            500                 505

<210>  71
<211>  1593
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Codon-optimized KO

<400>  71
aagcttaaaa tgagtaagtc taatagtatg aattctacat cacacgaaac ccttttttcaa       60

caattggtct tgggtttgga ccgtatgcca ttgatggatg ttcactggtt gatctacgtt      120

gctttcggcg catggttatg ttcttatgtg atacatgttt tatcatcttc ctctacagta      180

aaagtgccag ttgttggata caggtctgta ttcgaaccta catggttgct tagacttaga      240

ttcgtctggg aaggtggctc tatcataggt caagggtaca ataagtttaa agactctatt      300

ttccaagtta ggaaattggg aactgatatt gtcattatac cacctaacta tattgatgaa      360

gtgagaaaat tgtcacagga caagactaga tcagttgaac ctttcattaa tgattttgca      420

ggtcaataca caagaggcat ggttttcttg caatctgact tacaaaaccg tgttatacaa      480

caaagactaa ctccaaaatt ggtttccttg accaaggtca tgaaggaaga gttggattat      540

gctttaacaa aagagatgcc tgatatgaaa aatgacgaat gggtagaagt agatatcagt      600

agtataatgg tgagattgat ttccaggatc tccgccagag tctttctagg gcctgaacac      660

tgtcgtaacc aggaatggtt gactactaca gcagaatatt cagaatcact tttcattaca      720

gggtttatct taagagttgt acctcatatc ttaagaccat tcatcgcccc tctattacct      780
```

tcatacagga ctctacttag aaacgtttca agtggtagaa gagtcatcgg tgacatcata 840

agatctcagc aaggggatgg taacgaagat atactttcct ggatgagaga tgctgccaca 900

ggagaggaaa agcaaatcga taacattgct cagagaatgt taattctttc tttagcatca 960

atccacacta ctgcgatgac catgacacat gccatgtacg atctatgtgc ttgccctgag 1020

tacattgaac cattaagaga tgaagttaaa tctgttgttg gggcttctgg ctgggacaag 1080

acagcgttaa acagatttca taagttggac tccttcctaa aagagtcaca aagattcaac 1140

ccagtattct tattgacatt caatagaatc taccatcaat ctatgacctt atcagatggc 1200

actaacattc catctggaac acgtattgct gttccatcac acgcaatgtt gcaagattct 1260

gcacatgtcc caggtccaac cccacctact gaatttgatg gattcagata tagtaagata 1320

cgttctgata gtaactacgc acaaaagtac ctattctcca tgaccgattc ttcaaacatg 1380

gctttcggat acggcaagta tgcttgtcca ggtagatttt acgcgtctaa tgagatgaaa 1440

ctaacattag ccattttgtt gctacaattt gagttcaaac taccagatgg taaaggtcgt 1500

cctagaaata tcactatcga ttctgatatg attccagacc caagagctag actttgcgtc 1560

agaaaaagat cacttagaga tgaatgaccg cgg 1593

<210> 72
<211> 525
<212> PRT
<213> Gibberella fujikuroi

<400> 72

Met Ser Lys Ser Asn Ser Met Asn Ser Thr Ser His Glu Thr Leu Phe
1 5 10 15

Gln Gln Leu Val Leu Gly Leu Asp Arg Met Pro Leu Met Asp Val His
20 25 30

Trp Leu Ile Tyr Val Ala Phe Gly Ala Trp Leu Cys Ser Tyr Val Ile
35 40 45

His Val Leu Ser Ser Ser Ser Thr Val Lys Val Pro Val Val Gly Tyr
50 55 60

```
Arg Ser Val Phe Glu Pro Thr Trp Leu Leu Arg Leu Arg Phe Val Trp
65                  70                  75                  80

Glu Gly Gly Ser Ile Ile Gly Gln Gly Tyr Asn Lys Phe Lys Asp Ser
                85                  90                  95

Ile Phe Gln Val Arg Lys Leu Gly Thr Asp Ile Val Ile Ile Pro Pro
            100                 105                 110

Asn Tyr Ile Asp Glu Val Arg Lys Leu Ser Gln Asp Lys Thr Arg Ser
        115                 120                 125

Val Glu Pro Phe Ile Asn Asp Phe Ala Gly Gln Tyr Thr Arg Gly Met
    130                 135                 140

Val Phe Leu Gln Ser Asp Leu Gln Asn Arg Val Ile Gln Gln Arg Leu
145                 150                 155                 160

Thr Pro Lys Leu Val Ser Leu Thr Lys Val Met Lys Glu Glu Leu Asp
                165                 170                 175

Tyr Ala Leu Thr Lys Glu Met Pro Asp Met Lys Asn Asp Glu Trp Val
            180                 185                 190

Glu Val Asp Ile Ser Ser Ile Met Val Arg Leu Ile Ser Arg Ile Ser
        195                 200                 205

Ala Arg Val Phe Leu Gly Pro Glu His Cys Arg Asn Gln Glu Trp Leu
    210                 215                 220

Thr Thr Thr Ala Glu Tyr Ser Glu Ser Leu Phe Ile Thr Gly Phe Ile
225                 230                 235                 240

Leu Arg Val Val Pro His Ile Leu Arg Pro Phe Ile Ala Pro Leu Leu
                245                 250                 255
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```
Pro Ser Tyr Arg Thr Leu Leu Arg Asn Val Ser Ser Gly Arg Arg Val
            260                 265                 270

Ile Gly Asp Ile Ile Arg Ser Gln Gln Gly Asp Gly Asn Glu Asp Ile
        275                 280                 285

Leu Ser Trp Met Arg Asp Ala Ala Thr Gly Glu Glu Lys Gln Ile Asp
    290                 295                 300

Asn Ile Ala Gln Arg Met Leu Ile Leu Ser Leu Ala Ser Ile His Thr
305                 310                 315                 320

Thr Ala Met Thr Met Thr His Ala Met Tyr Asp Leu Cys Ala Cys Pro
                325                 330                 335

Glu Tyr Ile Glu Pro Leu Arg Asp Glu Val Lys Ser Val Val Gly Ala
            340                 345                 350

Ser Gly Trp Asp Lys Thr Ala Leu Asn Arg Phe His Lys Leu Asp Ser
        355                 360                 365

Phe Leu Lys Glu Ser Gln Arg Phe Asn Pro Val Phe Leu Leu Thr Phe
    370                 375                 380

Asn Arg Ile Tyr His Gln Ser Met Thr Leu Ser Asp Gly Thr Asn Ile
385                 390                 395                 400

Pro Ser Gly Thr Arg Ile Ala Val Pro Ser His Ala Met Leu Gln Asp
                405                 410                 415

Ser Ala His Val Pro Gly Pro Thr Pro Pro Thr Glu Phe Asp Gly Phe
            420                 425                 430

Arg Tyr Ser Lys Ile Arg Ser Asp Ser Asn Tyr Ala Gln Lys Tyr Leu
        435                 440                 445

Phe Ser Met Thr Asp Ser Ser Asn Met Ala Phe Gly Tyr Gly Lys Tyr
    450                 455                 460
```

```
Ala Cys Pro Gly Arg Phe Tyr Ala Ser Asn Glu Met Lys Leu Thr Leu
465                 470                 475                 480


Ala Ile Leu Leu Leu Gln Phe Glu Phe Lys Leu Pro Asp Gly Lys Gly
                485                 490                 495


Arg Pro Arg Asn Ile Thr Ile Asp Ser Asp Met Ile Pro Asp Pro Arg
            500                 505                 510


Ala Arg Leu Cys Val Arg Lys Arg Ser Leu Arg Asp Glu
        515                 520                 525


<210>  73
<211>  1515
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Codon-optimized KO

<400>  73
aagcttaaaa tggaagatcc tactgtctta tatgcttgtc ttgccattgc agttgcaact       60

ttcgttgtta gatggtacag agatccattg agatccatcc caacagttgg tggttccgat      120

ttgcctattc tatcttacat cggcgcacta agatggacaa gacgtggcag agagatactt      180

caagagggat atgatggcta cagaggatct acattcaaaa tcgcgatgtt agaccgttgg      240

atcgtgatcg caaatggtcc taaactagct gatgaagtca gacgtagacc agatgaagag      300

ttaaacttta tggacggatt aggagcattc gtccaaacta agtacacctt aggtgaagct      360

attcataacg atccatacca tgtcgatatc ataagagaaa aactaacaag aggccttcca      420

gccgtgcttc ctgatgtcat tgaagagttg acacttgcgg ttagacagta cattccaaca      480

gaaggtgatg aatgggtgtc cgtaaactgt tcaaaggccg caagagatat tgttgctaga      540

gcttctaata gagtctttgt aggtttgcct gcttgcagaa accaaggtta cttagatttg      600

gcaatagact ttacattgtc tgttgtcaag gatagagcca tcatcaatat gtttccagaa      660

ttgttgaagc caatagttgg cagagttgta ggtaacgcca ccagaaatgt tcgtagagct      720
```

gttccttttg ttgctccatt ggtggaggaa agacgtagac ttatggaaga gtacggtgaa 780

gactggtctg aaaaacctaa tgatatgtta cagtggataa tggatgaagc tgcatccaga 840

gatagttcag tgaaggcaat cgcagagaga ttgttaatgg tgaacttcgc ggctattcat 900

acctcatcaa acactatcac tcatgctttg taccaccttg ccgaaatgcc tgaaactttg 960

caaccactta gagaagagat cgaaccatta gtcaaagagg agggctggac caaggctgct 1020

atgggaaaaa tgtggtggtt agattcattt ctaagagaat ctcaaagata caatggcatt 1080

aacatcgtat ctttaactag aatggctgac aaagatatta cattgagtga tggcacattt 1140

ttgccaaaag gtactctagt ggccgttcca gcgtattcta ctcatagaga tgatgctgtc 1200

tacgctgatg ccttagtatt cgatcctttc agattctcac gtatgagagc gagagaaggt 1260

gaaggtacaa agcaccagtt cgttaatact tcagtcgagt acgttccatt tggtcacgga 1320

aagcatgctt gtccaggaag attcttcgcc gcaaacgaat tgaaagcaat gttggcttac 1380

attgttctaa actatgatgt aaagttgcct ggtgacggta aacgtccatt gaacatgtat 1440

tggggtccaa cagttttgcc tgcaccagca ggccaagtat tgttcagaaa gagacaagtt 1500

agtctataac cgcgg 1515

<210> 74
<211> 499
<212> PRT
<213> Trametes versicolor

<400> 74

Met Glu Asp Pro Thr Val Leu Tyr Ala Cys Leu Ala Ile Ala Val Ala
1 5 10 15

Thr Phe Val Val Arg Trp Tyr Arg Asp Pro Leu Arg Ser Ile Pro Thr
20 25 30

Val Gly Gly Ser Asp Leu Pro Ile Leu Ser Tyr Ile Gly Ala Leu Arg
35 40 45

Trp Thr Arg Arg Gly Arg Glu Ile Leu Gln Glu Gly Tyr Asp Gly Tyr

```
    50                  55                  60

Arg Gly Ser Thr Phe Lys Ile Ala Met Leu Asp Arg Trp Ile Val Ile
65                  70                  75                  80

Ala Asn Gly Pro Lys Leu Ala Asp Glu Val Arg Arg Arg Pro Asp Glu
                85                  90                  95

Glu Leu Asn Phe Met Asp Gly Leu Gly Ala Phe Val Gln Thr Lys Tyr
            100                 105                 110

Thr Leu Gly Glu Ala Ile His Asn Asp Pro Tyr His Val Asp Ile Ile
        115                 120                 125

Arg Glu Lys Leu Thr Arg Gly Leu Pro Ala Val Leu Pro Asp Val Ile
    130                 135                 140

Glu Glu Leu Thr Leu Ala Val Arg Gln Tyr Ile Pro Thr Glu Gly Asp
145                 150                 155                 160

Glu Trp Val Ser Val Asn Cys Ser Lys Ala Ala Arg Asp Ile Val Ala
                165                 170                 175

Arg Ala Ser Asn Arg Val Phe Val Gly Leu Pro Ala Cys Arg Asn Gln
            180                 185                 190

Gly Tyr Leu Asp Leu Ala Ile Asp Phe Thr Leu Ser Val Val Lys Asp
        195                 200                 205

Arg Ala Ile Ile Asn Met Phe Pro Glu Leu Leu Lys Pro Ile Val Gly
    210                 215                 220

Arg Val Val Gly Asn Ala Thr Arg Asn Val Arg Arg Ala Val Pro Phe
225                 230                 235                 240

Val Ala Pro Leu Val Glu Glu Arg Arg Arg Leu Met Glu Glu Tyr Gly
                245                 250                 255
```

```
Glu Asp Trp Ser Glu Lys Pro Asn Asp Met Leu Gln Trp Ile Met Asp
            260                 265                 270

Glu Ala Ala Ser Arg Asp Ser Ser Val Lys Ala Ile Ala Glu Arg Leu
        275                 280                 285

Leu Met Val Asn Phe Ala Ala Ile His Thr Ser Ser Asn Thr Ile Thr
    290                 295                 300

His Ala Leu Tyr His Leu Ala Glu Met Pro Glu Thr Leu Gln Pro Leu
305                 310                 315                 320

Arg Glu Glu Ile Glu Pro Leu Val Lys Glu Glu Gly Trp Thr Lys Ala
                325                 330                 335

Ala Met Gly Lys Met Trp Trp Leu Asp Ser Phe Leu Arg Glu Ser Gln
            340                 345                 350

Arg Tyr Asn Gly Ile Asn Ile Val Ser Leu Thr Arg Met Ala Asp Lys
        355                 360                 365

Asp Ile Thr Leu Ser Asp Gly Thr Phe Leu Pro Lys Gly Thr Leu Val
    370                 375                 380

Ala Val Pro Ala Tyr Ser Thr His Arg Asp Asp Ala Val Tyr Ala Asp
385                 390                 395                 400

Ala Leu Val Phe Asp Pro Phe Arg Phe Ser Arg Met Arg Ala Arg Glu
                405                 410                 415

Gly Glu Gly Thr Lys His Gln Phe Val Asn Thr Ser Val Glu Tyr Val
            420                 425                 430

Pro Phe Gly His Gly Lys His Ala Cys Pro Gly Arg Phe Phe Ala Ala
        435                 440                 445

Asn Glu Leu Lys Ala Met Leu Ala Tyr Ile Val Leu Asn Tyr Asp Val
```

```
    450                 455                 460

Lys Leu Pro Gly Asp Gly Lys Arg Pro Leu Asn Met Tyr Trp Gly Pro
465                 470                 475                 480

Thr Val Leu Pro Ala Pro Ala Gly Gln Val Leu Phe Arg Lys Arg Gln
                485                 490                 495

Val Ser Leu
```

<210> 75
<211> 1530
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized KO

<400> 75

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atggcatttt tctctatgat ttcaattttg ttgggatttg ttatttcttc tttcatcttc       60

atctttttct tcaaaaagtt acttagtttt agtaggaaaa acatgtcaga agtttctact      120

ttgccaagtg ttccagtagt gcctggtttt ccagttattg ggaatttgtt gcaactaaag      180

gagaaaaagc ctcataaaac tttcactaga tggtcagaga tatatggacc tatctactct      240

ataaagatgg gttcttcatc tcttattgta ttgaacagta cagaaactgc taaggaagca      300

atggtcacta gattttcatc aatatctacc agaaaattgt caaacgccct aacagttcta      360

acctgcgata agtctatggt cgccacttct gattatgatg acttccacaa attagttaag      420

agatgtttgc taaatggact tcttggtgct aatgctcaaa agagaaaaag acactacaga      480

gatgctttga ttgaaaatgt gagttccaag ctacatgcac acgctagaga tcatccacaa      540

gagccagtta actttagagc aattttcgaa cacgaattgt ttggtgtagc attaaagcaa      600

gccttcggta aagacgtaga atccatatac gtcaaggagt taggcgtaac attatcaaaa      660

gatgaaatct ttaaggtgct tgtacatgat atgatggagg gtgcaattga tgtagattgg      720

agagatttct tcccatattt gaaatggatc cctaataagt cttttgaagc taggatacaa      780
```

caaaagcaca agagaagact agctgttatg aacgcactta tacaggacag attgaagcaa 840

aatgggtctg aatcagatga tgattgttac cttaacttct taatgtctga ggctaaaaca 900

ttgactaagg aacagatcgc aatccttgtc tgggaaacaa tcattgaaac agcagatact 960

accttagtca caactgaatg ggccatatac gagctagcca aacatccatc tgtgcaagat 1020

aggttgtgta aggagatcca gaacgtgtgt ggtggagaga aattcaagga agagcagttg 1080

tcacaagttc cttaccttaa cggcgttttc catgaaacct tgagaaaata ctcacctgca 1140

ccattagttc ctattagata cgcccacgaa gatacacaaa tcggtggcta ccatgttcca 1200

gctgggtccg aaattgctat aaacatctac gggtgcaaca tggacaaaaa gagatgggaa 1260

agaccagaag attggtggcc agaaagattc ttagatgatg gcaaatatga aacatctgat 1320

ttgcataaaa caatggcttt cggagctggc aaaagagtgt gtgccggtgc tctacaagcc 1380

tccctaatgg ctggtatcgc tattggtaga ttggtccaag agttcgaatg gaaacttaga 1440

gatggtgaag aggaaaatgt cgatacttat gggttaacat ctcaaaagtt atacccacta 1500

atggcaatca tcaatcctag aagatcctaa 1530

<210> 76
<211> 509
<212> PRT
<213> Arabidopsis thaliana

<400> 76

Met Ala Phe Phe Ser Met Ile Ser Ile Leu Leu Gly Phe Val Ile Ser
1 5 10 15

Ser Phe Ile Phe Ile Phe Phe Phe Lys Lys Leu Leu Ser Phe Ser Arg
20 25 30

Lys Asn Met Ser Glu Val Ser Thr Leu Pro Ser Val Pro Val Val Pro
35 40 45

Gly Phe Pro Val Ile Gly Asn Leu Leu Gln Leu Lys Glu Lys Lys Pro
50 55 60

```
His Lys Thr Phe Thr Arg Trp Ser Glu Ile Tyr Gly Pro Ile Tyr Ser
65                  70                  75                  80

Ile Lys Met Gly Ser Ser Ser Leu Ile Val Leu Asn Ser Thr Glu Thr
                85                  90                  95

Ala Lys Glu Ala Met Val Thr Arg Phe Ser Ser Ile Ser Thr Arg Lys
            100                 105                 110

Leu Ser Asn Ala Leu Thr Val Leu Thr Cys Asp Lys Ser Met Val Ala
        115                 120                 125

Thr Ser Asp Tyr Asp Asp Phe His Lys Leu Val Lys Arg Cys Leu Leu
    130                 135                 140

Asn Gly Leu Leu Gly Ala Asn Ala Gln Lys Arg Lys Arg His Tyr Arg
145                 150                 155                 160

Asp Ala Leu Ile Glu Asn Val Ser Ser Lys Leu His Ala His Ala Arg
                165                 170                 175

Asp His Pro Gln Glu Pro Val Asn Phe Arg Ala Ile Phe Glu His Glu
            180                 185                 190

Leu Phe Gly Val Ala Leu Lys Gln Ala Phe Gly Lys Asp Val Glu Ser
        195                 200                 205

Ile Tyr Val Lys Glu Leu Gly Val Thr Leu Ser Lys Asp Glu Ile Phe
    210                 215                 220

Lys Val Leu Val His Asp Met Met Glu Gly Ala Ile Asp Val Asp Trp
225                 230                 235                 240

Arg Asp Phe Phe Pro Tyr Leu Lys Trp Ile Pro Asn Lys Ser Phe Glu
                245                 250                 255

Ala Arg Ile Gln Gln Lys His Lys Arg Arg Leu Ala Val Met Asn Ala
            260                 265                 270
```

```
Leu Ile Gln Asp Arg Leu Lys Gln Asn Gly Ser Glu Ser Asp Asp Asp
        275                 280                 285

Cys Tyr Leu Asn Phe Leu Met Ser Glu Ala Lys Thr Leu Thr Lys Glu
    290                 295                 300

Gln Ile Ala Ile Leu Val Trp Glu Thr Ile Ile Glu Thr Ala Asp Thr
305                 310                 315                 320

Thr Leu Val Thr Thr Glu Trp Ala Ile Tyr Glu Leu Ala Lys His Pro
                325                 330                 335

Ser Val Gln Asp Arg Leu Cys Lys Glu Ile Gln Asn Val Cys Gly Gly
            340                 345                 350

Glu Lys Phe Lys Glu Glu Gln Leu Ser Gln Val Pro Tyr Leu Asn Gly
        355                 360                 365

Val Phe His Glu Thr Leu Arg Lys Tyr Ser Pro Ala Pro Leu Val Pro
    370                 375                 380

Ile Arg Tyr Ala His Glu Asp Thr Gln Ile Gly Gly Tyr His Val Pro
385                 390                 395                 400

Ala Gly Ser Glu Ile Ala Ile Asn Ile Tyr Gly Cys Asn Met Asp Lys
                405                 410                 415

Lys Arg Trp Glu Arg Pro Glu Asp Trp Trp Pro Glu Arg Phe Leu Asp
            420                 425                 430

Asp Gly Lys Tyr Glu Thr Ser Asp Leu His Lys Thr Met Ala Phe Gly
        435                 440                 445

Ala Gly Lys Arg Val Cys Ala Gly Ala Leu Gln Ala Ser Leu Met Ala
    450                 455                 460
```

```
Gly Ile Ala Ile Gly Arg Leu Val Gln Glu Phe Glu Trp Lys Leu Arg
465                 470                 475                 480


Asp Gly Glu Glu Glu Asn Val Asp Thr Tyr Gly Leu Thr Ser Gln Lys
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Leu Tyr Pro Leu Met Ala Ile Ile Asn Pro Arg Arg Ser
            500                 505


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<212>  DNA
<213>  Artificial Sequence

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<223>  Codon-optimized CPR

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aagatgctag ttgaaaatag agaattgttg acactgttca caacttcctt cgcagttctt      180

attgggtgtc ttgtatttct aatgtggaga cgttcatcct ctaaaaagct ggtacaagat      240

ccagttccac aagttatcgt tgtaaagaag aaagagaagg agtcagaggt tgatgacggg      300

aaaaagaaag tttctatttt ctacggcaca caaacaggaa ctgccgaagg ttttgctaaa      360

gcattagtcg aggaagcaaa agtgagatat gaaaagacct ctttcaaggt tatcgatcta      420

gatgactacg ctgcagatga tgatgaatat gaggaaaaac tgaaaaagga atccttagcc      480

ttcttcttct tggccacata cggtgatggt gaacctactg ataatgctgc taacttctac      540

aagtggttca cagaaggcga cgataaaggt gaatggctga aaaagttaca atacggagta      600

tttggtttag gtaacagaca atatgaacat ttcaacaaga tcgctattgt agttgatgat      660

aaacttactg aaatgggagc caaaagatta gtaccagtag gattagggga tgatgatcag      720

tgtatagaag atgacttcac cgcctggaag gaattggtat ggccagaatt ggatcaactt      780

ttaagggacg aagatgatac ttctgtgact accccataca ctgcagccgt attggagtac      840

agagtggttt accatgataa accagcagac tcatatgctg aagatcaaac ccatacaaac      900
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ctacacacct ctcaatcaga taggtcttgt actcacttag aattcgatat ttctcacaca 1020

ggactgtctt acgaaactgg cgatcacgtt ggcgtttatt ccgagaactt gtccgaagtt 1080

gtcgatgaag cactaaaact gttagggtta tcaccagaca catacttctc agtccatgct 1140

gataaggagg atgggacacc tatcggtggt gcttcactac caccaccttt tcctccttgc 1200

acattgagag acgctctaac cagatacgca gatgtcttat cctcacctaa aaaggtagct 1260

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gcttcaccag ccggaaaaga tgaatatgca caatggatcg tcgccaacca acgttctttg 1380

ctagaagtga tgcaaagttt tccatctgcc aagcctccat taggtgtgtt cttcgcagca 1440

gtagctccac gtttacaacc aagatactac tctatcagtt catctcctaa gatgtctcct 1500

aacagaatac atgttacatg tgctttggtg tacgagacta ctccagcagg cagaattcac 1560

agaggattgt gttcaacctg gatgaaaaat gctgtccctt taacagagtc acctgattgc 1620

tctcaagcat ccattttcgt tagaacatca aatttcagac ttccagtgga tccaaaagtt 1680

ccagtcatta tgataggacc aggcactggt cttgccccat tcaggggctt tcttcaagag 1740

agattggcct tgaaggaatc tggtacagaa ttgggttctt ctatcttttt ctttggttgc 1800

cgtaatagaa aagttgactt tatctacgag gacgagctta acaattttgt tgagacagga 1860

gcattgtcag aattgatcgt cgcattttca agagaaggga ctgccaaaga gtacgttcag 1920

cacaagatga gtcaaaaagc ctccgatata tggaaacttc taagtgaagg tgcctatctt 1980

tatgtctgtg gcgatgcaaa gggcatggcc aaggatgtcc atagaactct gcatacaatt 2040

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atgtctggaa gatacttaag agatgtttgg taa 2133

<210> 78
<211> 710
<212> PRT
<213> Stevia rebaudiana

<400> 78

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Met Gln Ser Asp Ser Val Lys Val Ser Pro Phe Asp Leu Val Ser Ala
1               5                  10                  15

Ala Met Asn Gly Lys Ala Met Glu Lys Leu Asn Ala Ser Glu Ser Glu
            20                  25                  30

Asp Pro Thr Thr Leu Pro Ala Leu Lys Met Leu Val Glu Asn Arg Glu
        35                  40                  45

Leu Leu Thr Leu Phe Thr Thr Ser Phe Ala Val Leu Ile Gly Cys Leu
    50                  55                  60

Val Phe Leu Met Trp Arg Arg Ser Ser Ser Lys Lys Leu Val Gln Asp
65                  70                  75                  80

Pro Val Pro Gln Val Ile Val Val Lys Lys Lys Glu Lys Glu Ser Glu
                85                  90                  95

Val Asp Asp Gly Lys Lys Lys Val Ser Ile Phe Tyr Gly Thr Gln Thr
            100                 105                 110

Gly Thr Ala Glu Gly Phe Ala Lys Ala Leu Val Glu Glu Ala Lys Val
        115                 120                 125

Arg Tyr Glu Lys Thr Ser Phe Lys Val Ile Asp Leu Asp Asp Tyr Ala
    130                 135                 140

Ala Asp Asp Asp Glu Tyr Glu Glu Lys Leu Lys Lys Glu Ser Leu Ala
145                 150                 155                 160

Phe Phe Phe Leu Ala Thr Tyr Gly Asp Gly Glu Pro Thr Asp Asn Ala
                165                 170                 175

Ala Asn Phe Tyr Lys Trp Phe Thr Glu Gly Asp Asp Lys Gly Glu Trp
            180                 185                 190

Leu Lys Lys Leu Gln Tyr Gly Val Phe Gly Leu Gly Asn Arg Gln Tyr
```

```
        195                 200                 205

Glu His Phe Asn Lys Ile Ala Ile Val Val Asp Asp Lys Leu Thr Glu
    210                 215                 220

Met Gly Ala Lys Arg Leu Val Pro Val Gly Leu Gly Asp Asp Asp Gln
225                 230                 235                 240

Cys Ile Glu Asp Asp Phe Thr Ala Trp Lys Glu Leu Val Trp Pro Glu
                245                 250                 255

Leu Asp Gln Leu Leu Arg Asp Glu Asp Asp Thr Ser Val Thr Thr Pro
            260                 265                 270

Tyr Thr Ala Ala Val Leu Glu Tyr Arg Val Val Tyr His Asp Lys Pro
        275                 280                 285

Ala Asp Ser Tyr Ala Glu Asp Gln Thr His Thr Asn Gly His Val Val
    290                 295                 300

His Asp Ala Gln His Pro Ser Arg Ser Asn Val Ala Phe Lys Lys Glu
305                 310                 315                 320

Leu His Thr Ser Gln Ser Asp Arg Ser Cys Thr His Leu Glu Phe Asp
                325                 330                 335

Ile Ser His Thr Gly Leu Ser Tyr Glu Thr Gly Asp His Val Gly Val
            340                 345                 350

Tyr Ser Glu Asn Leu Ser Glu Val Val Asp Glu Ala Leu Lys Leu Leu
        355                 360                 365

Gly Leu Ser Pro Asp Thr Tyr Phe Ser Val His Ala Asp Lys Glu Asp
    370                 375                 380

Gly Thr Pro Ile Gly Gly Ala Ser Leu Pro Pro Pro Phe Pro Pro Cys
385                 390                 395                 400
```

```
Thr Leu Arg Asp Ala Leu Thr Arg Tyr Ala Asp Val Leu Ser Ser Pro
                405                 410                 415

Lys Lys Val Ala Leu Leu Ala Leu Ala Ala His Ala Ser Asp Pro Ser
            420                 425                 430

Glu Ala Asp Arg Leu Lys Phe Leu Ala Ser Pro Ala Gly Lys Asp Glu
        435                 440                 445

Tyr Ala Gln Trp Ile Val Ala Asn Gln Arg Ser Leu Leu Glu Val Met
    450                 455                 460

Gln Ser Phe Pro Ser Ala Lys Pro Pro Leu Gly Val Phe Phe Ala Ala
465                 470                 475                 480

Val Ala Pro Arg Leu Gln Pro Arg Tyr Tyr Ser Ile Ser Ser Ser Pro
                485                 490                 495

Lys Met Ser Pro Asn Arg Ile His Val Thr Cys Ala Leu Val Tyr Glu
            500                 505                 510

Thr Thr Pro Ala Gly Arg Ile His Arg Gly Leu Cys Ser Thr Trp Met
        515                 520                 525

Lys Asn Ala Val Pro Leu Thr Glu Ser Pro Asp Cys Ser Gln Ala Ser
    530                 535                 540

Ile Phe Val Arg Thr Ser Asn Phe Arg Leu Pro Val Asp Pro Lys Val
545                 550                 555                 560

Pro Val Ile Met Ile Gly Pro Gly Thr Gly Leu Ala Pro Phe Arg Gly
                565                 570                 575

Phe Leu Gln Glu Arg Leu Ala Leu Lys Glu Ser Gly Thr Glu Leu Gly
            580                 585                 590

Ser Ser Ile Phe Phe Phe Gly Cys Arg Asn Arg Lys Val Asp Phe Ile
```

595 600 605

Tyr Glu Asp Glu Leu Asn Asn Phe Val Glu Thr Gly Ala Leu Ser Glu
610 615 620

Leu Ile Val Ala Phe Ser Arg Glu Gly Thr Ala Lys Glu Tyr Val Gln
625 630 635 640

His Lys Met Ser Gln Lys Ala Ser Asp Ile Trp Lys Leu Leu Ser Glu
645 650 655

Gly Ala Tyr Leu Tyr Val Cys Gly Asp Ala Lys Gly Met Ala Lys Asp
660 665 670

Val His Arg Thr Leu His Thr Ile Val Gln Glu Gln Gly Ser Leu Asp
675 680 685

Ser Ser Lys Ala Glu Leu Tyr Val Lys Asn Leu Gln Met Ser Gly Arg
690 695 700

Tyr Leu Arg Asp Val Trp
705 710

<210> 79
<211> 2106
<212> DNA
<213> Siraitia grosvenorii

<400> 79
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agaagagctg gttctagaaa ggttaagaat gtcgaattgc caaagccatt gattgtccat 240

gaaccagaac ctgaagttga agatggtaag aagaaggttt ccatcttctt cggtactcaa 300

actggtactg ctgaaggttt tgctaaggct ttggctgatg aagctaaagc tagatacgaa 360

aaggctacct tcagagttgt tgatttggat gattatgctg ccgatgatga ccaatacgaa 420

gaaaaattga agaacgaatc cttcgccgtt ttcttgttgg ctacttatgg tgatggtgaa 480

cctactgata atgctgctag attttacaag tggttcgccg aaggtaaaga aagaggtgaa 540

tggttgcaaa acttgcacta tgctgttttt ggtttgggta acagacaata cgaacacttc 600

aacaagattg ctaaggttgc cgacgaatta ttggaagctc aaggtggtaa tagattggtt 660

aaggttggtt taggtgatga cgatcaatgc atcgaagatg atttttctgc ttggagagaa 720

tctttgtggc cagaattgga tatgttgttg agagatgaag atgatgctac tactgttact 780

actccatata ctgctgctgt cttggaatac agagttgtct ttcatgattc tgctgatgtt 840

gctgctgaag ataagtcttg gattaacgct aatggtcatg ctgttcatga tgctcaacat 900

ccattcagat ctaacgttgt cgtcagaaaa gaattgcata cttctgcctc tgatagatcc 960

tgttctcatt tggaattcaa catttccggt tccgctttga attacgaaac tggtgatcat 1020

gttggtgtct actgtgaaaa cttgactgaa actgttgatg aagccttgaa cttgttgggt 1080

ttgtctccag aaacttactt ctctatctac accgataacg aagatggtac tccattgggt 1140

ggttcttcat tgccaccacc atttccatca tgtactttga gaactgcttt gaccagatac 1200

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gcccaatctg ttatcggttc ccaaaagtct ttgttggaag ttatggctga attcccatct 1380

gctaaaccac cattaggtgt ttttttgct gctgttgctc caagattgca acctagattc 1440

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atctggaact tgatttctga aggtgcttac ttgtacgttt gtggtgatgc taaaggtatg 1980

gctaaggatg ttcatagaac cttgcatacc atcatgcaag aacaaggttc tttggattct 2040

tccaaagctg aatccatggt caagaacttg caaatgaatg gtagatactt aagagatgtt 2100

tggtaa 2106

<210> 80
<211> 701
<212> PRT
<213> Siraitia grosvenorii

<400> 80

Met Lys Val Ser Pro Phe Glu Phe Met Ser Ala Ile Ile Lys Gly Arg
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Met Asp Pro Ser Asn Ser Ser Phe Glu Ser Thr Gly Glu Val Ala Ser
20 25 30

Val Ile Phe Glu Asn Arg Glu Leu Val Ala Ile Leu Thr Thr Ser Ile
35 40 45

Ala Val Met Ile Gly Cys Phe Val Val Leu Met Trp Arg Arg Ala Gly
50 55 60

Ser Arg Lys Val Lys Asn Val Glu Leu Pro Lys Pro Leu Ile Val His
65 70 75 80

Glu Pro Glu Pro Glu Val Glu Asp Gly Lys Lys Lys Val Ser Ile Phe
85 90 95

Phe Gly Thr Gln Thr Gly Thr Ala Glu Gly Phe Ala Lys Ala Leu Ala
100 105 110

Asp Glu Ala Lys Ala Arg Tyr Glu Lys Ala Thr Phe Arg Val Val Asp
115 120 125

Leu Asp Asp Tyr Ala Ala Asp Asp Asp Gln Tyr Glu Glu Lys Leu Lys

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    130                 135                 140

Asn Glu Ser Phe Ala Val Phe Leu Leu Ala Thr Tyr Gly Asp Gly Glu
145                 150                 155                 160

Pro Thr Asp Asn Ala Ala Arg Phe Tyr Lys Trp Phe Ala Glu Gly Lys
                165                 170                 175

Glu Arg Gly Glu Trp Leu Gln Asn Leu His Tyr Ala Val Phe Gly Leu
            180                 185                 190

Gly Asn Arg Gln Tyr Glu His Phe Asn Lys Ile Ala Lys Val Ala Asp
        195                 200                 205

Glu Leu Leu Glu Ala Gln Gly Gly Asn Arg Leu Val Lys Val Gly Leu
    210                 215                 220

Gly Asp Asp Asp Gln Cys Ile Glu Asp Asp Phe Ser Ala Trp Arg Glu
225                 230                 235                 240

Ser Leu Trp Pro Glu Leu Asp Met Leu Leu Arg Asp Glu Asp Asp Ala
                245                 250                 255

Thr Thr Val Thr Thr Pro Tyr Thr Ala Ala Val Leu Glu Tyr Arg Val
            260                 265                 270

Val Phe His Asp Ser Ala Asp Val Ala Ala Glu Asp Lys Ser Trp Ile
        275                 280                 285

Asn Ala Asn Gly His Ala Val His Asp Ala Gln His Pro Phe Arg Ser
    290                 295                 300

Asn Val Val Val Arg Lys Glu Leu His Thr Ser Ala Ser Asp Arg Ser
305                 310                 315                 320

Cys Ser His Leu Glu Phe Asn Ile Ser Gly Ser Ala Leu Asn Tyr Glu
                325                 330                 335
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Thr Gly Asp His Val Gly Val Tyr Cys Glu Asn Leu Thr Glu Thr Val
            340                 345                 350

Asp Glu Ala Leu Asn Leu Leu Gly Leu Ser Pro Glu Thr Tyr Phe Ser
        355                 360                 365

Ile Tyr Thr Asp Asn Glu Asp Gly Thr Pro Leu Gly Gly Ser Ser Leu
    370                 375                 380

Pro Pro Pro Phe Pro Ser Cys Thr Leu Arg Thr Ala Leu Thr Arg Tyr
385                 390                 395                 400

Ala Asp Leu Leu Asn Ser Pro Lys Lys Ser Ala Leu Leu Ala Leu Ala
                405                 410                 415

Ala His Ala Ser Asn Pro Val Glu Ala Asp Arg Leu Arg Tyr Leu Ala
            420                 425                 430

Ser Pro Ala Gly Lys Asp Glu Tyr Ala Gln Ser Val Ile Gly Ser Gln
        435                 440                 445

Lys Ser Leu Leu Glu Val Met Ala Glu Phe Pro Ser Ala Lys Pro Pro
    450                 455                 460

Leu Gly Val Phe Phe Ala Ala Val Ala Pro Arg Leu Gln Pro Arg Phe
465                 470                 475                 480

Tyr Ser Ile Ser Ser Ser Pro Arg Met Ala Pro Ser Arg Ile His Val
                485                 490                 495

Thr Cys Ala Leu Val Tyr Asp Lys Met Pro Thr Gly Arg Ile His Lys
            500                 505                 510

Gly Val Cys Ser Thr Trp Met Lys Asn Ser Val Pro Met Glu Lys Ser
        515                 520                 525

His Glu Cys Ser Trp Ala Pro Ile Phe Val Arg Gln Ser Asn Phe Lys
```

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    530                 535                 540

Leu Pro Ala Glu Ser Lys Val Pro Ile Ile Met Val Gly Pro Gly Thr
545                 550                 555                 560

Gly Leu Ala Pro Phe Arg Gly Phe Leu Gln Glu Arg Leu Ala Leu Lys
                565                 570                 575

Glu Ser Gly Val Glu Leu Gly Pro Ser Ile Leu Phe Phe Gly Cys Arg
            580                 585                 590

Asn Arg Arg Met Asp Tyr Ile Tyr Glu Asp Glu Leu Asn Asn Phe Val
        595                 600                 605

Glu Thr Gly Ala Leu Ser Glu Leu Val Ile Ala Phe Ser Arg Glu Gly
    610                 615                 620

Pro Thr Lys Glu Tyr Val Gln His Lys Met Ala Glu Lys Ala Ser Asp
625                 630                 635                 640

Ile Trp Asn Leu Ile Ser Glu Gly Ala Tyr Leu Tyr Val Cys Gly Asp
                645                 650                 655

Ala Lys Gly Met Ala Lys Asp Val His Arg Thr Leu His Thr Ile Met
            660                 665                 670

Gln Glu Gln Gly Ser Leu Asp Ser Ser Lys Ala Glu Ser Met Val Lys
        675                 680                 685

Asn Leu Gln Met Asn Gly Arg Tyr Leu Arg Asp Val Trp
    690                 695                 700


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<211>  2142
<212>  DNA
<213>  Artificial Sequence

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<223>  Codon-optimized CPR
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gctgcaggtg gtgcttccaa gcctggcaga actagaaaca tcgtcgaagc tatggaggaa 180

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gaagattatg acttcgataa cttagacact gttccatctg ataacatcgt tatgtttgta 360

ttggctactt acggtgaagg cgaaccaaca gataacgccg tggatttcta tgagttcatt 420

actggcgaag atgcctcttt caatgagggc aacgatcctc cactaggtaa cttgaattac 480

gttgcgttcg gtctgggcaa caatacctac gaacactaca actcaatggt caggaacgtt 540

aacaaggctc tagaaaagtt aggagctcat agaattggag aagcaggtga gggtgacgac 600

ggagctggaa ctatggaaga ggacttttta gcttggaaag atccaatgtg ggaagccttg 660

gctaaaaaga tgggcttgga ggaaagagaa gctgtatatg aacctatttt cgctatcaat 720

gagagagatg atttgacccc tgaagcgaat gaggtatact tgggagaacc taataagcta 780

cacttggaag gtacagcgaa aggtccattc aactcccaca acccatatat cgcaccaatt 840

gcagaatcat acgaactttt ctcagctaag gatagaaatt gtctgcatat ggaaattgat 900

atttctggta gtaatctaaa gtatgaaaca ggcgaccata tcgcgatctg gcctaccaac 960

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ttggcctcag tctctaaagg tgaaaaatgg acaaagatac cattttctgc tttcatagaa 1320

ggccttacaa aactacaacc aagatactat tctatctctt cctctagttt agttcagcct 1380

aaaaagatta gtattactgc tgttgtcgaa tctcagcaaa ttccaggtag agatgaccca 1440

ttcagaggtg tagcgactaa ctacttgttc gctttgaagc agaaacaaaa cggtgatcca 1500

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cctattatca tgatcggtcc aggtaccggt gttgcccctt ttagaggctt cgtccaagag 1680

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ggcgacaaat tcgaaatgat tacagctttt tcaagagaag gatctaaaaa ggtttatgtt 1860

caacacagac tgaaggaaag atcaaaggaa gtttctgatc ttctatccca aaaagcatac 1920

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atcatagcag aaggccgtgg tgtatcagaa gccaagggtg aggaaattgt caaaaacatg 2040

agatcagcaa atcaatacca agtgtgttct gatttcgtaa ctttacactg taaagagaca 2100

acatacgcga attcagaatt gcaagaggat gtctggagtt aa 2142

<210> 82
<211> 713
<212> PRT
<213> Gibberella fujikuroi

<400> 82

Met Ala Glu Leu Asp Thr Leu Asp Ile Val Val Leu Gly Val Ile Phe
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Leu Gly Thr Val Ala Tyr Phe Thr Lys Gly Lys Leu Trp Gly Val Thr
20 25 30

Lys Asp Pro Tyr Ala Asn Gly Phe Ala Ala Gly Gly Ala Ser Lys Pro
35 40 45

Gly Arg Thr Arg Asn Ile Val Glu Ala Met Glu Glu Ser Gly Lys Asn
50 55 60

Cys Val Val Phe Tyr Gly Ser Gln Thr Gly Thr Ala Glu Asp Tyr Ala
65 70 75 80

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Ser Arg Leu Ala Lys Glu Gly Lys Ser Arg Phe Gly Leu Asn Thr Met
                85                  90                  95

Ile Ala Asp Leu Glu Asp Tyr Asp Phe Asp Asn Leu Asp Thr Val Pro
            100                 105                 110

Ser Asp Asn Ile Val Met Phe Val Leu Ala Thr Tyr Gly Glu Gly Glu
        115                 120                 125

Pro Thr Asp Asn Ala Val Asp Phe Tyr Glu Phe Ile Thr Gly Glu Asp
    130                 135                 140

Ala Ser Phe Asn Glu Gly Asn Asp Pro Pro Leu Gly Asn Leu Asn Tyr
145                 150                 155                 160

Val Ala Phe Gly Leu Gly Asn Asn Thr Tyr Glu His Tyr Asn Ser Met
                165                 170                 175

Val Arg Asn Val Asn Lys Ala Leu Glu Lys Leu Gly Ala His Arg Ile
            180                 185                 190

Gly Glu Ala Gly Glu Gly Asp Asp Gly Ala Gly Thr Met Glu Glu Asp
        195                 200                 205

Phe Leu Ala Trp Lys Asp Pro Met Trp Glu Ala Leu Ala Lys Lys Met
    210                 215                 220

Gly Leu Glu Glu Arg Glu Ala Val Tyr Glu Pro Ile Phe Ala Ile Asn
225                 230                 235                 240

Glu Arg Asp Asp Leu Thr Pro Glu Ala Asn Glu Val Tyr Leu Gly Glu
                245                 250                 255

Pro Asn Lys Leu His Leu Glu Gly Thr Ala Lys Gly Pro Phe Asn Ser
            260                 265                 270
```

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His Asn Pro Tyr Ile Ala Pro Ile Ala Glu Ser Tyr Glu Leu Phe Ser
        275                 280                 285

Ala Lys Asp Arg Asn Cys Leu His Met Glu Ile Asp Ile Ser Gly Ser
    290                 295                 300

Asn Leu Lys Tyr Glu Thr Gly Asp His Ile Ala Ile Trp Pro Thr Asn
305                 310                 315                 320

Pro Gly Glu Glu Val Asn Lys Phe Leu Asp Ile Leu Asp Leu Ser Gly
                325                 330                 335

Lys Gln His Ser Val Val Thr Val Lys Ala Leu Glu Pro Thr Ala Lys
            340                 345                 350

Val Pro Phe Pro Asn Pro Thr Thr Tyr Asp Ala Ile Leu Arg Tyr His
        355                 360                 365

Leu Glu Ile Cys Ala Pro Val Ser Arg Gln Phe Val Ser Thr Leu Ala
    370                 375                 380

Ala Phe Ala Pro Asn Asp Asp Ile Lys Ala Glu Met Asn Arg Leu Gly
385                 390                 395                 400

Ser Asp Lys Asp Tyr Phe His Glu Lys Thr Gly Pro His Tyr Tyr Asn
                405                 410                 415

Ile Ala Arg Phe Leu Ala Ser Val Ser Lys Gly Glu Lys Trp Thr Lys
            420                 425                 430

Ile Pro Phe Ser Ala Phe Ile Glu Gly Leu Thr Lys Leu Gln Pro Arg
        435                 440                 445

Tyr Tyr Ser Ile Ser Ser Ser Ser Leu Val Gln Pro Lys Lys Ile Ser
    450                 455                 460

Ile Thr Ala Val Val Glu Ser Gln Gln Ile Pro Gly Arg Asp Asp Pro
465                 470                 475                 480
```

```
Phe Arg Gly Val Ala Thr Asn Tyr Leu Phe Ala Leu Lys Gln Lys Gln
               485                 490                 495

Asn Gly Asp Pro Asn Pro Ala Pro Phe Gly Gln Ser Tyr Glu Leu Thr
            500                 505                 510

Gly Pro Arg Asn Lys Tyr Asp Gly Ile His Val Pro Val His Val Arg
        515                 520                 525

His Ser Asn Phe Lys Leu Pro Ser Asp Pro Gly Lys Pro Ile Ile Met
    530                 535                 540

Ile Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly Phe Val Gln Glu
545                 550                 555                 560

Arg Ala Lys Gln Ala Arg Asp Gly Val Glu Val Gly Lys Thr Leu Leu
               565                 570                 575

Phe Phe Gly Cys Arg Lys Ser Thr Glu Asp Phe Met Tyr Gln Lys Glu
            580                 585                 590

Trp Gln Glu Tyr Lys Glu Ala Leu Gly Asp Lys Phe Glu Met Ile Thr
        595                 600                 605

Ala Phe Ser Arg Glu Gly Ser Lys Lys Val Tyr Val Gln His Arg Leu
    610                 615                 620

Lys Glu Arg Ser Lys Glu Val Ser Asp Leu Leu Ser Gln Lys Ala Tyr
625                 630                 635                 640

Phe Tyr Val Cys Gly Asp Ala Ala His Met Ala Arg Glu Val Asn Thr
               645                 650                 655

Val Leu Ala Gln Ile Ile Ala Glu Gly Arg Gly Val Ser Glu Ala Lys
            660                 665                 670
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Gly Glu Glu Ile Val Lys Asn Met Arg Ser Ala Asn Gln Tyr Gln Val
        675   680   685

Cys Ser Asp Phe Val Thr Leu His Cys Lys Glu Thr Thr Tyr Ala Asn
    690   695   700

Ser Glu Leu Gln Glu Asp Val Trp Ser
705   710

<210> 83
<211> 2130
<212> DNA
<213> Stevia rebaudiana

<400> 83
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acagtgatcg atacagcgaa cgcatctgat aacggagact caaagatgcc gccggcgttg   120

gcgatgatgt tcgaaattcg tgatctgttg ctgattttga ctacgtcagt tgctgttttg   180

gtcggatgtt tcgttgtttt ggtgtggaag agatcgtccg ggaagaagtc cggcaaggaa   240

ttggagccgc cgaagatcgt tgtgccgaag aggcggctgg agcaggaggt tgatgatggt   300

aagaagaagg ttacgatttt cttcggaaca caaactggaa cggctgaagg tttcgctaag   360

gcacttttcg aagaagcgaa agcgcgatat gaaaaggcag cgtttaaagt gattgatttg   420

gatgattatg ctgctgattt ggatgagtat gcagagaagc tgaagaagga aacatatgct   480

ttcttcttct tggctacata tggagatggt gagccaactg ataatgctgc caaattttat   540

aaatggttta ctgagggaga cgagaaaggc gtttggcttc aaaaacttca atatggagta   600

tttggtcttg gcaacagaca atatgaacat ttcaacaaga ttggaatagt ggttgatgat   660

ggtctcaccg agcagggtgc aaaacgcatt gttcccgttg gtcttggaga cgacgatcaa   720

tcaattgaag acgatttttc ggcatggaaa gagttagtgt ggcccgaatt ggatctattg   780

cttcgcgatg aagatgacaa agctgctgca actccttaca cagctgcaat ccctgaatac   840

cgcgtcgtat ttcatgacaa acccgatgcg ttttctgatg atcatactca aaccaatggt   900

catgctgttc atgatgctca acatccatgc agatccaatg tggctgttaa aaaagagctt   960

catactcctg aatccgatcg ttcatgcaca catcttgaat ttgacatttc tcacactgga 1020

ttatcttatg aaactgggga tcatgttggt gtatactgtg aaaacctaat tgaagtagtg 1080

gaagaagctg ggaaattgtt aggattatca acagatactt atttctcgtt acatattgat 1140

aacgaagatg gttcaccact tggtggacct tcattacaac ctccttttcc tccttgtact 1200

ttaagaaaag cattgactaa ttatgcagat ctgttaagct ctcccaaaaa gtcaactttg 1260

cttgctctag ctgctcatgc ttccgatccc actgaagctg atcgtttaag atttcttgca 1320

tctcgcgagg gcaaggatga atatgctgaa tgggttgttg caaaccaaag aagtcttctt 1380

gaagtcatgg aagctttccc gtcagctaga ccgccacttg gtgttttctt tgcagcggtt 1440

gcaccgcgtt tacagcctcg ttactactct atttcttcct ccccaaagat ggaaccaaac 1500

aggattcatg ttacttgcgc gttggtttat gaaaaaactc ccgcaggtcg tatccacaaa 1560

ggaatctgct caacctggat gaagaacgct gtacctttga ccgaaagtca agattgcagt 1620

tgggcaccga tttttgttag aacatcaaac ttcagacttc caattgaccc gaaagtcccg 1680

gttatcatga ttggtcctgg aaccgggttg gctccattta ggggttttct tcaagaaaga 1740

ttggctctta aagaatccgg aaccgaactc gggtcatcta ttttattctt cggttgtaga 1800

aaccgcaaag tggattacat atatgagaat gaactcaaca actttgttga aaatggtgcg 1860

ctttctgagc ttgatgttgc tttctcccgc gatggcccga cgaaagaata cgtgcaacat 1920

aaaatgaccc aaaaggcttc tgaaatatgg aatatgcttt ctgagggagc atatttatat 1980

gtatgtggtg atgctaaagg catggctaaa gatgtacacc gtacacttca caccattgtg 2040

caagaacagg gaagtttgga ctcgtctaaa gcggagttgt atgtgaagaa tctacaaatg 2100

tcaggaagat acctccgtga tgtttggtaa 2130

<210> 84
<211> 709
<212> PRT
<213> Stevia rebaudiana

<400> 84

Met Gln Ser Glu Ser Val Glu Ala Ser Thr Ile Asp Leu Met Thr Ala
1 5 10 15

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Val Leu Lys Asp Thr Val Ile Asp Thr Ala Asn Ala Ser Asp Asn Gly
            20                  25                  30

Asp Ser Lys Met Pro Pro Ala Leu Ala Met Met Phe Glu Ile Arg Asp
        35                  40                  45

Leu Leu Leu Ile Leu Thr Thr Ser Val Ala Val Leu Val Gly Cys Phe
    50                  55                  60

Val Val Leu Val Trp Lys Arg Ser Ser Gly Lys Lys Ser Gly Lys Glu
65                  70                  75                  80

Leu Glu Pro Pro Lys Ile Val Val Pro Lys Arg Arg Leu Glu Gln Glu
                85                  90                  95

Val Asp Asp Gly Lys Lys Lys Val Thr Ile Phe Phe Gly Thr Gln Thr
            100                 105                 110

Gly Thr Ala Glu Gly Phe Ala Lys Ala Leu Phe Glu Glu Ala Lys Ala
        115                 120                 125

Arg Tyr Glu Lys Ala Ala Phe Lys Val Ile Asp Leu Asp Asp Tyr Ala
    130                 135                 140

Ala Asp Leu Asp Glu Tyr Ala Glu Lys Leu Lys Lys Glu Thr Tyr Ala
145                 150                 155                 160

Phe Phe Phe Leu Ala Thr Tyr Gly Asp Gly Glu Pro Thr Asp Asn Ala
                165                 170                 175

Ala Lys Phe Tyr Lys Trp Phe Thr Glu Gly Asp Glu Lys Gly Val Trp
            180                 185                 190

Leu Gln Lys Leu Gln Tyr Gly Val Phe Gly Leu Gly Asn Arg Gln Tyr
        195                 200                 205
```

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Glu His Phe Asn Lys Ile Gly Ile Val Val Asp Asp Gly Leu Thr Glu
    210                 215                 220

Gln Gly Ala Lys Arg Ile Val Pro Val Gly Leu Gly Asp Asp Asp Gln
225                 230                 235                 240

Ser Ile Glu Asp Asp Phe Ser Ala Trp Lys Glu Leu Val Trp Pro Glu
                245                 250                 255

Leu Asp Leu Leu Leu Arg Asp Glu Asp Asp Lys Ala Ala Ala Thr Pro
            260                 265                 270

Tyr Thr Ala Ala Ile Pro Glu Tyr Arg Val Val Phe His Asp Lys Pro
        275                 280                 285

Asp Ala Phe Ser Asp Asp His Thr Gln Thr Asn Gly His Ala Val His
    290                 295                 300

Asp Ala Gln His Pro Cys Arg Ser Asn Val Ala Val Lys Lys Glu Leu
305                 310                 315                 320

His Thr Pro Glu Ser Asp Arg Ser Cys Thr His Leu Glu Phe Asp Ile
                325                 330                 335

Ser His Thr Gly Leu Ser Tyr Glu Thr Gly Asp His Val Gly Val Tyr
            340                 345                 350

Cys Glu Asn Leu Ile Glu Val Val Glu Glu Ala Gly Lys Leu Leu Gly
        355                 360                 365

Leu Ser Thr Asp Thr Tyr Phe Ser Leu His Ile Asp Asn Glu Asp Gly
    370                 375                 380

Ser Pro Leu Gly Gly Pro Ser Leu Gln Pro Pro Phe Pro Pro Cys Thr
385                 390                 395                 400

Leu Arg Lys Ala Leu Thr Asn Tyr Ala Asp Leu Leu Ser Ser Pro Lys
                405                 410                 415
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Lys Ser Thr Leu Leu Ala Leu Ala Ala His Ala Ser Asp Pro Thr Glu
            420                 425                 430

Ala Asp Arg Leu Arg Phe Leu Ala Ser Arg Glu Gly Lys Asp Glu Tyr
        435                 440                 445

Ala Glu Trp Val Val Ala Asn Gln Arg Ser Leu Leu Glu Val Met Glu
    450                 455                 460

Ala Phe Pro Ser Ala Arg Pro Pro Leu Gly Val Phe Phe Ala Ala Val
465                 470                 475                 480

Ala Pro Arg Leu Gln Pro Arg Tyr Tyr Ser Ile Ser Ser Ser Pro Lys
                485                 490                 495

Met Glu Pro Asn Arg Ile His Val Thr Cys Ala Leu Val Tyr Glu Lys
            500                 505                 510

Thr Pro Ala Gly Arg Ile His Lys Gly Ile Cys Ser Thr Trp Met Lys
        515                 520                 525

Asn Ala Val Pro Leu Thr Glu Ser Gln Asp Cys Ser Trp Ala Pro Ile
    530                 535                 540

Phe Val Arg Thr Ser Asn Phe Arg Leu Pro Ile Asp Pro Lys Val Pro
545                 550                 555                 560

Val Ile Met Ile Gly Pro Gly Thr Gly Leu Ala Pro Phe Arg Gly Phe
                565                 570                 575

Leu Gln Glu Arg Leu Ala Leu Lys Glu Ser Gly Thr Glu Leu Gly Ser
            580                 585                 590

Ser Ile Leu Phe Phe Gly Cys Arg Asn Arg Lys Val Asp Tyr Ile Tyr
        595                 600                 605
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Glu Asn Glu Leu Asn Asn Phe Val Glu Asn Gly Ala Leu Ser Glu Leu
610 615 620

Asp Val Ala Phe Ser Arg Asp Gly Pro Thr Lys Glu Tyr Val Gln His
625 630 635 640

Lys Met Thr Gln Lys Ala Ser Glu Ile Trp Asn Met Leu Ser Glu Gly
645 650 655

Ala Tyr Leu Tyr Val Cys Gly Asp Ala Lys Gly Met Ala Lys Asp Val
660 665 670

His Arg Thr Leu His Thr Ile Val Gln Glu Gln Gly Ser Leu Asp Ser
675 680 685

Ser Lys Ala Glu Leu Tyr Val Lys Asn Leu Gln Met Ser Gly Arg Tyr
690 695 700

Leu Arg Asp Val Trp
705

<210> 85
<211> 2124
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized CPR

<400> 85
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gcgatgatta tggagaatcg tgagctgttg atgatactca caacgtcggt tgctgtattg 180

atcggatgcg ttgtcgtttt ggtgtggcgg agatcgtcta cgaagaagtc ggcgttggag 240

ccaccggtga ttgtggttcc gaagagagtg caagaggagg aagttgatga tggtaagaag 300

aaagttacgg ttttcttcgg cacccaaact ggaacagctg aaggcttcgc taaggcactt 360

gttgaggaag ctaaagctcg atatgaaaag gctgtcttta aagtaattga tttggatgat 420

tatgctgctg atgacgatga gtatgaggag aaactaaaga aagaatcttt ggccttttc 480

tttttggcta cgtatggaga tggtgagcca acagataatg ctgccagatt ttataaatgg 540

tttactgagg gagatgcgaa aggagaatgg cttaataagc ttcaatatgg agtatttggt 600

ttgggtaaca gacaatatga acattttaac aagatcgcaa aagtggttga tgatggtctt 660

gtagaacagg gtgcaaagcg tcttgttcct gttggacttg gagatgatga tcaatgtatt 720

gaagatgact tcaccgcatg gaaagagtta gtatggccgg agttggatca attacttcgt 780

gatgaggatg acacaactgt tgctactcca tacacagctg ctgttgcaga atatcgcgtt 840

gtttttcatg aaaaaccaga cgcgctttct gaagattata gttatacaaa tggccatgct 900

gttcatgatg ctcaacatcc atgcagatcc aacgtggctg tcaaaaagga acttcatagt 960

cctgaatctg accggtcttg cactcatctt gaatttgaca tctcgaacac cggactatca 1020

tatgaaactg gggaccatgt tggagtttac tgtgaaaact tgagtgaagt tgtgaatgat 1080

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gccggaaagg atgaatattc tcaatggata gttgcaagcc aaagaagtct ccttgaagtc 1380

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atgattggac ctggcactgg tttggctcct tttagaggtt tccttcaaga gcggttagct 1740

ttaaaggaag ccggaactga cctcggttta tccattttat tcttcggatg taggaatcgc 1800

aaagtggatt tcatatatga aaacgagctt aacaactttg tggagactgg tgctctttct 1860

gagcttattg ttgctttctc ccgtgaaggc ccgactaagg aatatgtgca acacaagatg 1920

agtgagaagg cttcggatat ctggaacttg ctttctgaag gagcatattt atacgtatgt 1980

ggtgatgcca aaggcatggc caaagatgta catcgaaccc tccacacaat tgtgcaagaa 2040

cagggatctc ttgactcgtc aaaggcagaa ctctacgtga agaatctaca aatgtcagga 2100

agatacctcc gtgacgtttg gtaa 2124

<210> 86
<211> 707
<212> PRT
<213> Stevia rebaudiana

<400> 86

Met Gln Ser Asn Ser Val Lys Ile Ser Pro Leu Asp Leu Val Thr Ala
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Leu Phe Ser Gly Lys Val Leu Asp Thr Ser Asn Ala Ser Glu Ser Gly
20 25 30

Glu Ser Ala Met Leu Pro Thr Ile Ala Met Ile Met Glu Asn Arg Glu
35 40 45

Leu Leu Met Ile Leu Thr Thr Ser Val Ala Val Leu Ile Gly Cys Val
50 55 60

Val Val Leu Val Trp Arg Arg Ser Ser Thr Lys Lys Ser Ala Leu Glu
65 70 75 80

Pro Pro Val Ile Val Val Pro Lys Arg Val Gln Glu Glu Glu Val Asp
85 90 95

Asp Gly Lys Lys Lys Val Thr Val Phe Phe Gly Thr Gln Thr Gly Thr
100 105 110

Ala Glu Gly Phe Ala Lys Ala Leu Val Glu Glu Ala Lys Ala Arg Tyr
115 120 125

Glu Lys Ala Val Phe Lys Val Ile Asp Leu Asp Asp Tyr Ala Ala Asp

```
    130                 135                 140

Asp Asp Glu Tyr Glu Glu Lys Leu Lys Lys Glu Ser Leu Ala Phe Phe
145                 150                 155                 160

Phe Leu Ala Thr Tyr Gly Asp Gly Glu Pro Thr Asp Asn Ala Ala Arg
                165                 170                 175

Phe Tyr Lys Trp Phe Thr Glu Gly Asp Ala Lys Gly Glu Trp Leu Asn
            180                 185                 190

Lys Leu Gln Tyr Gly Val Phe Gly Leu Gly Asn Arg Gln Tyr Glu His
        195                 200                 205

Phe Asn Lys Ile Ala Lys Val Val Asp Asp Gly Leu Val Glu Gln Gly
    210                 215                 220

Ala Lys Arg Leu Val Pro Val Gly Leu Gly Asp Asp Asp Gln Cys Ile
225                 230                 235                 240

Glu Asp Asp Phe Thr Ala Trp Lys Glu Leu Val Trp Pro Glu Leu Asp
                245                 250                 255

Gln Leu Leu Arg Asp Glu Asp Asp Thr Thr Val Ala Thr Pro Tyr Thr
            260                 265                 270

Ala Ala Val Ala Glu Tyr Arg Val Val Phe His Glu Lys Pro Asp Ala
        275                 280                 285

Leu Ser Glu Asp Tyr Ser Tyr Thr Asn Gly His Ala Val His Asp Ala
    290                 295                 300

Gln His Pro Cys Arg Ser Asn Val Ala Val Lys Lys Glu Leu His Ser
305                 310                 315                 320

Pro Glu Ser Asp Arg Ser Cys Thr His Leu Glu Phe Asp Ile Ser Asn
                325                 330                 335
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Thr Gly Leu Ser Tyr Glu Thr Gly Asp His Val Gly Val Tyr Cys Glu
            340                 345                 350

Asn Leu Ser Glu Val Val Asn Asp Ala Glu Arg Leu Val Gly Leu Pro
        355                 360                 365

Pro Asp Thr Tyr Ser Ser Ile His Thr Asp Ser Glu Asp Gly Ser Pro
    370                 375                 380

Leu Gly Gly Ala Ser Leu Pro Pro Pro Phe Pro Pro Cys Thr Leu Arg
385                 390                 395                 400

Lys Ala Leu Thr Cys Tyr Ala Asp Val Leu Ser Ser Pro Lys Lys Ser
                405                 410                 415

Ala Leu Leu Ala Leu Ala Ala His Ala Thr Asp Pro Ser Glu Ala Asp
            420                 425                 430

Arg Leu Lys Phe Leu Ala Ser Pro Ala Gly Lys Asp Glu Tyr Ser Gln
        435                 440                 445

Trp Ile Val Ala Ser Gln Arg Ser Leu Leu Glu Val Met Glu Ala Phe
    450                 455                 460

Pro Ser Ala Lys Pro Ser Leu Gly Val Phe Phe Ala Ser Val Ala Pro
465                 470                 475                 480

Arg Leu Gln Pro Arg Tyr Tyr Ser Ile Ser Ser Ser Pro Lys Met Ala
                485                 490                 495

Pro Asp Arg Ile His Val Thr Cys Ala Leu Val Tyr Glu Lys Thr Pro
            500                 505                 510

Ala Gly Arg Ile His Lys Gly Val Cys Ser Thr Trp Met Lys Asn Ala
        515                 520                 525

Val Pro Met Thr Glu Ser Gln Asp Cys Ser Trp Ala Pro Ile Tyr Val
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    530                 535                 540

Arg Thr Ser Asn Phe Arg Leu Pro Ser Asp Pro Lys Val Pro Val Ile
545                 550                 555                 560

Met Ile Gly Pro Gly Thr Gly Leu Ala Pro Phe Arg Gly Phe Leu Gln
                565                 570                 575

Glu Arg Leu Ala Leu Lys Glu Ala Gly Thr Asp Leu Gly Leu Ser Ile
            580                 585                 590

Leu Phe Phe Gly Cys Arg Asn Arg Lys Val Asp Phe Ile Tyr Glu Asn
        595                 600                 605

Glu Leu Asn Asn Phe Val Glu Thr Gly Ala Leu Ser Glu Leu Ile Val
    610                 615                 620

Ala Phe Ser Arg Glu Gly Pro Thr Lys Glu Tyr Val Gln His Lys Met
625                 630                 635                 640

Ser Glu Lys Ala Ser Asp Ile Trp Asn Leu Leu Ser Glu Gly Ala Tyr
                645                 650                 655

Leu Tyr Val Cys Gly Asp Ala Lys Gly Met Ala Lys Asp Val His Arg
            660                 665                 670

Thr Leu His Thr Ile Val Gln Glu Gln Gly Ser Leu Asp Ser Ser Lys
        675                 680                 685

Ala Glu Leu Tyr Val Lys Asn Leu Gln Met Ser Gly Arg Tyr Leu Arg
    690                 695                 700

Asp Val Trp
705
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<210> 87
<211> 2070
<212> DNA

<213> Artificial Sequence

<220>
<223> Codon-optimized CPR

<400> 87
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ggttctgtta ctgattccgt tgttgttatt gctaccacct ctattgcttt ggttatcggt 120

gttttggttt tgttgtggag aagatcctct gacagatcta gagaagttaa gcaattggct 180

gttccaaagc cagttactat cgttgaagaa gaagatgaat tcgaagttgc ttctggtaag 240

accagagttt ctattttcta cggtactcaa actggtactg ctgaaggttt tgctaaggct 300

ttggctgaag aaatcaaagc cagatacgaa aaagctgccg ttaaggttat tgatttggat 360

gattacacag ccgaagatga caaatacggt gaaaagttga agaaagaaac tatggccttc 420

ttcatgttgg ctacttatgg tgatggtgaa cctactgata atgctgctag attttacaag 480

tggttcaccg aaggtactga tagaggtgtt tggttggaac atttgagata cggtgtattc 540

ggtttgggta acagacaata cgaacacttc aacaagattg ccaaggttgt tgatgatttg 600

ttggttgaac aaggtgccaa gagattggtt actgttggtt tgggtgatga tgatcaatgc 660

atcgaagatg atttctccgc ttggaaagaa gccttgtggc cagaattgga tcaattattg 720

caagatgata ccaacaccgt ttctactcca tacactgctg ttattccaga atacagagtt 780

gttatccacg atccatctgt tacctcttat gaagatccat actctaacat ggctaacggt 840

aatgcctctt acgatattca tcatccatgt agagctaacg ttgccgtcca aaaagaattg 900

cataagccag aatctgacag aagttgcatc catttggaat tcgatatttt cgctactggt 960

ttgacttacg aaaccggtga tcatgttggt gtttacgctg ataattgtga tgatactgta 1020

gaagaagccg ctaagttgtt gggtcaacca ttggatttgt tgttctccat tcataccgat 1080

aacaacgacg gtacttcttt gggttcttct ttgccaccac catttccagg tccatgtact 1140

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agagttcatg ttacttgcgc tttggtttat ggtccaactc caactggtag aattcacaga 1500

ggtgtatgtt cattctggat gaagaatgtt gtcccattgg aaaagtctca aaactgttct 1560

tgggccccaa ttttcatcag acaatctaat ttcaagttgc cagccgatca ttctgttcca 1620

atagttatgg ttggtccagg tactggttta gctcctttta gaggtttctt acaagaaaga 1680

ttggccttga aagaagaagg tgctcaagtt ggtcctgctt tgttgttttt tggttgcaga 1740

aacagacaaa tggacttcat ctacgaagtc gaattgaaca actttgtcga acaaggtgct 1800

ttgtccgaat tgatcgttgc tttttcaaga gaaggtccat ccaaagaata cgtccaacat 1860

aagatggttg aaaaggcagc ttacatgtgg aacttgattt ctcaaggtgg ttacttctac 1920

gtttgtggtg atgctaaagg tatggctaga gatgttcata gaacattgca taccatcgtc 1980

caacaagaag aaaaggttga ttctaccaag gccgaatcca tcgttaagaa attgcaaatg 2040

gacggtagat acttgagaga tgtttggtga 2070

<210> 88
<211> 689
<212> PRT
<213> Rubus suavissimus

<400> 88

Met Ser Ser Asn Ser Asp Leu Val Arg Arg Leu Glu Ser Val Leu Gly
1 5 10 15

Val Ser Phe Gly Gly Ser Val Thr Asp Ser Val Val Val Ile Ala Thr
20 25 30

Thr Ser Ile Ala Leu Val Ile Gly Val Leu Val Leu Leu Trp Arg Arg
35 40 45

Ser Ser Asp Arg Ser Arg Glu Val Lys Gln Leu Ala Val Pro Lys Pro
50 55 60

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Val Thr Ile Val Glu Glu Glu Asp Glu Phe Glu Val Ala Ser Gly Lys
65                  70                  75                  80


Thr Arg Val Ser Ile Phe Tyr Gly Thr Gln Thr Gly Thr Ala Glu Gly
                85                  90                  95


Phe Ala Lys Ala Leu Ala Glu Glu Ile Lys Ala Arg Tyr Glu Lys Ala
            100                 105                 110


Ala Val Lys Val Ile Asp Leu Asp Asp Tyr Thr Ala Glu Asp Asp Lys
        115                 120                 125


Tyr Gly Glu Lys Leu Lys Lys Glu Thr Met Ala Phe Phe Met Leu Ala
    130                 135                 140


Thr Tyr Gly Asp Gly Glu Pro Thr Asp Asn Ala Ala Arg Phe Tyr Lys
145                 150                 155                 160


Trp Phe Thr Glu Gly Thr Asp Arg Gly Val Trp Leu Glu His Leu Arg
                165                 170                 175


Tyr Gly Val Phe Gly Leu Gly Asn Arg Gln Tyr Glu His Phe Asn Lys
            180                 185                 190


Ile Ala Lys Val Val Asp Asp Leu Leu Val Glu Gln Gly Ala Lys Arg
        195                 200                 205


Leu Val Thr Val Gly Leu Gly Asp Asp Asp Gln Cys Ile Glu Asp Asp
    210                 215                 220


Phe Ser Ala Trp Lys Glu Ala Leu Trp Pro Glu Leu Asp Gln Leu Leu
225                 230                 235                 240


Gln Asp Asp Thr Asn Thr Val Ser Thr Pro Tyr Thr Ala Val Ile Pro
                245                 250                 255


Glu Tyr Arg Val Val Ile His Asp Pro Ser Val Thr Ser Tyr Glu Asp
            260                 265                 270
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```
Pro Tyr Ser Asn Met Ala Asn Gly Asn Ala Ser Tyr Asp Ile His His
        275                 280                 285

Pro Cys Arg Ala Asn Val Ala Val Gln Lys Glu Leu His Lys Pro Glu
    290                 295                 300

Ser Asp Arg Ser Cys Ile His Leu Glu Phe Asp Ile Phe Ala Thr Gly
305                 310                 315                 320

Leu Thr Tyr Glu Thr Gly Asp His Val Gly Val Tyr Ala Asp Asn Cys
                325                 330                 335

Asp Asp Thr Val Glu Glu Ala Ala Lys Leu Leu Gly Gln Pro Leu Asp
            340                 345                 350

Leu Leu Phe Ser Ile His Thr Asp Asn Asn Asp Gly Thr Ser Leu Gly
        355                 360                 365

Ser Ser Leu Pro Pro Pro Phe Pro Gly Pro Cys Thr Leu Arg Thr Ala
    370                 375                 380

Leu Ala Arg Tyr Ala Asp Leu Leu Asn Pro Pro Lys Lys Ala Ala Leu
385                 390                 395                 400

Ile Ala Leu Ala Ala His Ala Asp Glu Pro Ser Glu Ala Glu Arg Leu
                405                 410                 415

Lys Phe Leu Ser Ser Pro Gln Gly Lys Asp Glu Tyr Ser Lys Trp Val
            420                 425                 430

Val Gly Ser Gln Arg Ser Leu Val Glu Val Met Ala Glu Phe Pro Ser
        435                 440                 445

Ala Lys Pro Pro Leu Gly Val Phe Phe Ala Ala Val Val Pro Arg Leu
    450                 455                 460
```

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Gln Pro Arg Tyr Tyr Ser Ile Ser Ser Ser Pro Arg Phe Ala Pro His
465                 470                 475                 480


Arg Val His Val Thr Cys Ala Leu Val Tyr Gly Pro Thr Pro Thr Gly
                485                 490                 495


Arg Ile His Arg Gly Val Cys Ser Phe Trp Met Lys Asn Val Val Pro
            500                 505                 510


Leu Glu Lys Ser Gln Asn Cys Ser Trp Ala Pro Ile Phe Ile Arg Gln
        515                 520                 525


Ser Asn Phe Lys Leu Pro Ala Asp His Ser Val Pro Ile Val Met Val
    530                 535                 540


Gly Pro Gly Thr Gly Leu Ala Pro Phe Arg Gly Phe Leu Gln Glu Arg
545                 550                 555                 560


Leu Ala Leu Lys Glu Glu Gly Ala Gln Val Gly Pro Ala Leu Leu Phe
                565                 570                 575


Phe Gly Cys Arg Asn Arg Gln Met Asp Phe Ile Tyr Glu Val Glu Leu
            580                 585                 590


Asn Asn Phe Val Glu Gln Gly Ala Leu Ser Glu Leu Ile Val Ala Phe
        595                 600                 605


Ser Arg Glu Gly Pro Ser Lys Glu Tyr Val Gln His Lys Met Val Glu
    610                 615                 620


Lys Ala Ala Tyr Met Trp Asn Leu Ile Ser Gln Gly Gly Tyr Phe Tyr
625                 630                 635                 640


Val Cys Gly Asp Ala Lys Gly Met Ala Arg Asp Val His Arg Thr Leu
                645                 650                 655


His Thr Ile Val Gln Gln Glu Glu Lys Val Asp Ser Thr Lys Ala Glu
            660                 665                 670
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Ser Ile Val Lys Lys Leu Gln Met Asp Gly Arg Tyr Leu Arg Asp Val
675 680 685

Trp

<210> 89
<211> 2079
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized CPR

<400> 89
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gctttctttt gtgtagccac gtatggtgat ggtgaaccaa ccgataacgc cgcaagattc 480

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gaagagttat gcaaaaaggg tgcgaagaga ttgattgaag tcggtttagg agatgatgat 660

caatctatcg aggatgactt taatgcatgg aaggaatctt tgtggtctga attagataag 720

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tatagagtag ttactcatga tccaagattc acaacacaga aatcaatgga aagtaatgtg 840

gctaatggta atactaccat cgatattcat catccatgta gagtagacgt tgcagttcaa 900

aaggaattgc acactcatga atcagacaga tcttgcatac atcttgaatt tgatatatca 960

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<211> 692
<212> PRT
<213> Arabidopsis thaliana

<400> 90

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Thr Thr Ser Leu Ala Leu Val Ala Gly Phe Val Val Leu Leu Trp Lys
        35                  40                  45

Lys Thr Thr Ala Asp Arg Ser Gly Glu Leu Lys Pro Leu Met Ile Pro
    50                  55                  60

Lys Ser Leu Met Ala Lys Asp Glu Asp Asp Asp Leu Asp Leu Gly Ser
65                  70                  75                  80

Gly Lys Thr Arg Val Ser Ile Phe Phe Gly Thr Gln Thr Gly Thr Ala
                85                  90                  95

Glu Gly Phe Ala Lys Ala Leu Ser Glu Glu Ile Lys Ala Arg Tyr Glu
            100                 105                 110

Lys Ala Ala Val Lys Val Ile Asp Leu Asp Asp Tyr Ala Ala Asp Asp
        115                 120                 125

Asp Gln Tyr Glu Glu Lys Leu Lys Lys Glu Thr Leu Ala Phe Phe Cys
    130                 135                 140

Val Ala Thr Tyr Gly Asp Gly Glu Pro Thr Asp Asn Ala Ala Arg Phe
145                 150                 155                 160

Tyr Lys Trp Phe Thr Glu Glu Asn Glu Arg Asp Ile Lys Leu Gln Gln
                165                 170                 175

Leu Ala Tyr Gly Val Phe Ala Leu Gly Asn Arg Gln Tyr Glu His Phe
            180                 185                 190

Asn Lys Ile Gly Ile Val Leu Asp Glu Glu Leu Cys Lys Lys Gly Ala
        195                 200                 205

Lys Arg Leu Ile Glu Val Gly Leu Gly Asp Asp Asp Gln Ser Ile Glu
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    210                 215                 220

Asp Asp Phe Asn Ala Trp Lys Glu Ser Leu Trp Ser Glu Leu Asp Lys
225                 230                 235                 240

Leu Leu Lys Asp Glu Asp Asp Lys Ser Val Ala Thr Pro Tyr Thr Ala
                245                 250                 255

Val Ile Pro Glu Tyr Arg Val Val Thr His Asp Pro Arg Phe Thr Thr
            260                 265                 270

Gln Lys Ser Met Glu Ser Asn Val Ala Asn Gly Asn Thr Thr Ile Asp
        275                 280                 285

Ile His His Pro Cys Arg Val Asp Val Ala Val Gln Lys Glu Leu His
    290                 295                 300

Thr His Glu Ser Asp Arg Ser Cys Ile His Leu Glu Phe Asp Ile Ser
305                 310                 315                 320

Arg Thr Gly Ile Thr Tyr Glu Thr Gly Asp His Val Gly Val Tyr Ala
                325                 330                 335

Glu Asn His Val Glu Ile Val Glu Glu Ala Gly Lys Leu Leu Gly His
            340                 345                 350

Ser Leu Asp Leu Val Phe Ser Ile His Ala Asp Lys Glu Asp Gly Ser
        355                 360                 365

Pro Leu Glu Ser Ala Val Pro Pro Pro Phe Pro Gly Pro Cys Thr Leu
    370                 375                 380

Gly Thr Gly Leu Ala Arg Tyr Ala Asp Leu Leu Asn Pro Pro Arg Lys
385                 390                 395                 400

Ser Ala Leu Val Ala Leu Ala Ala Tyr Ala Thr Glu Pro Ser Glu Ala
                405                 410                 415
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Glu Lys Leu Lys His Leu Thr Ser Pro Asp Gly Lys Asp Glu Tyr Ser
            420                 425                 430

Gln Trp Ile Val Ala Ser Gln Arg Ser Leu Leu Glu Val Met Ala Ala
        435                 440                 445

Phe Pro Ser Ala Lys Pro Pro Leu Gly Val Phe Phe Ala Ala Ile Ala
    450                 455                 460

Pro Arg Leu Gln Pro Arg Tyr Tyr Ser Ile Ser Ser Ser Pro Arg Leu
465                 470                 475                 480

Ala Pro Ser Arg Val His Val Thr Ser Ala Leu Val Tyr Gly Pro Thr
                485                 490                 495

Pro Thr Gly Arg Ile His Lys Gly Val Cys Ser Thr Trp Met Lys Asn
            500                 505                 510

Ala Val Pro Ala Glu Lys Ser His Glu Cys Ser Gly Ala Pro Ile Phe
        515                 520                 525

Ile Arg Ala Ser Asn Phe Lys Leu Pro Ser Asn Pro Ser Thr Pro Ile
    530                 535                 540

Val Met Val Gly Pro Gly Thr Gly Leu Ala Pro Phe Arg Gly Phe Leu
545                 550                 555                 560

Gln Glu Arg Met Ala Leu Lys Glu Asp Gly Glu Glu Leu Gly Ser Ser
                565                 570                 575

Leu Leu Phe Phe Gly Cys Arg Asn Arg Gln Met Asp Phe Ile Tyr Glu
            580                 585                 590

Asp Glu Leu Asn Asn Phe Val Asp Gln Gly Val Ile Ser Glu Leu Ile
        595                 600                 605

Met Ala Phe Ser Arg Glu Gly Ala Gln Lys Glu Tyr Val Gln His Lys
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610 615 620

Met Met Glu Lys Ala Ala Gln Val Trp Asp Leu Ile Lys Glu Glu Gly
625 630 635 640

Tyr Leu Tyr Val Cys Gly Asp Ala Lys Gly Met Ala Arg Asp Val His
645 650 655

Arg Thr Leu His Thr Ile Val Gln Glu Gln Glu Gly Val Ser Ser Ser
660 665 670

Glu Ala Glu Ala Ile Val Lys Lys Leu Gln Thr Glu Gly Arg Tyr Leu
675 680 685

Arg Asp Val Trp
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<210> 91
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<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized CPR

<400> 91
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gaattgtctt caatgttgat cgaaaacaga caattcgcca tgatcgtaac tacatcaatc 180

gctgttttga tcggttgtat tgtcatgttg gtatggagaa gatccggtag tggtaattct 240

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ggtagaaaga aagttacaat atttttcggt acccaaactg gtacagctga aggttttgca 360

aaagccttag gtgaagaagc taaggcaaga tacgaaaaga ctagattcaa gatagtcgat 420

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gatattttgg tcgaacaagg tgctcaaaga ttagtccaag taggtttggg tgacgatgac 720

caatgtatag aagatgactt tactgcctgg agagaagctt tgtggcctga attagacaca 780

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tacagagttt ccatccatga tagtgaagac gcaaagttta atgatatcac tttggccaat 900

ggtaacggtt atacagtttt cgatgcacaa cacccttaca aagctaacgt tgcagtcaag 960

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gaaactgttg atgaagcatt gagattgttg gatatgtccc ctgacactta ttttagtttg 1140

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tctggtgcat tggccgaatt atctgtagct ttttcaagag aaggtccaac taaggaatac 1920

gttcaacata agatgatgga taaggcatcc gacatatgga acatgatcag tcaaggtgct 1980

tatttgtacg tttgcggtga cgcaaagggt atggccagag atgtccatag atctttgcac 2040

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<400> 92

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Ser Ala Tyr Glu Ser Val Ala Ala Glu Leu Ser Ser Met Leu Ile Glu
35 40 45

Asn Arg Gln Phe Ala Met Ile Val Thr Thr Ser Ile Ala Val Leu Ile
50 55 60

Gly Cys Ile Val Met Leu Val Trp Arg Arg Ser Gly Ser Gly Asn Ser
65 70 75 80

Lys Arg Val Glu Pro Leu Lys Pro Leu Val Ile Lys Pro Arg Glu Glu
85 90 95

Glu Ile Asp Asp Gly Arg Lys Lys Val Thr Ile Phe Phe Gly Thr Gln
100 105 110

Thr Gly Thr Ala Glu Gly Phe Ala Lys Ala Leu Gly Glu Glu Ala Lys
115 120 125

Ala Arg Tyr Glu Lys Thr Arg Phe Lys Ile Val Asp Leu Asp Asp Tyr
130 135 140

Ala Ala Asp Asp Asp Glu Tyr Glu Glu Lys Leu Lys Lys Glu Asp Val
145 150 155 160

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Ala Phe Phe Phe Leu Ala Thr Tyr Gly Asp Gly Glu Pro Thr Asp Asn
                165                 170                 175

Ala Ala Arg Phe Tyr Lys Trp Phe Thr Glu Gly Asn Asp Arg Gly Glu
            180                 185                 190

Trp Leu Lys Asn Leu Lys Tyr Gly Val Phe Gly Leu Gly Asn Arg Gln
        195                 200                 205

Tyr Glu His Phe Asn Lys Val Ala Lys Val Val Asp Asp Ile Leu Val
    210                 215                 220

Glu Gln Gly Ala Gln Arg Leu Val Gln Val Gly Leu Gly Asp Asp Asp
225                 230                 235                 240

Gln Cys Ile Glu Asp Asp Phe Thr Ala Trp Arg Glu Ala Leu Trp Pro
                245                 250                 255

Glu Leu Asp Thr Ile Leu Arg Glu Glu Gly Asp Thr Ala Val Ala Thr
            260                 265                 270

Pro Tyr Thr Ala Ala Val Leu Glu Tyr Arg Val Ser Ile His Asp Ser
        275                 280                 285

Glu Asp Ala Lys Phe Asn Asp Ile Thr Leu Ala Asn Gly Asn Gly Tyr
    290                 295                 300

Thr Val Phe Asp Ala Gln His Pro Tyr Lys Ala Asn Val Ala Val Lys
305                 310                 315                 320

Arg Glu Leu His Thr Pro Glu Ser Asp Arg Ser Cys Ile His Leu Glu
                325                 330                 335

Phe Asp Ile Ala Gly Ser Gly Leu Thr Met Lys Leu Gly Asp His Val
            340                 345                 350
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Gly Val Leu Cys Asp Asn Leu Ser Glu Thr Val Asp Glu Ala Leu Arg
        355                 360                 365

Leu Leu Asp Met Ser Pro Asp Thr Tyr Phe Ser Leu His Ala Glu Lys
    370                 375                 380

Glu Asp Gly Thr Pro Ile Ser Ser Ser Leu Pro Pro Pro Phe Pro Pro
385                 390                 395                 400

Cys Asn Leu Arg Thr Ala Leu Thr Arg Tyr Ala Cys Leu Leu Ser Ser
                405                 410                 415

Pro Lys Lys Ser Ala Leu Val Ala Leu Ala Ala His Ala Ser Asp Pro
            420                 425                 430

Thr Glu Ala Glu Arg Leu Lys His Leu Ala Ser Pro Ala Gly Lys Asp
        435                 440                 445

Glu Tyr Ser Lys Trp Val Val Glu Ser Gln Arg Ser Leu Leu Glu Val
    450                 455                 460

Met Ala Glu Phe Pro Ser Ala Lys Pro Pro Leu Gly Val Phe Phe Ala
465                 470                 475                 480

Gly Val Ala Pro Arg Leu Gln Pro Arg Phe Tyr Ser Ile Ser Ser Ser
                485                 490                 495

Pro Lys Ile Ala Glu Thr Arg Ile His Val Thr Cys Ala Leu Val Tyr
            500                 505                 510

Glu Lys Met Pro Thr Gly Arg Ile His Lys Gly Val Cys Ser Thr Trp
        515                 520                 525

Met Lys Asn Ala Val Pro Tyr Glu Lys Ser Glu Lys Leu Phe Leu Gly
    530                 535                 540

Arg Pro Ile Phe Val Arg Gln Ser Asn Phe Lys Leu Pro Ser Asp Ser
545                 550                 555                 560
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Lys Val Pro Ile Ile Met Ile Gly Pro Gly Thr Gly Leu Ala Pro Phe
                565                 570                 575


Arg Gly Phe Leu Gln Glu Arg Leu Ala Leu Val Glu Ser Gly Val Glu
            580                 585                 590


Leu Gly Pro Ser Val Leu Phe Phe Gly Cys Arg Asn Arg Arg Met Asp
        595                 600                 605


Phe Ile Tyr Glu Glu Glu Leu Gln Arg Phe Val Glu Ser Gly Ala Leu
    610                 615                 620


Ala Glu Leu Ser Val Ala Phe Ser Arg Glu Gly Pro Thr Lys Glu Tyr
625                 630                 635                 640


Val Gln His Lys Met Met Asp Lys Ala Ser Asp Ile Trp Asn Met Ile
                645                 650                 655


Ser Gln Gly Ala Tyr Leu Tyr Val Cys Gly Asp Ala Lys Gly Met Ala
            660                 665                 670


Arg Asp Val His Arg Ser Leu His Thr Ile Ala Gln Glu Gln Gly Ser
        675                 680                 685


Met Asp Ser Thr Lys Ala Glu Gly Phe Val Lys Asn Leu Gln Thr Ser
    690                 695                 700


Gly Arg Tyr Leu Arg Asp Val Trp
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<211> 1503
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized KAH

<400> 93
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attggacact tatacttact caaaaagcct ctttatagaa ctttagcaaa aattgccgct 180

aagtacggac caatactgca attacaactc ggctacagac gtgttctggt gatttcctca 240

ccatcagcag cagaagagtg ctttaccaat aacgatgtaa tcttcgcaaa tagacctaag 300

acattgtttg gcaaaatagt gggtggaaca tcccttggca gtttatccta cggcgatcaa 360

tggcgtaatc taaggagagt agcttctatc gaaatcctat cagttcatag gttgaacgaa 420

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tctcctgtta ctcttataac agtcttttat gctctaacat tgaacgtcat tatgagaatg 540

atctctggca aaagatattt cgacagtggg gatagagaat tggaggagga aggtaagaga 600

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agtgatactt cagcgggcac tatggaatgg gccatgagct tactggtcaa tcacccacat 960

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gagtcagaca ttggaaatat cccttacatc gggtgtatta tcaatgaaac tctaagactc 1080

tatccagcag ggccattgtt gttcccacat gaaagttctg ccgactgcgt tatttccggt 1140

tacaatatac ctagaggtac aatgttaatc gtaaaccaat gggcgattca tcacgatcct 1200

aaagtctggg atgatcctga aacctttaaa cctgaaagat ttcaaggatt agaaggaact 1260

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ttggcaataa ggctgttagg gatgacacta ggctcagtga tccaatgttt tgattgggag 1380

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taa 1503

<210> 94
<211> 500
<212> PRT
<213> Stevia rebaudiana

<400> 94

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20 25 30

Thr Val Phe Pro Ser Ile Pro Ile Ile Gly His Leu Tyr Leu Leu Lys
35 40 45

Lys Pro Leu Tyr Arg Thr Leu Ala Lys Ile Ala Ala Lys Tyr Gly Pro
50 55 60

Ile Leu Gln Leu Gln Leu Gly Tyr Arg Arg Val Leu Val Ile Ser Ser
65 70 75 80

Pro Ser Ala Ala Glu Glu Cys Phe Thr Asn Asn Asp Val Ile Phe Ala
85 90 95

Asn Arg Pro Lys Thr Leu Phe Gly Lys Ile Val Gly Gly Thr Ser Leu
100 105 110

Gly Ser Leu Ser Tyr Gly Asp Gln Trp Arg Asn Leu Arg Arg Val Ala
115 120 125

Ser Ile Glu Ile Leu Ser Val His Arg Leu Asn Glu Phe His Asp Ile
130 135 140

Arg Val Asp Glu Asn Arg Leu Leu Ile Arg Lys Leu Arg Ser Ser Ser
145 150 155 160

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Ser Pro Val Thr Leu Ile Thr Val Phe Tyr Ala Leu Thr Leu Asn Val
                165                 170                 175

Ile Met Arg Met Ile Ser Gly Lys Arg Tyr Phe Asp Ser Gly Asp Arg
            180                 185                 190

Glu Leu Glu Glu Glu Gly Lys Arg Phe Arg Glu Ile Leu Asp Glu Thr
        195                 200                 205

Leu Leu Leu Ala Gly Ala Ser Asn Val Gly Asp Tyr Leu Pro Ile Leu
    210                 215                 220

Asn Trp Leu Gly Val Lys Ser Leu Glu Lys Lys Leu Ile Ala Leu Gln
225                 230                 235                 240

Lys Lys Arg Asp Asp Phe Phe Gln Gly Leu Ile Glu Gln Val Arg Lys
                245                 250                 255

Ser Arg Gly Ala Lys Val Gly Lys Gly Arg Lys Thr Met Ile Glu Leu
            260                 265                 270

Leu Leu Ser Leu Gln Glu Ser Glu Pro Glu Tyr Tyr Thr Asp Ala Met
        275                 280                 285

Ile Arg Ser Phe Val Leu Gly Leu Leu Ala Ala Gly Ser Asp Thr Ser
    290                 295                 300

Ala Gly Thr Met Glu Trp Ala Met Ser Leu Leu Val Asn His Pro His
305                 310                 315                 320

Val Leu Lys Lys Ala Gln Ala Glu Ile Asp Arg Val Ile Gly Asn Asn
                325                 330                 335

Arg Leu Ile Asp Glu Ser Asp Ile Gly Asn Ile Pro Tyr Ile Gly Cys
            340                 345                 350

Ile Ile Asn Glu Thr Leu Arg Leu Tyr Pro Ala Gly Pro Leu Leu Phe
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        355                 360                 365

Pro His Glu Ser Ser Ala Asp Cys Val Ile Ser Gly Tyr Asn Ile Pro
    370                 375                 380

Arg Gly Thr Met Leu Ile Val Asn Gln Trp Ala Ile His His Asp Pro
385                 390                 395                 400

Lys Val Trp Asp Asp Pro Glu Thr Phe Lys Pro Glu Arg Phe Gln Gly
                405                 410                 415

Leu Glu Gly Thr Arg Asp Gly Phe Lys Leu Met Pro Phe Gly Ser Gly
            420                 425                 430

Arg Arg Gly Cys Pro Gly Glu Gly Leu Ala Ile Arg Leu Leu Gly Met
        435                 440                 445

Thr Leu Gly Ser Val Ile Gln Cys Phe Asp Trp Glu Arg Val Gly Asp
    450                 455                 460

Glu Met Val Asp Met Thr Glu Gly Leu Gly Val Thr Leu Pro Lys Ala
465                 470                 475                 480

Val Pro Leu Val Ala Lys Cys Lys Pro Arg Ser Glu Met Thr Asn Leu
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Leu Ser Glu Leu
            500
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<210> 95
<211> 1572
<212> DNA
<213> Rubus suavissimus

<400> 95
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ttgagggagc aaggccttaa aggcaattcc tacaggtttt tatatggaga catgaaggag 180

aactctatcc tgctcaaaca agcaagatcc aaacccatga acctctccac ctcccatgac 240

atagcacctc aagtcacccc ttttgtcgac caaaccgtga aagcttacgg taagaactct 300

tttaattggg ttggccccat accaagggtg aacataatga atccagaaga tttgaaggac 360

gtcttaacaa aaaatgttga ctttgttaag ccaatatcaa acccacttat caagttgcta 420

gctacaggta ttgcaatcta tgaaggtgag aaatggacta aacacagaag gattatcaac 480

ccaacattcc attcggagag gctaaagcgt atgttacctt catttcacca aagttgtaat 540

gagatggtca aggaatggga gagcttggtg tcaaaagagg gttcatcatg tgagttggat 600

gtctggcctt ttcttgaaaa tatgtcggca gatgtgatct cgagaacagc atttggaact 660

agctacaaaa aaggacagaa aatctttgaa ctcttgagag agcaagtaat atatgtaacg 720

aaaggctttc aaagttttta cattccagga tggaggtttc tcccaactaa gatgaacaag 780

aggatgaatg agattaacga agaaataaaa ggattaatca ggggtattat aattgacaga 840

gagcaaatca ttaaggcagg tgaagaaacc aacgatgact tattaggtgc acttatggag 900

tcaaacttga aggacattcg ggaacatggg aaaaacaaca aaaatgttgg gatgagtatt 960

gaagatgtaa ttcaggagtg taagctgttt tactttgctg ggcaagaaac cacttcagtg 1020

ttgctggctt ggacaatggt tttacttggt caaaatcaga actggcaaga tcgagcaaga 1080

caagaggttt tgcaagtctt tggaagcagc aagccagatt ttgatggtct agctcacctt 1140

aaagtcgtaa ccatgatttt gcttgaagtt cttcgattat acccaccagt cattgaactt 1200

attcgaacca ttcacaagaa aacacaactt gggaagctct cactaccaga aggagttgaa 1260

gtccgcttac caacactgct cattcaccat gacaaggaac tgtggggtga tgatgcaaac 1320

cagttcaatc cagagaggtt ttcggaagga gtttccaaag caacaaagaa ccgactctca 1380

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gcaaagttgg ccttagcatt gatcttgcaa cacttcacct ttgagctttc tccatctcat 1500

gcacatgctc cttcccatcg tataaccctt caaccacagt atggtgttcg tatcatttta 1560

catcgacgtt ag 1572

<210> 96
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized KAH

<400> 96
atggaagtca ctgtcgcctc ttctgtcgct ttatccttag tcttcatttc cattgtcgtc 60

agatgggctt ggtccgttgt caactgggtt tggttcaaac caaagaagtt ggaaagattc 120

ttgagagagc aaggtttgaa gggtaattct tatagattct tgtacggtga catgaaggaa 180

aattctattt tgttgaagca agccagatcc aaaccaatga acttgtctac ctctcatgat 240

attgctccac aagttactcc attcgtcgat caaactgtta aagcctacgg taagaactct 300

ttcaattggg ttggtccaat tcctagagtt aacatcatga acccagaaga tttgaaggat 360

gtcttgacca agaacgttga cttcgttaag ccaatttcca acccattgat taaattgttg 420

gctactggta ttgccattta cgaaggtgaa aagtggacta agcatagaag aatcatcaac 480

cctaccttcc actctgaaag attgaagaga atgttaccat ctttccatca atcctgtaat 540

gaaatggtta aggaatggga atccttggtt tctaaagaag gttcttcttg cgaattggat 600

gtttggccat tcttggaaaa tatgtctgct gatgtcattt ccagaaccgc tttcggtacc 660

tcctacaaga agggtcaaaa gattttcgaa ttgttgagag agcaagttat ttacgttacc 720

aagggtttcc aatccttcta catcccaggt tggagattct tgccaactaa aatgaacaag 780

cgtatgaacg agatcaacga agaaattaaa ggtttgatca gaggtattat tatcgacaga 840

gaacaaatta ttaaagctgg tgaagaaacc aacgatgatt tgttgggtgc tttgatggag 900

tccaacttga aggatattag agaacatggt aagaacaaca agaatgttgg tatgtctatt 960

gaagatgtta ttcaagaatg taagttattc tacttcgctg gtcaagagac cacttctgtt 1020

ttgttagcct ggactatggt cttgttaggt caaaaccaaa attggcaaga tagagctaga 1080

caagaagttt tgcaagtctt cggttcttcc aagccagact ttgatggttt ggcccacttg 1140

aaggttgtta ctatgatttt gttagaagtt ttgagattgt acccaccagt cattgagtta 1200

atcagaacca ttcataaaaa gactcaattg ggtaaattat ctttgccaga aggtgttgaa 1260

gtcagattac caaccttgtt gattcaccac gataaggaat tatggggtga cgacgctaat 1320

caatttaatc cagaaagatt ttccgaaggt gtttccaagg ctaccaaaaa ccgtttgtcc 1380

ttcttcccat ttggtgctgg tccacgtatt tgtatcggtc aaaacttttc catgatggaa 1440

gccaagttgg ctttggcttt aatcttgcaa cacttcactt tcgaattgtc tccatcccat 1500

gcccacgctc cttctcatag aatcacttta caaccacaat acggtgtcag aatcatctta 1560

cacagaagat aa 1572

<210> 97
<211> 523
<212> PRT
<213> Rubus suavissimus

<400> 97

Met Glu Val Thr Val Ala Ser Ser Val Ala Leu Ser Leu Val Phe Ile
1 5 10 15

Ser Ile Val Val Arg Trp Ala Trp Ser Val Val Asn Trp Val Trp Phe
20 25 30

Lys Pro Lys Lys Leu Glu Arg Phe Leu Arg Glu Gln Gly Leu Lys Gly
35 40 45

Asn Ser Tyr Arg Phe Leu Tyr Gly Asp Met Lys Glu Asn Ser Ile Leu
50 55 60

Leu Lys Gln Ala Arg Ser Lys Pro Met Asn Leu Ser Thr Ser His Asp
65 70 75 80

Ile Ala Pro Gln Val Thr Pro Phe Val Asp Gln Thr Val Lys Ala Tyr
85 90 95

Gly Lys Asn Ser Phe Asn Trp Val Gly Pro Ile Pro Arg Val Asn Ile
100 105 110

Met Asn Pro Glu Asp Leu Lys Asp Val Leu Thr Lys Asn Val Asp Phe

```
        115                 120                 125

Val Lys Pro Ile Ser Asn Pro Leu Ile Lys Leu Leu Ala Thr Gly Ile
    130                 135                 140

Ala Ile Tyr Glu Gly Glu Lys Trp Thr Lys His Arg Arg Ile Ile Asn
145                 150                 155                 160

Pro Thr Phe His Ser Glu Arg Leu Lys Arg Met Leu Pro Ser Phe His
                165                 170                 175

Gln Ser Cys Asn Glu Met Val Lys Glu Trp Glu Ser Leu Val Ser Lys
            180                 185                 190

Glu Gly Ser Ser Cys Glu Leu Asp Val Trp Pro Phe Leu Glu Asn Met
        195                 200                 205

Ser Ala Asp Val Ile Ser Arg Thr Ala Phe Gly Thr Ser Tyr Lys Lys
    210                 215                 220

Gly Gln Lys Ile Phe Glu Leu Leu Arg Glu Gln Val Ile Tyr Val Thr
225                 230                 235                 240

Lys Gly Phe Gln Ser Phe Tyr Ile Pro Gly Trp Arg Phe Leu Pro Thr
                245                 250                 255

Lys Met Asn Lys Arg Met Asn Glu Ile Asn Glu Glu Ile Lys Gly Leu
            260                 265                 270

Ile Arg Gly Ile Ile Ile Asp Arg Glu Gln Ile Ile Lys Ala Gly Glu
        275                 280                 285

Glu Thr Asn Asp Asp Leu Leu Gly Ala Leu Met Glu Ser Asn Leu Lys
    290                 295                 300

Asp Ile Arg Glu His Gly Lys Asn Asn Lys Asn Val Gly Met Ser Ile
305                 310                 315                 320
```

```
Glu Asp Val Ile Gln Glu Cys Lys Leu Phe Tyr Phe Ala Gly Gln Glu
                325                 330                 335

Thr Thr Ser Val Leu Leu Ala Trp Thr Met Val Leu Leu Gly Gln Asn
            340                 345                 350

Gln Asn Trp Gln Asp Arg Ala Arg Gln Glu Val Leu Gln Val Phe Gly
        355                 360                 365

Ser Ser Lys Pro Asp Phe Asp Gly Leu Ala His Leu Lys Val Val Thr
    370                 375                 380

Met Ile Leu Leu Glu Val Leu Arg Leu Tyr Pro Pro Val Ile Glu Leu
385                 390                 395                 400

Ile Arg Thr Ile His Lys Lys Thr Gln Leu Gly Lys Leu Ser Leu Pro
                405                 410                 415

Glu Gly Val Glu Val Arg Leu Pro Thr Leu Leu Ile His His Asp Lys
            420                 425                 430

Glu Leu Trp Gly Asp Asp Ala Asn Gln Phe Asn Pro Glu Arg Phe Ser
        435                 440                 445

Glu Gly Val Ser Lys Ala Thr Lys Asn Arg Leu Ser Phe Phe Pro Phe
    450                 455                 460

Gly Ala Gly Pro Arg Ile Cys Ile Gly Gln Asn Phe Ser Met Met Glu
465                 470                 475                 480

Ala Lys Leu Ala Leu Ala Leu Ile Leu Gln His Phe Thr Phe Glu Leu
                485                 490                 495

Ser Pro Ser His Ala His Ala Pro Ser His Arg Ile Thr Leu Gln Pro
            500                 505                 510

Gln Tyr Gly Val Arg Ile Ile Leu His Arg Arg
```

515 520

<210> 98
<211> 1566
<212> DNA
<213> Prunus avium

<400> 98
atggaagcat caagggctag ttgtgttgcg ctatgtgttg tttgggtgag catagtaatt 60

acattggcat ggagggtgct gaattgggtg tggttgaggc caaagaaact agaaagatgc 120

ttgagggagc aaggccttac aggcaattct tacaggcttt tgtttggaga caccaaggat 180

ctctcgaaga tgctggaaca aacacaatcc aaacccatca aactctccac ctcccatgat 240

atagcgccac gagtcacccc atttttccat cgaactgtga actctaatgg caagaattct 300

tttgtttgga tgggccctat accaagagtg cacatcatga atccagaaga tttgaaagat 360

gccttcaaca gacatgatga ttttcataag acagtaaaaa atcctatcat gaagtctcca 420

ccaccgggca ttgtaggcat tgaaggtgag caatgggcta aacacagaaa gattatcaac 480

ccagcattcc atttagagaa gctaaagggt atggtaccaa tattttacca aagttgtagc 540

gagatgatta acaaatggga gagcttggtg tccaaagaga gttcatgtga gttggatgtg 600

tggccttatc ttgaaaattt taccagcgat gtgatttccc gagctgcatt tggaagtagc 660

tatgaagagg gaaggaaaat atttcaacta ctaagagagg aagcaaaagt ttattcggta 720

gctctacgaa gtgtttacat tccaggatgg aggtttctac caaccaagca gaacaagaag 780

acgaaggaaa ttcacaatga aattaaaggc ttacttaagg gcattataaa taaaagggaa 840

gaggcgatga aggcagggga agccactaaa gatgacttac taggaatact tatggagtcc 900

aacttcaggg aaattcagga acatgggaac aacaaaaatg ctggaatgag tattgaagat 960

gtaattggag agtgtaagtt gttttacttt gctgggcaag agaccacttc ggtgttgctt 1020

gtttggacaa tgattttact aagccaaaat caggattggc aagctcgtgc aagagaagag 1080

gtcttgaaag tctttggaag caacatccca acctatgaag agctaagtca cctaaaagtt 1140

gtgaccatga ttttacttga agttcttcga ttatacccat cagtcgttgc gcttcctcga 1200

accactcaca agaaaacaca gcttggaaaa ttatcattac cagctggagt ggaagtctcc 1260

ttgcccatac tgcttgttca ccatgacaaa gagttgtggg gtgaggatgc aaatgagttc 1320

aagccagaga ggttttcaga gggagtttca aaggcaacaa agaacaaatt tacatactta 1380

cctttcggag ggggtccaag gatttgcatt ggacaaaact ttgccatggt ggaagctaaa 1440

ttggccttgg ccctgatttt acaacacttt gcctttgagc tttctccatc ctatgctcat 1500

gctccttctg cagttataac ccttcaacct caatttggtg ctcatatcat tttgcataaa 1560

cgttga 1566

<210> 99
<211> 1567
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized KAH

<400> 99
atggaagctt ctagagcatc ttgtgttgct ttgtgtgttg tttgggtttc catcgttatt 60

actttggctt ggagagtttt gaattgggtc tggttaagac caaaaaagtt ggaaagatgc 120

ttgagagaac aaggtttgac tggtaactct tacagattgt tgttcggtga taccaaggac 180

ttgtctaaga tgttggaaca aactcaatcc aagcctatca agttgtctac ctctcatgat 240

attgctccaa gagttactcc attcttccat agaactgtta actccaacgg taagaactct 300

tttgtttgga tgggtccaat tccaagagtc catattatga accctgaaga tttgaaggac 360

gctttcaaca gacatgatga tttccataag accgtcaaga acccaattat gaagtctcca 420

ccaccaggta tagttggtat tgaaggtgaa caatgggcca aacatagaaa gattattaac 480

ccagccttcc acttggaaaa gttgaaaggt atggttccaa tcttctacca atcctgctct 540

gaaatgatta acaagtggga atccttggtt tccaaagaat cttcctgtga attggatgtc 600

tggccatatt tggaaaactt cacctccgat gttatttcca gagctgcttt tggttcttct 660

tacgaagaag gtagaaagat cttccaatta ttgagagaag aagccaaggt ttactccgtt 720

gctttgagat ctgtttacat tccaggttgg agattcttgc caactaagca aaacaaaaag 780

accaaagaaa tccacaacga aatcaagggt ttgttgaagg gtatcatcaa caagagagaa 840

gaagctatga aggctggtga agctacaaaa gatgatttgt tgggtatctt gatggaatcc 900

aacttcagag aaatccaaga acacggtaac aacaagaatg ccggtatgtc tattgaagat 960

gttatcggtg aatgcaagtt gttctacttt gctggtcaag aaactacctc cgttttgttg 1020

gtttggacca tgattttgtt gtcccaaaat caagattggc aagctagagc tagagaagaa 1080

gtcttgaaag ttttcggttc taacatccca acctacgaag aattgtctca cttgaaggtt 1140

gtcactatga tcttgttgga agtattgaga ttatacccat ccgttgttgc attgccaaga 1200

actactcata agaaaactca attgggtaaa ttgtccttgc cagctggtgt tgaagtttct 1260

ttgccaattt tgttagtcca ccacgacaaa gaattgtggg gtgaagatgc taatgaattc 1320

aagccagaaa gattctccga aggtgtttct aaagctacca agaacaagtt cacttacttg 1380

ccatttggtg gtggtccaag aatatgtatt ggtcaaaatt tcgctatggt cgaagctaaa 1440

ttggctttgg ctttgatctt gcaacatttc gctttcgaat tgtcaccatc ttatgctcat 1500

gctccatctg ctgttattac attgcaacca caatttggtg cccatatcat cttgcataag 1560

agataac 1567

<210> 100
<211> 521
<212> PRT
<213> Prunus avium

<400> 100

Met Glu Ala Ser Arg Ala Ser Cys Val Ala Leu Cys Val Val Trp Val
1 5 10 15

Ser Ile Val Ile Thr Leu Ala Trp Arg Val Leu Asn Trp Val Trp Leu
20 25 30

Arg Pro Lys Lys Leu Glu Arg Cys Leu Arg Glu Gln Gly Leu Thr Gly
35 40 45

Asn Ser Tyr Arg Leu Leu Phe Gly Asp Thr Lys Asp Leu Ser Lys Met
50 55 60

```
Leu Glu Gln Thr Gln Ser Lys Pro Ile Lys Leu Ser Thr Ser His Asp
65                  70                  75                  80

Ile Ala Pro Arg Val Thr Pro Phe Phe His Arg Thr Val Asn Ser Asn
                85                  90                  95

Gly Lys Asn Ser Phe Val Trp Met Gly Pro Ile Pro Arg Val His Ile
            100                 105                 110

Met Asn Pro Glu Asp Leu Lys Asp Ala Phe Asn Arg His Asp Asp Phe
        115                 120                 125

His Lys Thr Val Lys Asn Pro Ile Met Lys Ser Pro Pro Pro Gly Ile
    130                 135                 140

Val Gly Ile Glu Gly Glu Gln Trp Ala Lys His Arg Lys Ile Ile Asn
145                 150                 155                 160

Pro Ala Phe His Leu Glu Lys Leu Lys Gly Met Val Pro Ile Phe Tyr
                165                 170                 175

Gln Ser Cys Ser Glu Met Ile Asn Lys Trp Glu Ser Leu Val Ser Lys
            180                 185                 190

Glu Ser Ser Cys Glu Leu Asp Val Trp Pro Tyr Leu Glu Asn Phe Thr
        195                 200                 205

Ser Asp Val Ile Ser Arg Ala Ala Phe Gly Ser Ser Tyr Glu Glu Gly
    210                 215                 220

Arg Lys Ile Phe Gln Leu Leu Arg Glu Glu Ala Lys Val Tyr Ser Val
225                 230                 235                 240

Ala Leu Arg Ser Val Tyr Ile Pro Gly Trp Arg Phe Leu Pro Thr Lys
                245                 250                 255

Gln Asn Lys Lys Thr Lys Glu Ile His Asn Glu Ile Lys Gly Leu Leu
```

```
            260                 265                 270

Lys Gly Ile Ile Asn Lys Arg Glu Glu Ala Met Lys Ala Gly Glu Ala
        275                 280                 285

Thr Lys Asp Asp Leu Leu Gly Ile Leu Met Glu Ser Asn Phe Arg Glu
    290                 295                 300

Ile Gln Glu His Gly Asn Asn Lys Asn Ala Gly Met Ser Ile Glu Asp
305                 310                 315                 320

Val Ile Gly Glu Cys Lys Leu Phe Tyr Phe Ala Gly Gln Glu Thr Thr
                325                 330                 335

Ser Val Leu Leu Val Trp Thr Met Ile Leu Leu Ser Gln Asn Gln Asp
            340                 345                 350

Trp Gln Ala Arg Ala Arg Glu Glu Val Leu Lys Val Phe Gly Ser Asn
        355                 360                 365

Ile Pro Thr Tyr Glu Glu Leu Ser His Leu Lys Val Val Thr Met Ile
    370                 375                 380

Leu Leu Glu Val Leu Arg Leu Tyr Pro Ser Val Val Ala Leu Pro Arg
385                 390                 395                 400

Thr Thr His Lys Lys Thr Gln Leu Gly Lys Leu Ser Leu Pro Ala Gly
                405                 410                 415

Val Glu Val Ser Leu Pro Ile Leu Leu Val His His Asp Lys Glu Leu
            420                 425                 430

Trp Gly Glu Asp Ala Asn Glu Phe Lys Pro Glu Arg Phe Ser Glu Gly
        435                 440                 445

Val Ser Lys Ala Thr Lys Asn Lys Phe Thr Tyr Leu Pro Phe Gly Gly
    450                 455                 460
```

```
Gly Pro Arg Ile Cys Ile Gly Gln Asn Phe Ala Met Val Glu Ala Lys
465                 470                 475                 480


Leu Ala Leu Ala Leu Ile Leu Gln His Phe Ala Phe Glu Leu Ser Pro
                485                 490                 495


Ser Tyr Ala His Ala Pro Ser Ala Val Ile Thr Leu Gln Pro Gln Phe
            500                 505                 510


Gly Ala His Ile Ile Leu His Lys Arg
        515                 520


<210>  101
<211>  517
<212>  PRT
<213>  Prunus mume

<400>  101

Ala Ser Trp Val Ala Val Leu Ser Val Val Trp Val Ser Met Val Ile
1               5                   10                  15


Ala Trp Ala Trp Arg Val Leu Asn Trp Val Trp Leu Arg Pro Lys Lys
            20                  25                  30


Leu Glu Lys Cys Leu Arg Glu Gln Gly Leu Ala Gly Asn Ser Tyr Arg
        35                  40                  45


Leu Leu Phe Gly Asp Thr Lys Asp Leu Ser Lys Met Leu Glu Gln Thr
    50                  55                  60


Gln Ser Lys Pro Ile Lys Leu Ser Thr Ser His Asp Ile Ala Pro His
65                  70                  75                  80


Val Thr Pro Phe Phe His Gln Thr Val Asn Ser Tyr Gly Lys Asn Ser
                85                  90                  95


Phe Val Trp Met Gly Pro Ile Pro Arg Val His Ile Met Asn Pro Glu
            100                 105                 110
```

```
Asp Leu Lys Asp Thr Phe Asn Arg His Asp Asp Phe His Lys Val Val
        115                 120                 125

Lys Asn Pro Ile Met Lys Ser Leu Pro Gln Gly Ile Val Gly Ile Glu
    130                 135                 140

Gly Glu Gln Trp Ala Lys His Arg Lys Ile Ile Asn Pro Ala Phe His
145                 150                 155                 160

Leu Glu Lys Leu Lys Gly Met Val Pro Ile Phe Tyr Arg Ser Cys Ser
                165                 170                 175

Glu Met Ile Asn Lys Trp Glu Ser Leu Val Ser Lys Glu Ser Ser Cys
            180                 185                 190

Glu Leu Asp Val Trp Pro Tyr Leu Glu Asn Phe Thr Ser Asp Val Ile
        195                 200                 205

Ser Arg Ala Ala Phe Gly Ser Ser Tyr Glu Glu Gly Arg Lys Ile Phe
    210                 215                 220

Gln Leu Leu Arg Glu Glu Ala Lys Ile Tyr Thr Val Ala Met Arg Ser
225                 230                 235                 240

Val Tyr Ile Pro Gly Trp Arg Phe Leu Pro Thr Lys Gln Asn Lys Lys
                245                 250                 255

Ala Lys Glu Ile His Asn Glu Ile Lys Gly Leu Leu Lys Gly Ile Ile
            260                 265                 270

Asn Lys Arg Glu Glu Ala Met Lys Ala Gly Glu Ala Thr Lys Asp Asp
        275                 280                 285

Leu Leu Gly Ile Leu Met Glu Ser Asn Phe Arg Glu Ile Gln Glu His
    290                 295                 300
```

```
Gly Asn Asn Lys Asn Ala Gly Met Ser Ile Glu Asp Val Ile Gly Glu
305                 310                 315                 320


Cys Lys Leu Phe Tyr Phe Ala Gly Gln Glu Thr Thr Ser Val Leu Leu
                325                 330                 335


Val Trp Thr Met Val Leu Leu Ser Gln Asn Gln Asp Trp Gln Ala Arg
            340                 345                 350


Ala Arg Glu Glu Val Leu Gln Val Phe Gly Ser Asn Ile Pro Thr Tyr
        355                 360                 365


Glu Glu Leu Ser Gln Leu Lys Val Val Thr Met Ile Leu Leu Glu Val
    370                 375                 380


Leu Arg Leu Tyr Pro Ser Val Val Ala Leu Pro Arg Thr Thr His Lys
385                 390                 395                 400


Lys Thr Gln Leu Gly Lys Leu Ser Leu Pro Ala Gly Val Glu Val Ser
                405                 410                 415


Leu Pro Ile Leu Leu Val His His Asp Lys Glu Leu Trp Gly Glu Asp
            420                 425                 430


Ala Asn Glu Phe Lys Pro Glu Arg Phe Ser Glu Gly Val Ser Lys Ala
        435                 440                 445


Thr Lys Asn Gln Phe Thr Tyr Phe Pro Phe Gly Gly Gly Pro Arg Ile
    450                 455                 460


Cys Ile Gly Gln Asn Phe Ala Met Met Glu Ala Lys Leu Ala Leu Ser
465                 470                 475                 480


Leu Ile Leu Arg His Phe Ala Leu Glu Leu Ser Pro Leu Tyr Ala His
                485                 490                 495


Ala Pro Ser Val Thr Ile Thr Leu Gln Pro Gln Tyr Gly Ala His Ile
            500                 505                 510
```

Ile Leu His Lys Arg
515

<210> 102
<211> 521
<212> PRT
<213> Prunus mume

<400> 102

Met Glu Ala Ser Arg Pro Ser Cys Val Ala Leu Ser Val Val Leu Val
1 5 10 15

Ser Ile Val Ile Ala Trp Ala Trp Arg Val Leu Asn Trp Val Trp Leu
20 25 30

Arg Pro Asn Lys Leu Glu Arg Cys Leu Arg Glu Gln Gly Leu Thr Gly
35 40 45

Asn Ser Tyr Arg Leu Leu Phe Gly Asp Thr Lys Glu Ile Ser Met Met
50 55 60

Val Glu Gln Ala Gln Ser Lys Pro Ile Lys Leu Ser Thr Thr His Asp
65 70 75 80

Ile Ala Pro Arg Val Ile Pro Phe Ser His Gln Ile Val Tyr Thr Tyr
85 90 95

Gly Arg Asn Ser Phe Val Trp Met Gly Pro Thr Pro Arg Val Thr Ile
100 105 110

Met Asn Pro Glu Asp Leu Lys Asp Ala Phe Asn Lys Ser Asp Glu Phe
115 120 125

Gln Arg Ala Ile Ser Asn Pro Ile Val Lys Ser Ile Ser Gln Gly Leu
130 135 140

Ser Ser Leu Glu Gly Glu Lys Trp Ala Lys His Arg Lys Ile Ile Asn

```
145                 150                 155                 160

Pro Ala Phe His Leu Glu Lys Leu Lys Gly Met Leu Pro Thr Phe Tyr
                165                 170                 175

Gln Ser Cys Ser Glu Met Ile Asn Lys Trp Glu Ser Leu Val Phe Lys
            180                 185                 190

Glu Gly Ser Arg Glu Met Asp Val Trp Pro Tyr Leu Glu Asn Leu Thr
        195                 200                 205

Ser Asp Val Ile Ser Arg Ala Ala Phe Gly Ser Ser Tyr Glu Glu Gly
    210                 215                 220

Arg Lys Ile Phe Gln Leu Leu Arg Glu Glu Ala Lys Phe Tyr Thr Ile
225                 230                 235                 240

Ala Ala Arg Ser Val Tyr Ile Pro Gly Trp Arg Phe Leu Pro Thr Lys
                245                 250                 255

Gln Asn Lys Arg Met Lys Glu Ile His Lys Glu Val Arg Gly Leu Leu
            260                 265                 270

Lys Gly Ile Ile Asn Lys Arg Glu Asp Ala Ile Lys Ala Gly Glu Ala
        275                 280                 285

Ala Lys Gly Asn Leu Leu Gly Ile Leu Met Glu Ser Asn Phe Arg Glu
    290                 295                 300

Ile Gln Glu His Gly Asn Asn Lys Asn Ala Gly Met Ser Ile Glu Asp
305                 310                 315                 320

Val Ile Gly Glu Cys Lys Leu Phe Tyr Phe Ala Gly Gln Glu Thr Thr
                325                 330                 335

Ser Val Leu Leu Val Trp Thr Leu Val Leu Leu Ser Gln Asn Gln Asp
            340                 345                 350
```

```
Trp Gln Ala Arg Ala Arg Glu Glu Val Leu Gln Val Phe Gly Thr Asn
        355                 360                 365

Ile Pro Thr Tyr Asp Gln Leu Ser His Leu Lys Val Val Thr Met Ile
    370                 375                 380

Leu Leu Glu Val Leu Arg Leu Tyr Pro Ala Val Val Glu Leu Pro Arg
385                 390                 395                 400

Thr Thr Tyr Lys Lys Thr Gln Leu Gly Lys Phe Leu Leu Pro Ala Gly
                405                 410                 415

Val Glu Val Ser Leu His Ile Met Leu Ala His His Asp Lys Glu Leu
            420                 425                 430

Trp Gly Glu Asp Ala Lys Glu Phe Lys Pro Glu Arg Phe Ser Glu Gly
        435                 440                 445

Val Ser Lys Ala Thr Lys Asn Gln Phe Thr Tyr Phe Pro Phe Gly Ala
    450                 455                 460

Gly Pro Arg Ile Cys Ile Gly Gln Asn Phe Ala Met Leu Glu Ala Lys
465                 470                 475                 480

Leu Ala Leu Ser Leu Ile Leu Gln His Phe Thr Phe Glu Leu Ser Pro
                485                 490                 495

Ser Tyr Ala His Ala Pro Ser Val Thr Ile Thr Leu His Pro Gln Phe
            500                 505                 510

Gly Ala His Phe Ile Leu His Lys Arg
        515                 520
```

<210> 103
<211> 514
<212> PRT
<213> Prunus mume

<400> 103

```
Cys Val Ala Leu Ser Val Val Leu Val Ser Ile Val Ile Ala Trp Ala
1               5                   10                  15


Trp Arg Val Leu Asn Trp Val Trp Leu Arg Pro Asn Lys Leu Glu Arg
            20                  25                  30


Cys Leu Arg Glu Gln Gly Leu Thr Gly Asn Ser Tyr Arg Leu Leu Phe
        35                  40                  45


Gly Asp Thr Lys Glu Ile Ser Met Met Val Glu Gln Ala Gln Ser Lys
    50                  55                  60


Pro Ile Lys Leu Ser Thr Thr His Asp Ile Ala Pro Arg Val Ile Pro
65                  70                  75                  80


Phe Ser His Gln Ile Val Tyr Thr Tyr Gly Arg Asn Ser Phe Val Trp
                85                  90                  95


Met Gly Pro Thr Pro Arg Val Thr Ile Met Asn Pro Glu Asp Leu Lys
            100                 105                 110


Asp Ala Phe Asn Lys Ser Asp Glu Phe Gln Arg Ala Ile Ser Asn Pro
        115                 120                 125


Ile Val Lys Ser Ile Ser Gln Gly Leu Ser Ser Leu Glu Gly Glu Lys
    130                 135                 140


Trp Ala Lys His Arg Lys Ile Ile Asn Pro Ala Phe His Leu Glu Lys
145                 150                 155                 160


Leu Lys Gly Met Leu Pro Thr Phe Tyr Gln Ser Cys Ser Glu Met Ile
                165                 170                 175


Asn Lys Trp Glu Ser Leu Val Phe Lys Glu Gly Ser Arg Glu Met Asp
            180                 185                 190
```

```
Val Trp Pro Tyr Leu Glu Asn Leu Thr Ser Asp Val Ile Ser Arg Ala
        195                 200                 205

Ala Phe Gly Ser Ser Tyr Glu Glu Gly Arg Lys Ile Phe Gln Leu Leu
    210                 215                 220

Arg Glu Glu Ala Lys Phe Tyr Thr Ile Ala Ala Arg Ser Val Tyr Ile
225                 230                 235                 240

Pro Gly Trp Arg Phe Leu Pro Thr Lys Gln Asn Lys Arg Met Lys Glu
                245                 250                 255

Ile His Lys Glu Val Arg Gly Leu Leu Lys Gly Ile Ile Asn Lys Arg
            260                 265                 270

Glu Asp Ala Ile Lys Ala Gly Glu Ala Ala Lys Gly Asn Leu Leu Gly
        275                 280                 285

Ile Leu Met Glu Ser Asn Phe Arg Glu Ile Gln Glu His Gly Asn Asn
    290                 295                 300

Lys Asn Ala Gly Met Ser Ile Glu Asp Val Ile Gly Glu Cys Lys Leu
305                 310                 315                 320

Phe Tyr Phe Ala Gly Gln Glu Thr Thr Ser Val Leu Leu Val Trp Thr
                325                 330                 335

Leu Val Leu Leu Ser Gln Asn Gln Asp Trp Gln Ala Arg Ala Arg Glu
            340                 345                 350

Glu Val Leu Gln Val Phe Gly Thr Asn Ile Pro Thr Tyr Asp Gln Leu
        355                 360                 365

Ser His Leu Lys Val Val Thr Met Ile Leu Leu Glu Val Leu Arg Leu
    370                 375                 380

Tyr Pro Ala Val Val Glu Leu Pro Arg Thr Thr Tyr Lys Lys Thr Gln
385                 390                 395                 400
```

```
Leu Gly Lys Phe Leu Leu Pro Ala Gly Val Glu Val Ser Leu His Ile
                405                 410                 415


Met Leu Ala His His Asp Lys Glu Leu Trp Gly Glu Asp Ala Lys Glu
            420                 425                 430


Phe Lys Pro Glu Arg Phe Ser Glu Gly Val Ser Lys Ala Thr Lys Asn
        435                 440                 445


Gln Phe Thr Tyr Phe Pro Phe Gly Ala Gly Pro Arg Ile Cys Ile Gly
    450                 455                 460


Gln Asn Phe Ala Met Leu Glu Ala Lys Leu Ala Leu Ser Leu Ile Leu
465                 470                 475                 480


Gln His Phe Thr Phe Glu Leu Ser Pro Ser Tyr Ala His Ala Pro Ser
                485                 490                 495


Val Thr Ile Thr Leu His Pro Gln Phe Gly Ala His Phe Ile Leu His
            500                 505                 510


Lys Arg
```

<210> 104
<211> 418
<212> PRT
<213> Prunus persica

<400> 104

```
Met Gly Pro Ile Pro Arg Val His Ile Met Asn Pro Glu Asp Leu Lys
1               5                   10                  15


Asp Thr Phe Asn Arg His Asp Asp Phe His Lys Val Val Lys Asn Pro
            20                  25                  30


Ile Met Lys Ser Leu Pro Gln Gly Ile Val Gly Ile Glu Gly Asp Gln
```

```
        35                  40                  45

Trp Ala Lys His Arg Lys Ile Ile Asn Pro Ala Phe His Leu Glu Lys
    50                  55                  60

Leu Lys Gly Met Val Pro Ile Phe Tyr Gln Ser Cys Ser Glu Met Ile
65                  70                  75                  80

Asn Ile Trp Lys Ser Leu Val Ser Lys Glu Ser Ser Cys Glu Leu Asp
                85                  90                  95

Val Trp Pro Tyr Leu Glu Asn Phe Thr Ser Asp Val Ile Ser Arg Ala
            100                 105                 110

Ala Phe Gly Ser Ser Tyr Glu Glu Gly Arg Lys Ile Phe Gln Leu Leu
        115                 120                 125

Arg Glu Glu Ala Lys Val Tyr Thr Val Ala Val Arg Ser Val Tyr Ile
    130                 135                 140

Pro Gly Trp Arg Phe Leu Pro Thr Lys Gln Asn Lys Lys Thr Lys Glu
145                 150                 155                 160

Ile His Asn Glu Ile Lys Gly Leu Leu Lys Gly Ile Ile Asn Lys Arg
                165                 170                 175

Glu Glu Ala Met Lys Ala Gly Glu Ala Thr Lys Asp Asp Leu Leu Gly
            180                 185                 190

Ile Leu Met Glu Ser Asn Phe Arg Glu Ile Gln Glu His Gly Asn Asn
        195                 200                 205

Lys Asn Ala Gly Met Ser Ile Glu Asp Val Ile Gly Glu Cys Lys Leu
    210                 215                 220

Phe Tyr Phe Ala Gly Gln Glu Thr Thr Ser Val Leu Leu Val Trp Thr
225                 230                 235                 240
```

```
Met Val Leu Leu Ser Gln Asn Gln Asp Trp Gln Ala Arg Ala Arg Glu
                245                 250                 255

Glu Val Leu Gln Val Phe Gly Ser Asn Ile Pro Thr Tyr Glu Glu Leu
            260                 265                 270

Ser His Leu Lys Val Val Thr Met Ile Leu Leu Glu Val Leu Arg Leu
        275                 280                 285

Tyr Pro Ser Val Val Ala Leu Pro Arg Thr Thr His Lys Lys Thr Gln
    290                 295                 300

Leu Gly Lys Leu Ser Leu Pro Ala Gly Val Glu Val Ser Leu Pro Ile
305                 310                 315                 320

Leu Leu Val His His Asp Lys Glu Leu Trp Gly Glu Asp Ala Asn Glu
                325                 330                 335

Phe Lys Pro Glu Arg Phe Ser Glu Gly Val Ser Lys Ala Thr Lys Asn
            340                 345                 350

Gln Phe Thr Tyr Phe Pro Phe Gly Gly Gly Pro Arg Ile Cys Ile Gly
        355                 360                 365

Gln Asn Phe Ala Met Met Glu Ala Lys Leu Ala Leu Ser Leu Ile Leu
    370                 375                 380

Gln His Phe Thr Phe Glu Leu Ser Pro Gln Tyr Ser His Ala Pro Ser
385                 390                 395                 400

Val Thr Ile Thr Leu Gln Pro Gln Tyr Gly Ala His Leu Ile Leu His
                405                 410                 415

Lys Arg
```

<210> 105

<211> 1578
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized KAH

<400> 105
atgggtttgt tcccattaga ggattcctac gcgctggtct ttgaaggact agcaataaca 60

ctggctttgt actatctact gtctttcatc tacaaaacat ctaaaaagac atgtacacct 120

cctaaagcat ctggtgaaat cattccaatt acaggaatca tattgaatct gctatctggc 180

tcaagtggtc tacctattat cttagcactt gcctctttag cagacagatg tggtcctatt 240

ttcaccatta ggctgggtat taggagagtg ctagtagtat caaattggga aatcgctaag 300

gagattttca ctacccacga tttgatagtt tctaatagac caaaatactt agccgctaag 360

attcttggtt tcaattatgt ttcattctct ttcgctccat acggcccata ttgggtcgga 420

atcagaaaga ttattgctac aaaactaatg tcttcttcca gacttcagaa gttgcaattt 480

gtaagagttt ttgaactaga aaactctatg aaatctatca gagaatcatg gaaggagaaa 540

aaggatgaag agggaaaggt attagttgag atgaaaaagt ggttctggga actgaatatg 600

aacatagtgt taaggacagt tgctggtaaa caatacactg gtacagttga tgatgccgat 660

gcaaagcgta tctccgagtt attcagagaa tggtttcact acactggcag atttgtcgtt 720

ggagacgctt ttccttttct aggttggttg gacctgggcg gatacaaaaa gacaatggaa 780

ttagttgcta gtagattgga ctcaatggtc agtaaatggt tagatgagca tcgtaaaaag 840

caagctaacg atgacaaaaa ggaggatatg gatttcatgg atatcatgat ctccatgaca 900

gaagcaaatt caccacttga aggatacggc actgatacta ttatcaagac cacatgtatg 960

actttgattg tttcaggagt tgatacaacc tcaatcgtac ttacttgggc cttatcactt 1020

ttgttaaaca acagagatac tttgaaaaag gcacaagagg aattagatat gtgcgtaggt 1080

aaaggaagac aagtcaacga gtctgatctt gttaacttga tatacttgga agcagtgctt 1140

aaagaggctt taagacttta cccagcagcg ttcttaggcg gaccaagagc attcttggaa 1200

gattgtactg ttgctggtta tagaattcca aagggcacct gcttgttgat taacatgtgg 1260

aaactgcata gagatccaaa catttggagt gatccttgcg aattcaagcc agaaagattt 1320

ttgacaccta atcaaaagga tgttgatgtg atcggtatgg atttcgaatt gataccattt 1380

ggtgccggca gaagatattg tccaggtact agattggctt tacagatgtt gcatatcgta 1440

ttagcgacat tgctgcaaaa cttcgaaatg tcaacaccaa acgatgcgcc agtcgatatg 1500

actgcttctg ttggcatgac aaatgccaaa gcatcacctt tagaagtctt gctatcacct 1560

cgtgttaaat ggtcctaa 1578

<210> 106
<211> 522
<212> PRT
<213> Stevia rebaudiana

<400> 106

Met Gly Leu Phe Pro Leu Glu Asp Ser Tyr Ala Leu Val Phe Glu Gly
1 5 10 15

Leu Ala Ile Thr Leu Ala Leu Tyr Tyr Leu Leu Ser Phe Ile Tyr Lys
20 25 30

Thr Ser Lys Lys Thr Cys Thr Pro Pro Lys Ala Ser Gly Glu His Pro
35 40 45

Ile Thr Gly His Leu Asn Leu Leu Ser Gly Ser Ser Gly Leu Pro His
50 55 60

Leu Ala Leu Ala Ser Leu Ala Asp Arg Cys Gly Pro Ile Phe Thr Ile
65 70 75 80

Arg Leu Gly Ile Arg Arg Val Leu Val Val Ser Asn Trp Glu Ile Ala
85 90 95

Lys Glu Ile Phe Thr Thr His Asp Leu Ile Val Ser Asn Arg Pro Lys
100 105 110

Tyr Leu Ala Ala Lys Ile Leu Gly Phe Asn Tyr Val Ser Phe Ser Phe
115 120 125

```
Ala Pro Tyr Gly Pro Tyr Trp Val Gly Ile Arg Lys Ile Ile Ala Thr
    130                 135                 140

Lys Leu Met Ser Ser Ser Arg Leu Gln Lys Leu Gln Phe Val Arg Val
145                 150                 155                 160

Phe Glu Leu Glu Asn Ser Met Lys Ser Ile Arg Glu Ser Trp Lys Glu
                165                 170                 175

Lys Lys Asp Glu Glu Gly Lys Val Leu Val Glu Met Lys Lys Trp Phe
            180                 185                 190

Trp Glu Leu Asn Met Asn Ile Val Leu Arg Thr Val Ala Gly Lys Gln
        195                 200                 205

Tyr Thr Gly Thr Val Asp Asp Ala Asp Ala Lys Arg Ile Ser Glu Leu
    210                 215                 220

Phe Arg Glu Trp Phe His Tyr Thr Gly Arg Phe Val Val Gly Asp Ala
225                 230                 235                 240

Phe Pro Phe Leu Gly Trp Leu Asp Leu Gly Gly Tyr Lys Lys Thr Met
                245                 250                 255

Glu Leu Val Ala Ser Arg Leu Asp Ser Met Val Ser Lys Trp Leu Asp
            260                 265                 270

Glu His Arg Lys Lys Gln Ala Asn Asp Asp Lys Lys Glu Asp Met Asp
        275                 280                 285

Phe Met Asp Ile Met Ile Ser Met Thr Glu Ala Asn Ser Pro Leu Glu
    290                 295                 300

Gly Tyr Gly Thr Asp Thr Ile Ile Lys Thr Thr Cys Met Thr Leu Ile
305                 310                 315                 320
```

```
Val Ser Gly Val Asp Thr Thr Ser Ile Val Leu Thr Trp Ala Leu Ser
                325                 330                 335

Leu Leu Leu Asn Asn Arg Asp Thr Leu Lys Lys Ala Gln Glu Glu Leu
            340                 345                 350

Asp Met Cys Val Gly Lys Gly Arg Gln Val Asn Glu Ser Asp Leu Val
        355                 360                 365

Asn Leu Ile Tyr Leu Glu Ala Val Leu Lys Glu Ala Leu Arg Leu Tyr
    370                 375                 380

Pro Ala Ala Phe Leu Gly Gly Pro Arg Ala Phe Leu Glu Asp Cys Thr
385                 390                 395                 400

Val Ala Gly Tyr Arg Ile Pro Lys Gly Thr Cys Leu Leu Ile Asn Met
                405                 410                 415

Trp Lys Leu His Arg Asp Pro Asn Ile Trp Ser Asp Pro Cys Glu Phe
            420                 425                 430

Lys Pro Glu Arg Phe Leu Thr Pro Asn Gln Lys Asp Val Asp Val Ile
        435                 440                 445

Gly Met Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Tyr Cys
    450                 455                 460

Pro Gly Thr Arg Leu Ala Leu Gln Met Leu His Ile Val Leu Ala Thr
465                 470                 475                 480

Leu Leu Gln Asn Phe Glu Met Ser Thr Pro Asn Asp Ala Pro Val Asp
                485                 490                 495

Met Thr Ala Ser Val Gly Met Thr Asn Ala Lys Ala Ser Pro Leu Glu
            500                 505                 510

Val Leu Leu Ser Pro Arg Val Lys Trp Ser
        515                 520
```

<210> 107
<211> 1431
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized KAH

<400> 107
atgatacaag ttttaactcc aattctactc ttcctcatct tcttcgtttt ctggaaagtc 60

tacaaacatc aaaagactaa aatcaatcta ccaccaggtt ccttcggctg gccatttttg 120

ggtgaaacct tagccttact tagagcaggc tgggattctg agccagaaag attcgtaaga 180

gagcgtatca aaaagcatgg atctccactt gttttcaaga catcactatt tggagacaga 240

ttcgctgttc tttgcggtcc agctggtaat aagtttttgt tctgcaacga aaacaaatta 300

gtggcatctt ggtggccagt ccctgtaagg aagttgttcg gtaaaagttt actcacaata 360

agaggagatg aagcaaaatg gatgagaaaa atgctattgt cttacttggg tccagatgca 420

tttgccacac attatgccgt tactatggat gttgtaacac gtagacatat tgatgtccat 480

tggaggggca aggaggaagt taatgtattt caaacagtta agttgtacgc attcgaatta 540

gcttgtagat tattcatgaa cctagatgac ccaaaccaca tcgcgaaact cggtagtctt 600

ttcaacattt tcctcaaagg gatcatcgag cttcctatag acgttcctgg aactagattt 660

tactccagta aaaaggccgc agctgccatt agaattgaat tgaaaaagct cattaaagct 720

agaaaactcg aattgaagga gggtaaggcg tcttcttcac aggacttgct ttctcatcta 780

ttaacatcac ctgatgagaa tgggatgttc ttgacagaag aggaaatagt cgataacatt 840

ctacttttgt tattcgctgg tcacgatacc tctgcactat caataacact tttgatgaaa 900

accttaggtg aacacagtga tgtgtacgac aaggttttga aggaacaatt agaaatttcc 960

aaaacaaagg aggcttggga atcactaaag tgggaagata tccagaagat gaagtactca 1020

tggtcagtaa tctgtgaagt catgagattg aatcctcctg tcatagggac atacagagag 1080

gcgttggttg atatcgacta tgctggttac actatcccaa aaggatggaa gttgcattgg 1140

tcagctgttt ctactcaaag agacgaagcc aatttcgaag atgtaactag attcgatcca 1200

tccagatttg aaggggcagg ccctactcca ttcacatttg tgcctttcgg tggaggtcct 1260

agaatgtgtt taggcaaaga gtttgccagg ttagaagtgt tagcatttct ccacaacatt 1320

gttaccaact ttaagtggga tcttctaatc cctgatgaga agatcgaata tgatccaatg 1380

gctactccag ctaagggctt gccaattaga cttcatccac accaagtcta a 1431

<210> 108
<211> 476
<212> PRT
<213> Stevia rebaudiana

<400> 108

Met Ile Gln Val Leu Thr Pro Ile Leu Leu Phe Leu Ile Phe Phe Val
1 5 10 15

Phe Trp Lys Val Tyr Lys His Gln Lys Thr Lys Ile Asn Leu Pro Pro
20 25 30

Gly Ser Phe Gly Trp Pro Phe Leu Gly Glu Thr Leu Ala Leu Leu Arg
35 40 45

Ala Gly Trp Asp Ser Glu Pro Glu Arg Phe Val Arg Glu Arg Ile Lys
50 55 60

Lys His Gly Ser Pro Leu Val Phe Lys Thr Ser Leu Phe Gly Asp Arg
65 70 75 80

Phe Ala Val Leu Cys Gly Pro Ala Gly Asn Lys Phe Leu Phe Cys Asn
85 90 95

Glu Asn Lys Leu Val Ala Ser Trp Trp Pro Val Pro Val Arg Lys Leu
100 105 110

Phe Gly Lys Ser Leu Leu Thr Ile Arg Gly Asp Glu Ala Lys Trp Met
115 120 125

Arg Lys Met Leu Leu Ser Tyr Leu Gly Pro Asp Ala Phe Ala Thr His

```
    130                 135                 140

Tyr Ala Val Thr Met Asp Val Val Thr Arg Arg His Ile Asp Val His
145                 150                 155                 160

Trp Arg Gly Lys Glu Glu Val Asn Val Phe Gln Thr Val Lys Leu Tyr
                165                 170                 175

Ala Phe Glu Leu Ala Cys Arg Leu Phe Met Asn Leu Asp Asp Pro Asn
            180                 185                 190

His Ile Ala Lys Leu Gly Ser Leu Phe Asn Ile Phe Leu Lys Gly Ile
        195                 200                 205

Ile Glu Leu Pro Ile Asp Val Pro Gly Thr Arg Phe Tyr Ser Ser Lys
    210                 215                 220

Lys Ala Ala Ala Ala Ile Arg Ile Glu Leu Lys Lys Leu Ile Lys Ala
225                 230                 235                 240

Arg Lys Leu Glu Leu Lys Glu Gly Lys Ala Ser Ser Ser Gln Asp Leu
                245                 250                 255

Leu Ser His Leu Leu Thr Ser Pro Asp Glu Asn Gly Met Phe Leu Thr
            260                 265                 270

Glu Glu Glu Ile Val Asp Asn Ile Leu Leu Leu Leu Phe Ala Gly His
        275                 280                 285

Asp Thr Ser Ala Leu Ser Ile Thr Leu Leu Met Lys Thr Leu Gly Glu
    290                 295                 300

His Ser Asp Val Tyr Asp Lys Val Leu Lys Glu Gln Leu Glu Ile Ser
305                 310                 315                 320

Lys Thr Lys Glu Ala Trp Glu Ser Leu Lys Trp Glu Asp Ile Gln Lys
                325                 330                 335
```

```
Met Lys Tyr Ser Trp Ser Val Ile Cys Glu Val Met Arg Leu Asn Pro
            340                 345                 350

Pro Val Ile Gly Thr Tyr Arg Glu Ala Leu Val Asp Ile Asp Tyr Ala
        355                 360                 365

Gly Tyr Thr Ile Pro Lys Gly Trp Lys Leu His Trp Ser Ala Val Ser
    370                 375                 380

Thr Gln Arg Asp Glu Ala Asn Phe Glu Asp Val Thr Arg Phe Asp Pro
385                 390                 395                 400

Ser Arg Phe Glu Gly Ala Gly Pro Thr Pro Phe Thr Phe Val Pro Phe
                405                 410                 415

Gly Gly Gly Pro Arg Met Cys Leu Gly Lys Glu Phe Ala Arg Leu Glu
            420                 425                 430

Val Leu Ala Phe Leu His Asn Ile Val Thr Asn Phe Lys Trp Asp Leu
        435                 440                 445

Leu Ile Pro Asp Glu Lys Ile Glu Tyr Asp Pro Met Ala Thr Pro Ala
    450                 455                 460

Lys Gly Leu Pro Ile Arg Leu His Pro His Gln Val
465                 470                 475
```

<210> 109
<211> 1578
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized KAH

<400> 109
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ttctcagttg gttatcacgt ttacggtaga gctgtggtcg aacaatggag aatgagaaga 120

tcactgaagc tacaaggtgt taaaggccca ccaccatcca tcttcaatgg taacgtctca 180

gaaatgcaac gtatccaatc cgaagctaaa cactgctctg gcgataacat tatctcacat 240

gattattctt cttcattatt cccacacttc gatcactgga gaaaacagta cggcagaatc 300

tacacatact ctactggatt aaagcaacac ttgtacatca atcatccaga aatggtgaag 360

gagctatctc agactaacac attgaacttg ggtagaatca cccatataac caaaagattg 420

aatcctatct taggtaacgg aatcataacc tctaatggtc ctcattgggc ccatcagcgt 480

agaattatcg cctacgagtt tactcatgat aagatcaagg gtatggttgg tttgatggtt 540

gagtctgcta tgcctatgtt gaataagtgg gaggagatgg taaagagagg cggagaaatg 600

ggatgcgaca taagagttga tgaggacttg aaagatgttt cagcagatgt gattgcaaaa 660

gcctgtttcg gatcctcatt ttctaaaggt aaggctattt tctctatgat aagagatttg 720

cttacagcta tcacaaagag aagtgttcta ttcagattca acggattcac tgatatggtc 780

tttgggagta aaaagcatgg tgacgttgat atagacgctt tagaaatgga attggaatca 840

tccatttggg aaactgtcaa ggaacgtgaa atagaatgta aagatactca caaaaaggat 900

ctgatgcaat tgattttgga aggggcaatg cgttcatgtg acggtaacct ttgggataaa 960

tcagcatata gaagatttgt tgtagataat tgtaaatcta tctacttcgc agggcatgat 1020

agtacagctg tctcagtgtc atggtgtttg atgttactgg ccctaaaccc atcatggcaa 1080

gttaagatcc gtgatgaaat tctgtcttct tgcaaaaatg gtattccaga tgccgaaagt 1140

atcccaaacc ttaaaacagt gactatggtt attcaagaga caatgagatt ataccctcca 1200

gcaccaatcg tcgggagaga agcctctaaa gatatcagat tgggcgatct agttgttcct 1260

aaaggcgtct gtatatggac actaatacca gctttacaca gagatcctga gatttgggga 1320

ccagatgcaa acgatttcaa accagaaaga ttttctgaag gaatttcaaa ggcttgtaag 1380

tatcctcaaa gttacattcc atttggtctg ggtcctagaa catgcgttgg taaaaacttt 1440

ggcatgatgg aagtaaaggt tcttgtttcc ctgattgtct ccaagttctc tttcactcta 1500

tctcctacct accaacatag tcctagtcac aaacttttag tagaaccaca acatggggtg 1560

gtaattagag tggtttaa 1578

<210> 110
<211> 525
<212> PRT
<213> Arabidopsis thaliana

<400> 110

Met Glu Ser Leu Val Val His Thr Val Asn Ala Ile Trp Cys Ile Val
1   5   10   15

Ile Val Gly Ile Phe Ser Val Gly Tyr His Val Tyr Gly Arg Ala Val
            20   25   30

Val Glu Gln Trp Arg Met Arg Arg Ser Leu Lys Leu Gln Gly Val Lys
        35   40   45

Gly Pro Pro Pro Ser Ile Phe Asn Gly Asn Val Ser Glu Met Gln Arg
    50   55   60

Ile Gln Ser Glu Ala Lys His Cys Ser Gly Asp Asn Ile Ile Ser His
65   70   75   80

Asp Tyr Ser Ser Ser Leu Phe Pro His Phe Asp His Trp Arg Lys Gln
                85   90   95

Tyr Gly Arg Ile Tyr Thr Tyr Ser Thr Gly Leu Lys Gln His Leu Tyr
            100   105   110

Ile Asn His Pro Glu Met Val Lys Glu Leu Ser Gln Thr Asn Thr Leu
        115   120   125

Asn Leu Gly Arg Ile Thr His Ile Thr Lys Arg Leu Asn Pro Ile Leu
    130   135   140

Gly Asn Gly Ile Ile Thr Ser Asn Gly Pro His Trp Ala His Gln Arg
145   150   155   160

Arg Ile Ile Ala Tyr Glu Phe Thr His Asp Lys Ile Lys Gly Met Val
                165   170   175

```
Gly Leu Met Val Glu Ser Ala Met Pro Met Leu Asn Lys Trp Glu Glu
            180                 185                 190

Met Val Lys Arg Gly Gly Glu Met Gly Cys Asp Ile Arg Val Asp Glu
        195                 200                 205

Asp Leu Lys Asp Val Ser Ala Asp Val Ile Ala Lys Ala Cys Phe Gly
    210                 215                 220

Ser Ser Phe Ser Lys Gly Lys Ala Ile Phe Ser Met Ile Arg Asp Leu
225                 230                 235                 240

Leu Thr Ala Ile Thr Lys Arg Ser Val Leu Phe Arg Phe Asn Gly Phe
                245                 250                 255

Thr Asp Met Val Phe Gly Ser Lys Lys His Gly Asp Val Asp Ile Asp
            260                 265                 270

Ala Leu Glu Met Glu Leu Glu Ser Ser Ile Trp Glu Thr Val Lys Glu
        275                 280                 285

Arg Glu Ile Glu Cys Lys Asp Thr His Lys Lys Asp Leu Met Gln Leu
    290                 295                 300

Ile Leu Glu Gly Ala Met Arg Ser Cys Asp Gly Asn Leu Trp Asp Lys
305                 310                 315                 320

Ser Ala Tyr Arg Arg Phe Val Val Asp Asn Cys Lys Ser Ile Tyr Phe
                325                 330                 335

Ala Gly His Asp Ser Thr Ala Val Ser Val Ser Trp Cys Leu Met Leu
            340                 345                 350

Leu Ala Leu Asn Pro Ser Trp Gln Val Lys Ile Arg Asp Glu Ile Leu
        355                 360                 365
```

```
Ser Ser Cys Lys Asn Gly Ile Pro Asp Ala Glu Ser Ile Pro Asn Leu
    370                 375                 380

Lys Thr Val Thr Met Val Ile Gln Glu Thr Met Arg Leu Tyr Pro Pro
385                 390                 395                 400

Ala Pro Ile Val Gly Arg Glu Ala Ser Lys Asp Ile Arg Leu Gly Asp
                405                 410                 415

Leu Val Val Pro Lys Gly Val Cys Ile Trp Thr Leu Ile Pro Ala Leu
            420                 425                 430

His Arg Asp Pro Glu Ile Trp Gly Pro Asp Ala Asn Asp Phe Lys Pro
        435                 440                 445

Glu Arg Phe Ser Glu Gly Ile Ser Lys Ala Cys Lys Tyr Pro Gln Ser
    450                 455                 460

Tyr Ile Pro Phe Gly Leu Gly Pro Arg Thr Cys Val Gly Lys Asn Phe
465                 470                 475                 480

Gly Met Met Glu Val Lys Val Leu Val Ser Leu Ile Val Ser Lys Phe
                485                 490                 495

Ser Phe Thr Leu Ser Pro Thr Tyr Gln His Ser Pro Ser His Lys Leu
            500                 505                 510

Leu Val Glu Pro Gln His Gly Val Val Ile Arg Val Val
        515                 520                 525
```

<210> 111
<211> 1590
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized KAH

<400> 111
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ctctcttatt gtttacttct ctggagaagt agagcgggta acaaaaagat tgccccagaa 120

gctgccgctg catggcctat tatcggccac ctccacttac ttgcaggtgg atcccatcaa 180

ctaccacata ttacattggg taacatggca gataagtacg gtcctgtatt cacaatcaga 240

ataggcttgc atagagctgt agttgtctca tcttgggaaa tggcaaagga atgttcaaca 300

gctaatgatc aagtgtcttc ttcaagacct gaactattag cttctaagtt gttgggttat 360

aactacgcca tgtttggttt ttcaccatac ggttcatact ggagagaaat gagaaagatc 420

atctctctcg aattactatc taattccaga ttggaactat tgaaagatgt tagagcctca 480

gaagttgtca catctattaa ggaactatac aaattgtggg cggaaaagaa gaatgagtca 540

ggattggttt ctgtcgagat gaaacaatgg ttcggagatt tgactttaaa cgtgatcttg 600

agaatggtgg ctggtaaaag atacttctcc gcgagtgacg cttcagaaaa caaacaggcc 660

cagcgttgta gaagagtctt cagagaattc ttccatctct ccggcttgtt tgtggttgct 720

gatgctatac cttttcttgg atggctcgat tggggaagac acgagaagac cttgaaaaag 780

accgccatag aaatggattc catcgcccag gagtggcttg aggaacatag acgtagaaaa 840

gattctggag atgataattc tacccaagat ttcatggacg ttatgcaatc tgtgctagat 900

ggcaaaaatc taggcggata cgatgctgat acgattaaca aggctacatg cttaactctt 960

atatcaggtg gcagtgatac tactgtagtt tctttgacat gggctcttag tcttgtgtta 1020

aacaatagag atactttgaa aaaggcacag gaagagttag acatccaagt cggtaaggaa 1080

agattggtta acgagcaaga catcagtaag ttagtttact tgcaagcaat agtaaaagag 1140

acactcagac tttatccacc aggtcctttg ggtggtttga gacaattcac tgaagattgt 1200

acactaggtg gctatcacgt ttcaaaagga actagattaa tcatgaactt atccaagatt 1260

caaaaagatc cacgtatttg gtctgatcct actgaattcc aaccagagag attccttacg 1320

actcataaag atgtcgatcc acgtggtaaa cactttgaat tcattccatt cggtgcagga 1380

agacgtgcat gtcctggtat cacattcgga ttacaagtac tacatctaac attggcatct 1440

ttcttgcatg cgtttgaatt ttcaacacca tcaaatgagc aggttaacat gagagaatca 1500

ttaggtctta cgaatatgaa atctacccca ttagaagttt tgatttctcc aagactatcc 1560

cttaattgct tcaaccttat gaaaatttga 1590

<210> 112
<211> 526
<212> PRT
<213> Vitis vinifera

<400> 112

Met Tyr Phe Leu Leu Gln Tyr Leu Asn Ile Thr Thr Val Gly Val Phe
1 5 10 15

Ala Thr Leu Phe Leu Ser Tyr Cys Leu Leu Leu Trp Arg Ser Arg Ala
20 25 30

Gly Asn Lys Lys Ile Ala Pro Glu Ala Ala Ala Ala Trp Pro Ile Ile
35 40 45

Gly His Leu His Leu Leu Ala Gly Gly Ser His Gln Leu Pro His Ile
50 55 60

Thr Leu Gly Asn Met Ala Asp Lys Tyr Gly Pro Val Phe Thr Ile Arg
65 70 75 80

Ile Gly Leu His Arg Ala Val Val Val Ser Ser Trp Glu Met Ala Lys
85 90 95

Glu Cys Ser Thr Ala Asn Asp Gln Val Ser Ser Ser Arg Pro Glu Leu
100 105 110

Leu Ala Ser Lys Leu Leu Gly Tyr Asn Tyr Ala Met Phe Gly Phe Ser
115 120 125

Pro Tyr Gly Ser Tyr Trp Arg Glu Met Arg Lys Ile Ile Ser Leu Glu
130 135 140

Leu Leu Ser Asn Ser Arg Leu Glu Leu Leu Lys Asp Val Arg Ala Ser
145 150 155 160

```
Glu Val Val Thr Ser Ile Lys Glu Leu Tyr Lys Leu Trp Ala Glu Lys
                165                 170                 175

Lys Asn Glu Ser Gly Leu Val Ser Val Glu Met Lys Gln Trp Phe Gly
            180                 185                 190

Asp Leu Thr Leu Asn Val Ile Leu Arg Met Val Ala Gly Lys Arg Tyr
        195                 200                 205

Phe Ser Ala Ser Asp Ala Ser Glu Asn Lys Gln Ala Gln Arg Cys Arg
    210                 215                 220

Arg Val Phe Arg Glu Phe Phe His Leu Ser Gly Leu Phe Val Val Ala
225                 230                 235                 240

Asp Ala Ile Pro Phe Leu Gly Trp Leu Asp Trp Gly Arg His Glu Lys
                245                 250                 255

Thr Leu Lys Lys Thr Ala Ile Glu Met Asp Ser Ile Ala Gln Glu Trp
            260                 265                 270

Leu Glu Glu His Arg Arg Arg Lys Asp Ser Gly Asp Asp Asn Ser Thr
        275                 280                 285

Gln Asp Phe Met Asp Val Met Gln Ser Val Leu Asp Gly Lys Asn Leu
    290                 295                 300

Gly Gly Tyr Asp Ala Asp Thr Ile Asn Lys Ala Thr Cys Leu Thr Leu
305                 310                 315                 320

Ile Ser Gly Gly Ser Asp Thr Thr Val Val Ser Leu Thr Trp Ala Leu
                325                 330                 335

Ser Leu Val Leu Asn Asn Arg Asp Thr Leu Lys Lys Ala Gln Glu Glu
            340                 345                 350

Leu Asp Ile Gln Val Gly Lys Glu Arg Leu Val Asn Glu Gln Asp Ile
```

```
        355                 360                 365

Ser Lys Leu Val Tyr Leu Gln Ala Ile Val Lys Glu Thr Leu Arg Leu
    370                 375                 380

Tyr Pro Pro Gly Pro Leu Gly Gly Leu Arg Gln Phe Thr Glu Asp Cys
385                 390                 395                 400

Thr Leu Gly Gly Tyr His Val Ser Lys Gly Thr Arg Leu Ile Met Asn
                405                 410                 415

Leu Ser Lys Ile Gln Lys Asp Pro Arg Ile Trp Ser Asp Pro Thr Glu
            420                 425                 430

Phe Gln Pro Glu Arg Phe Leu Thr Thr His Lys Asp Val Asp Pro Arg
        435                 440                 445

Gly Lys His Phe Glu Phe Ile Pro Phe Gly Ala Gly Arg Arg Ala Cys
    450                 455                 460

Pro Gly Ile Thr Phe Gly Leu Gln Val Leu His Leu Thr Leu Ala Ser
465                 470                 475                 480

Phe Leu His Ala Phe Glu Phe Ser Thr Pro Ser Asn Glu Gln Val Asn
                485                 490                 495

Met Arg Glu Ser Leu Gly Leu Thr Asn Met Lys Ser Thr Pro Leu Glu
            500                 505                 510

Val Leu Ile Ser Pro Arg Leu Ser Ser Cys Ser Leu Tyr Asn
        515                 520                 525
```

<210> 113
<211> 1440
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized KAH

<400> 113
atggaaccta acttttactt gtcattacta ttgttgttcg tgaccttcat ttctttaagt 60

ctgtttttca tcttttacaa acaaaagtcc ccattgaatt tgccaccagg gaaaatgggt 120

taccctatca taggtgaaag tttagaattc ctatccacag gctggaaggg acatcctgaa 180

aagttcatat ttgatagaat gcgtaagtac agtagtgagt tattcaagac ttctattgta 240

ggcgaatcca cagttgtttg ctgtggggca gctagtaaca aattcctatt ctctaacgaa 300

aacaaactgg taactgcctg gtggccagat tctgttaaca aaatcttccc aacaacttca 360

ctggattcta atttgaagga ggaatctata aagatgagaa agttgctgcc acagttcttc 420

aaaccagaag cacttcaaag atacgtcggc gttatggatg taatcgcaca aagacatttt 480

gtcactcact gggacaacaa aaatgagatc acagtttatc cacttgctaa aagatacact 540

ttcttgcttg cgtgtagact gttcatgtct gttgaggatg aaaatcatgt ggcgaaattc 600

tcagacccat tccaactaat cgctgcaggc atcatttcac ttcctatcga tcttcctggt 660

actccattca acaaggccat aaaggcttca aatttcatta gaaaagagct gataaagatt 720

atcaaacaaa gacgtgttga tctggcagag ggtacagcat ctccaaccca ggatatcttg 780

tcacatatgc tattaacatc tgatgaaaac ggtaaatcta tgaacgagtt gaacattgcc 840

gacaagattc ttggactatt gataggaggc cacgatacag cttcagtagc ttgcacattt 900

ctagtgaagt acttaggaga attaccacat atctacgata aagtctacca agagcaaatg 960

gaaattgcca agtccaaacc tgctggggaa ttgttgaatt gggatgactt gaaaaagatg 1020

aagtattcat ggaatgtggc atgtgaggta atgagattgt caccaccttt acaaggtggt 1080

tttagagagg ctataactga ctttatgttt aacggtttct ctattccaaa agggtggaag 1140

ttatactggt ccgccaactc tacacacaaa aatgcagaat gtttcccaat gcctgagaaa 1200

ttcgatccta ccagatttga aggtaatggt ccagcgcctt atacatttgt accattcggt 1260

ggaggcccta gaatgtgtcc tggaaaggaa tacgctagat tagaaatctt ggttttcatg 1320

cataatctgg tcaaacgttt taagtgggaa aaggttattc cagacgaaaa gattattgtc 1380

gatccattcc caatcccagc taaagatctt ccaatccgtt tgtatcctca caaagcttaa 1440

<210> 114
<211> 479
<212> PRT
<213> Medicago truncatula

<400> 114

```
Met Glu Pro Asn Phe Tyr Leu Ser Leu Leu Leu Leu Phe Val Thr Phe
1               5                   10                  15


Ile Ser Leu Ser Leu Phe Phe Ile Phe Tyr Lys Gln Lys Ser Pro Leu
            20                  25                  30


Asn Leu Pro Pro Gly Lys Met Gly Tyr Pro Ile Ile Gly Glu Ser Leu
        35                  40                  45


Glu Phe Leu Ser Thr Gly Trp Lys Gly His Pro Glu Lys Phe Ile Phe
    50                  55                  60


Asp Arg Met Arg Lys Tyr Ser Ser Glu Leu Phe Lys Thr Ser Ile Val
65                  70                  75                  80


Gly Glu Ser Thr Val Val Cys Cys Gly Ala Ala Ser Asn Lys Phe Leu
                85                  90                  95


Phe Ser Asn Glu Asn Lys Leu Val Thr Ala Trp Trp Pro Asp Ser Val
            100                 105                 110


Asn Lys Ile Phe Pro Thr Thr Ser Leu Asp Ser Asn Leu Lys Glu Glu
        115                 120                 125


Ser Ile Lys Met Arg Lys Leu Leu Pro Gln Phe Phe Lys Pro Glu Ala
    130                 135                 140


Leu Gln Arg Tyr Val Gly Val Met Asp Val Ile Ala Gln Arg His Phe
145                 150                 155                 160


Val Thr His Trp Asp Asn Lys Asn Glu Ile Thr Val Tyr Pro Leu Ala
                165                 170                 175
```

```
Lys Arg Tyr Thr Phe Leu Leu Ala Cys Arg Leu Phe Met Ser Val Glu
            180                 185                 190

Asp Glu Asn His Val Ala Lys Phe Ser Asp Pro Phe Gln Leu Ile Ala
        195                 200                 205

Ala Gly Ile Ile Ser Leu Pro Ile Asp Leu Pro Gly Thr Pro Phe Asn
    210                 215                 220

Lys Ala Ile Lys Ala Ser Asn Phe Ile Arg Lys Glu Leu Ile Lys Ile
225                 230                 235                 240

Ile Lys Gln Arg Arg Val Asp Leu Ala Glu Gly Thr Ala Ser Pro Thr
                245                 250                 255

Gln Asp Ile Leu Ser His Met Leu Leu Thr Ser Asp Glu Asn Gly Lys
            260                 265                 270

Ser Met Asn Glu Leu Asn Ile Ala Asp Lys Ile Leu Gly Leu Leu Ile
        275                 280                 285

Gly Gly His Asp Thr Ala Ser Val Ala Cys Thr Phe Leu Val Lys Tyr
    290                 295                 300

Leu Gly Glu Leu Pro His Ile Tyr Asp Lys Val Tyr Gln Glu Gln Met
305                 310                 315                 320

Glu Ile Ala Lys Ser Lys Pro Ala Gly Glu Leu Leu Asn Trp Asp Asp
                325                 330                 335

Leu Lys Lys Met Lys Tyr Ser Trp Asn Val Ala Cys Glu Val Met Arg
            340                 345                 350

Leu Ser Pro Pro Leu Gln Gly Gly Phe Arg Glu Ala Ile Thr Asp Phe
        355                 360                 365
```

```
Met Phe Asn Gly Phe Ser Ile Pro Lys Gly Trp Lys Leu Tyr Trp Ser
    370                 375                 380

Ala Asn Ser Thr His Lys Asn Ala Glu Cys Phe Pro Met Pro Glu Lys
385                 390                 395                 400

Phe Asp Pro Thr Arg Phe Glu Gly Asn Gly Pro Ala Pro Tyr Thr Phe
                405                 410                 415

Val Pro Phe Gly Gly Gly Pro Arg Met Cys Pro Gly Lys Glu Tyr Ala
            420                 425                 430

Arg Leu Glu Ile Leu Val Phe Met His Asn Leu Val Lys Arg Phe Lys
        435                 440                 445

Trp Glu Lys Val Ile Pro Asp Glu Lys Ile Ile Val Asp Pro Phe Pro
    450                 455                 460

Ile Pro Ala Lys Asp Leu Pro Ile Arg Leu Tyr Pro His Lys Ala
465                 470                 475
```

<210> 115
<211> 1116
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized GGPPS

<400> 115

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atggcctctg ttactttggg ttcctggatc gtcgtccacc accataacca tcaccatcca       60

tcatctatcc taactaaatc tcgttcaaga tcctgtccta ttacactaac caaaccaatc      120

tcttttcgtt caaagagaac agtttcctct agtagttcta tcgtgtcctc tagtgtcgtc      180

actaaggaag acaatctgag acagtctgaa ccttcttcct ttgatttcat gtcatatatc      240

attactaagg cagaactagt gaataaggct cttgattcag cagttccatt aagagagcca      300

ttgaaaatcc atgaagcaat gagatactct cttctagctg gcgggaagag agtcagacct      360

gtactctgca tagcagcgtg cgaattagtt ggtggcgagg aatcaaccgc tatgcctgcc      420
```

gcttgtgctg tagaaatgat tcatacaatg tcactgatac acgatgattt gccatgtatg 480

gataacgatg atctgagaag gggtaagcca actaaccata aggttttcgg cgaagatgtt 540

gccgtcttag ctggtgatgc tttgttatct ttcgcgttcg aacatttggc atccgcaaca 600

tcaagtgatg ttgtgtcacc agtaagagta gttagagcag ttggagaact ggctaaagct 660

attggaactg agggtttagt tgcaggtcaa gtcgtcgata tctcttccga aggtcttgat 720

ttgaatgatg taggtcttga acatctcgaa ttcatccatc ttcacaagac agctgcactt 780

ttagaagcca gtgcggttct cggcgcaatt gttggcggag ggagtgatga cgaaattgag 840

agattgagga agtttgctag atgtatagga ttactgttcc aagtagtaga cgatatacta 900

gatgtgacaa agtcttccaa agagttggga aaaacagctg gtaaagattt gattgccgac 960

aaattgacct accctaagat tatggggcta gaaaaatcaa gagaatttgc cgagaaactc 1020

aatagagagg cgcgtgatca actgttgggt ttcgattctg ataaagttgc accactctta 1080

gccttagcca actacatcgc ttacagacaa aactaa 1116

<210> 116
<211> 371
<212> PRT
<213> Arabidopsis thaliana

<400> 116

Met Ala Ser Val Thr Leu Gly Ser Trp Ile Val Val His His His Asn
1 5 10 15

His His His Pro Ser Ser Ile Leu Thr Lys Ser Arg Ser Arg Ser Cys
20 25 30

Pro Ile Thr Leu Thr Lys Pro Ile Ser Phe Arg Ser Lys Arg Thr Val
35 40 45

Ser Ser Ser Ser Ser Ile Val Ser Ser Ser Val Val Thr Lys Glu Asp
50 55 60

Asn Leu Arg Gln Ser Glu Pro Ser Ser Phe Asp Phe Met Ser Tyr Ile

```
65                  70                  75                  80

Ile Thr Lys Ala Glu Leu Val Asn Lys Ala Leu Asp Ser Ala Val Pro
                85                  90                  95

Leu Arg Glu Pro Leu Lys Ile His Glu Ala Met Arg Tyr Ser Leu Leu
            100                 105                 110

Ala Gly Gly Lys Arg Val Arg Pro Val Leu Cys Ile Ala Ala Cys Glu
        115                 120                 125

Leu Val Gly Gly Glu Glu Ser Thr Ala Met Pro Ala Ala Cys Ala Val
    130                 135                 140

Glu Met Ile His Thr Met Ser Leu Ile His Asp Asp Leu Pro Cys Met
145                 150                 155                 160

Asp Asn Asp Asp Leu Arg Arg Gly Lys Pro Thr Asn His Lys Val Phe
                165                 170                 175

Gly Glu Asp Val Ala Val Leu Ala Gly Asp Ala Leu Leu Ser Phe Ala
            180                 185                 190

Phe Glu His Leu Ala Ser Ala Thr Ser Ser Asp Val Val Ser Pro Val
        195                 200                 205

Arg Val Val Arg Ala Val Gly Glu Leu Ala Lys Ala Ile Gly Thr Glu
    210                 215                 220

Gly Leu Val Ala Gly Gln Val Val Asp Ile Ser Ser Glu Gly Leu Asp
225                 230                 235                 240

Leu Asn Asp Val Gly Leu Glu His Leu Glu Phe Ile His Leu His Lys
                245                 250                 255

Thr Ala Ala Leu Leu Glu Ala Ser Ala Val Leu Gly Ala Ile Val Gly
            260                 265                 270
```

```
Gly Gly Ser Asp Asp Glu Ile Glu Arg Leu Arg Lys Phe Ala Arg Cys
        275                 280                 285


Ile Gly Leu Leu Phe Gln Val Val Asp Asp Ile Leu Asp Val Thr Lys
    290                 295                 300


Ser Ser Lys Glu Leu Gly Lys Thr Ala Gly Lys Asp Leu Ile Ala Asp
305                 310                 315                 320


Lys Leu Thr Tyr Pro Lys Ile Met Gly Leu Glu Lys Ser Arg Glu Phe
                325                 330                 335


Ala Glu Lys Leu Asn Arg Glu Ala Arg Asp Gln Leu Leu Gly Phe Asp
            340                 345                 350


Ser Asp Lys Val Ala Pro Leu Leu Ala Leu Ala Asn Tyr Ile Ala Tyr
        355                 360                 365


Arg Gln Asn
    370
```

<210> 117
<211> 511
<212> PRT
<213> Rubus suavissimus

<400> 117

```
Met Ala Thr Leu Leu Glu His Phe Gln Ala Met Pro Phe Ala Ile Pro
1               5                   10                  15


Ile Ala Leu Ala Ala Leu Ser Trp Leu Phe Leu Phe Tyr Ile Lys Val
            20                  25                  30


Ser Phe Phe Ser Asn Lys Ser Ala Gln Ala Lys Leu Pro Pro Val Pro
        35                  40                  45


Val Val Pro Gly Leu Pro Val Ile Gly Asn Leu Leu Gln Leu Lys Glu
    50                  55                  60
```

```
Lys Lys Pro Tyr Gln Thr Phe Thr Arg Trp Ala Glu Glu Tyr Gly Pro
65                  70                  75                  80

Ile Tyr Ser Ile Arg Thr Gly Ala Ser Thr Met Val Val Leu Asn Thr
                85                  90                  95

Thr Gln Val Ala Lys Glu Ala Met Val Thr Arg Tyr Leu Ser Ile Ser
            100                 105                 110

Thr Arg Lys Leu Ser Asn Ala Leu Lys Ile Leu Thr Ala Asp Lys Cys
        115                 120                 125

Met Val Ala Ile Ser Asp Tyr Asn Asp Phe His Lys Met Ile Lys Arg
    130                 135                 140

Tyr Ile Leu Ser Asn Val Leu Gly Pro Ser Ala Gln Lys Arg His Arg
145                 150                 155                 160

Ser Asn Arg Asp Thr Leu Arg Ala Asn Val Cys Ser Arg Leu His Ser
                165                 170                 175

Gln Val Lys Asn Ser Pro Arg Glu Ala Val Asn Phe Arg Arg Val Phe
            180                 185                 190

Glu Trp Glu Leu Phe Gly Ile Ala Leu Lys Gln Ala Phe Gly Lys Asp
        195                 200                 205

Ile Glu Lys Pro Ile Tyr Val Glu Glu Leu Gly Thr Thr Leu Ser Arg
    210                 215                 220

Asp Glu Ile Phe Lys Val Leu Val Leu Asp Ile Met Glu Gly Ala Ile
225                 230                 235                 240

Glu Val Asp Trp Arg Asp Phe Phe Pro Tyr Leu Arg Trp Ile Pro Asn
                245                 250                 255
```

```
Thr Arg Met Glu Thr Lys Ile Gln Arg Leu Tyr Phe Arg Arg Lys Ala
            260                 265                 270

Val Met Thr Ala Leu Ile Asn Glu Gln Lys Lys Arg Ile Ala Ser Gly
        275                 280                 285

Glu Glu Ile Asn Cys Tyr Ile Asp Phe Leu Leu Lys Glu Gly Lys Thr
    290                 295                 300

Leu Thr Met Asp Gln Ile Ser Met Leu Leu Trp Glu Thr Val Ile Glu
305                 310                 315                 320

Thr Ala Asp Thr Thr Met Val Thr Thr Glu Trp Ala Met Tyr Glu Val
                325                 330                 335

Ala Lys Asp Ser Lys Arg Gln Asp Arg Leu Tyr Gln Glu Ile Gln Lys
            340                 345                 350

Val Cys Gly Ser Glu Met Val Thr Glu Glu Tyr Leu Ser Gln Leu Pro
        355                 360                 365

Tyr Leu Asn Ala Val Phe His Glu Thr Leu Arg Lys His Ser Pro Ala
    370                 375                 380

Ala Leu Val Pro Leu Arg Tyr Ala His Glu Asp Thr Gln Leu Gly Gly
385                 390                 395                 400

Tyr Tyr Ile Pro Ala Gly Thr Glu Ile Ala Ile Asn Ile Tyr Gly Cys
                405                 410                 415

Asn Met Asp Lys His Gln Trp Glu Ser Pro Glu Glu Trp Lys Pro Glu
            420                 425                 430

Arg Phe Leu Asp Pro Lys Phe Asp Pro Met Asp Leu Tyr Lys Thr Met
        435                 440                 445

Ala Phe Gly Ala Gly Lys Arg Val Cys Ala Gly Ser Leu Gln Ala Met
    450                 455                 460
```

```
Leu Ile Ala Cys Pro Thr Ile Gly Arg Leu Val Gln Glu Phe Glu Trp
465                 470                 475                 480


Lys Leu Arg Asp Gly Glu Glu Glu Asn Val Asp Thr Val Gly Leu Thr
                485                 490                 495


Thr His Lys Arg Tyr Pro Met His Ala Ile Leu Lys Pro Arg Ser
            500                 505                 510


<210>  118
<211>  473
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  UGT91D2e L211M

<400>  118

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15


Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30


Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45


Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60


Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80


Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95


Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110
```

```
His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Met Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300
```

```
Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460

Arg Ala Val Ala Ile Asp His Glu Ser
465                 470
```

<210> 119
<211> 473
<212> PRT
<213> Artificial Sequence

<220>

<223> UGT91D2e L195G

<400> 119

```
Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15


Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30


Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45


Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60


Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80


Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95


Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110


His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125


Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140


Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160


Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175


Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190
```

```
Ala Arg Gly Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380
```

```
Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400


Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415


Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430


Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445


Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460


Arg Ala Val Ala Ile Asp His Glu Ser
465                 470


<210>  120
<211>  473
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  UGT91D2e V196P

<400>  120

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15


Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30


Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45


Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60
```

```
Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110

His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Pro Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270
```

```
Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460
```

Arg Ala Val Ala Ile Asp His Glu Ser
465 470

<210> 121
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e L211H

<400> 121

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1 5 10 15

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
20 25 30

Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
35 40 45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
50 55 60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65 70 75 80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
85 90 95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
100 105 110

His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
115 120 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
130 135 140

```
Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160


Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175


Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190


Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205


Met Gly His Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220


His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240


Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255


Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270


Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285


Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300


Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320


Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335


Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350
```

```
Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365


Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380


Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400


Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415


Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430


Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445


Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460


Arg Ala Val Ala Ile Asp His Glu Ser
465                 470


<210>  122
<211>  469
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  UGT91D2e-b-EUGT11 chimera 2

<400>  122

Met Asp Ser Gly Tyr Ser Ser Ser Tyr Ala Ala Ala Ala Gly Met His
1               5                   10                  15


Val Val Ile Cys Pro Trp Leu Ala Phe Gly His Leu Leu Pro Cys Leu
            20                  25                  30
```

```
Asp Leu Ala Gln Arg Leu Ala Ser Arg Gly His Arg Val Ser Phe Val
        35                  40                  45

Ser Thr Pro Arg Asn Ile Ser Arg Leu Pro Pro Val Arg Pro Ala Leu
    50                  55                  60

Ala Pro Leu Val Ala Phe Val Ala Leu Pro Leu Pro Arg Val Glu Gly
65                  70                  75                  80

Leu Pro Asp Gly Ala Glu Ser Thr Asn Asp Val Pro His Asp Arg Pro
                85                  90                  95

Asp Met Val Glu Leu His Arg Arg Ala Phe Asp Gly Leu Ala Ala Pro
            100                 105                 110

Phe Ser Glu Phe Leu Gly Thr Ala Cys Ala Asp Trp Val Ile Val Asp
        115                 120                 125

Val Phe His His Trp Ala Ala Ala Ala Ala Leu Glu His Lys Val Pro
    130                 135                 140

Cys Ala Met Met Leu Leu Gly Ser Ala His Met Ile Ala Ser Ile Ala
145                 150                 155                 160

Asp Arg Arg Leu Glu Arg Ala Glu Thr Glu Ser Pro Ala Ala Ala Gly
                165                 170                 175

Gln Gly Arg Pro Ala Ala Ala Pro Thr Phe Glu Val Ala Arg Met Lys
            180                 185                 190

Leu Ile Arg Thr Lys Gly Ser Ser Gly Met Ser Leu Ala Glu Arg Phe
        195                 200                 205

Ser Leu Thr Leu Ser Arg Ser Ser Leu Val Val Gly Arg Ser Cys Val
    210                 215                 220
```

```
Glu Phe Glu Pro Glu Thr Val Pro Leu Leu Ser Thr Leu Arg Gly Lys
225                 230                 235                 240

Pro Ile Thr Phe Leu Gly Leu Met Pro Pro Leu His Glu Gly Arg Arg
                245                 250                 255

Glu Asp Gly Glu Asp Ala Thr Val Arg Trp Leu Asp Ala Gln Pro Ala
            260                 265                 270

Lys Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Pro Leu Gly Val
        275                 280                 285

Glu Lys Val His Glu Leu Ala Leu Gly Leu Glu Leu Ala Gly Thr Arg
    290                 295                 300

Phe Leu Trp Ala Leu Arg Lys Pro Thr Gly Val Ser Asp Ala Asp Leu
305                 310                 315                 320

Leu Pro Ala Gly Phe Glu Glu Arg Thr Arg Gly Arg Gly Val Val Ala
                325                 330                 335

Thr Arg Trp Val Pro Gln Met Ser Ile Leu Ala His Ala Ala Val Gly
            340                 345                 350

Ala Phe Leu Thr His Cys Gly Trp Asn Ser Thr Ile Glu Gly Leu Met
        355                 360                 365

Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly Asp Gln Gly Pro
    370                 375                 380

Asn Ala Arg Leu Ile Glu Ala Lys Asn Ala Gly Leu Gln Val Pro Arg
385                 390                 395                 400

Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val Ala Arg Ser Leu
                405                 410                 415

Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr Lys Ala Asn Ala
            420                 425                 430
```

Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val Glu Lys Glu Tyr
        435   440   445

Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala Arg Ala Val Ala
    450   455   460

Ile Asp His Glu Ser
465

<210> 123
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e L195C

<400> 123

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1   5   10   15

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20   25   30

Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35   40   45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50   55   60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65   70   75   80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85   90   95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100   105   110

```
His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Cys Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300
```

```
Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460

Arg Ala Val Ala Ile Asp His Glu Ser
465                 470
```

<210> 124
<211> 470
<212> PRT
<213> Artificial Sequence

<220>

<223> UGT91D2e-b-EUGT11 chimera 4

<400> 124

```
Met Asp Ser Gly Tyr Ser Ser Ser Tyr Ala Ala Ala Ala Gly Met His
1               5                  10                  15


Val Val Ile Cys Pro Trp Leu Ala Phe Gly His Leu Leu Pro Cys Leu
            20                  25                  30


Asp Leu Ala Gln Arg Leu Ala Ser Arg Gly His Arg Val Ser Phe Val
        35                  40                  45


Ser Thr Pro Arg Asn Ile Ser Arg Leu Pro Pro Val Arg Pro Ala Leu
    50                  55                  60


Ala Pro Leu Val Ala Phe Val Ala Leu Pro Leu Pro Arg Val Glu Gly
65                  70                  75                  80


Leu Pro Asp Gly Ala Glu Ser Thr Asn Asp Val Pro His Asp Arg Pro
                85                  90                  95


Asp Met Val Glu Leu His Arg Arg Ala Phe Asp Gly Leu Ala Ala Pro
            100                 105                 110


Phe Ser Glu Phe Leu Gly Thr Ala Cys Ala Asp Trp Val Ile Val Asp
        115                 120                 125


Val Phe His His Trp Leu Pro Ser Ile Ala Ala Ser Leu Gly Ile Ser
    130                 135                 140


Arg Ala His Phe Ser Val Thr Thr Pro Trp Ala Ile Ala Tyr Met Gly
145                 150                 155                 160


Pro Ser Ala Asp Ala Met Ile Asn Gly Ser Asp Gly Arg Thr Thr Val
                165                 170                 175


Glu Asp Leu Thr Thr Pro Pro Lys Trp Phe Pro Phe Pro Thr Lys Val
            180                 185                 190
```

```
Cys Trp Arg Lys His Asp Leu Ala Arg Leu Val Pro Tyr Lys Ala Pro
        195                 200                 205

Gly Ile Ser Asp Gly Tyr Arg Met Gly Met Val Leu Lys Gly Ser Asp
    210                 215                 220

Cys Leu Leu Ser Lys Cys Tyr His Glu Phe Gly Thr Gln Trp Leu Pro
225                 230                 235                 240

Leu Leu Glu Thr Leu His Gln Val Pro Val Val Pro Val Gly Leu Met
                245                 250                 255

Pro Pro Leu His Glu Gly Arg Arg Glu Asp Gly Glu Asp Ala Thr Val
            260                 265                 270

Arg Trp Leu Asp Ala Gln Pro Ala Lys Ser Val Val Tyr Val Ala Leu
        275                 280                 285

Gly Ser Glu Val Pro Leu Gly Val Glu Lys Val His Glu Leu Ala Leu
    290                 295                 300

Gly Leu Glu Leu Ala Gly Thr Arg Phe Leu Trp Ala Leu Arg Lys Pro
305                 310                 315                 320

Thr Gly Val Ser Asp Ala Asp Leu Leu Pro Ala Gly Phe Glu Glu Arg
                325                 330                 335

Thr Arg Gly Arg Gly Val Val Ala Thr Arg Trp Val Pro Gln Met Ser
            340                 345                 350

Ile Leu Ala His Ala Ala Val Gly Ala Phe Leu Thr His Cys Gly Trp
        355                 360                 365

Asn Ser Thr Ile Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu
    370                 375                 380
```

```
Pro Ile Phe Gly Asp Gln Gly Pro Asn Ala Arg Leu Ile Glu Ala Lys
385                 390                 395                 400


Asn Ala Gly Leu Gln Val Ala Arg Asn Asp Gly Asp Gly Ser Phe Asp
                405                 410                 415


Arg Glu Gly Val Ala Ala Ala Ile Arg Ala Val Ala Val Glu Glu Glu
            420                 425                 430


Ser Ser Lys Val Phe Gln Ala Lys Ala Lys Lys Leu Gln Glu Ile Val
        435                 440                 445


Ala Asp Met Ala Cys His Glu Arg Tyr Ile Asp Gly Phe Ile Gln Gln
    450                 455                 460


Leu Arg Ser Tyr Lys Asp
465                 470


<210>  125
<211>  455
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  UGT91D2e-b-EUGT11 chimera 5

<400>  125

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15


Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30


Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45


Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60
```

```
Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110

His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Ala Ala
        115                 120                 125

Ala Ala Ala Leu Glu His Lys Val Pro Cys Ala Met Met Leu Leu Gly
    130                 135                 140

Ser Ala His Met Ile Ala Ser Ile Ala Asp Arg Arg Leu Glu Arg Ala
145                 150                 155                 160

Glu Thr Glu Ser Pro Ala Ala Ala Gly Gln Gly Arg Pro Ala Ala Ala
                165                 170                 175

Pro Thr Phe Glu Val Ala Arg Met Lys Leu Ile Arg Thr Lys Gly Ser
            180                 185                 190

Ser Gly Met Ser Leu Ala Glu Arg Phe Ser Leu Thr Leu Ser Arg Ser
        195                 200                 205

Ser Leu Val Val Gly Arg Ser Cys Val Glu Phe Glu Pro Glu Thr Val
    210                 215                 220

Pro Leu Leu Ser Thr Leu Arg Gly Lys Pro Ile Thr Phe Leu Gly Leu
225                 230                 235                 240

Met Pro Pro Leu His Glu Gly Arg Arg Glu Asp Gly Glu Asp Ala Thr
                245                 250                 255

Val Arg Trp Leu Asp Ala Gln Pro Ala Lys Ser Val Val Tyr Val Ala
            260                 265                 270
```

```
Leu Gly Ser Glu Val Pro Leu Gly Val Glu Lys Val His Glu Leu Ala
        275                 280                 285

Leu Gly Leu Glu Leu Ala Gly Thr Arg Phe Leu Trp Ala Leu Arg Lys
    290                 295                 300

Pro Thr Gly Val Ser Asp Ala Asp Leu Leu Pro Ala Gly Phe Glu Glu
305                 310                 315                 320

Arg Thr Arg Gly Arg Gly Val Val Ala Thr Arg Trp Val Pro Gln Met
                325                 330                 335

Ser Ile Leu Ala His Ala Ala Val Gly Ala Phe Leu Thr His Cys Gly
            340                 345                 350

Trp Asn Ser Thr Ile Glu Gly Leu Met Phe Gly His Pro Leu Ile Met
        355                 360                 365

Leu Pro Ile Phe Gly Asp Gln Gly Pro Asn Ala Arg Leu Ile Glu Ala
    370                 375                 380

Lys Asn Ala Gly Leu Gln Val Ala Arg Asn Asp Gly Asp Gly Ser Phe
385                 390                 395                 400

Asp Arg Glu Gly Val Ala Ala Ala Ile Arg Ala Val Ala Val Glu Glu
                405                 410                 415

Glu Ser Ser Lys Val Phe Gln Ala Lys Ala Lys Lys Leu Gln Glu Ile
            420                 425                 430

Val Ala Asp Met Ala Cys His Glu Arg Tyr Ile Asp Gly Phe Ile Gln
        435                 440                 445

Gln Leu Arg Ser Tyr Lys Asp
    450                 455
```

<210> 126
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e-b-EUGT11 chimera 6

<400> 126

```
Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15


Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30


Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45


Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60


Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80


Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95


Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110


His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125


Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140


Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160
```

```
Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Met Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Ala Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365
```

```
Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Ala Arg Asn Asp Gly Asp Gly Ser Phe Asp Arg Glu Gly Val
                405                 410                 415

Ala Ala Ala Ile Arg Ala Val Ala Val Glu Glu Glu Ser Ser Lys Val
            420                 425                 430

Phe Gln Ala Lys Ala Lys Lys Leu Gln Glu Ile Val Ala Asp Met Ala
        435                 440                 445

Cys His Glu Arg Tyr Ile Asp Gly Phe Ile Gln Gln Leu Arg Ser Tyr
    450                 455                 460

Lys Asp
465
```

<210> 127
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 T304S

<400> 127

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                   10                  15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35                  40                  45
```

```
Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80

Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240
```

```
Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Ser
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445
```

```
Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460


Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480


Asn
```

<210> 128
<211> 465
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e-b-EUGT11 chimera 8

<400> 128

```
Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15


Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30


Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45


Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60


Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80


Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95


Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110
```

```
His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Ala Ala
        115                 120                 125

Ala Ala Ala Leu Glu His Lys Val Pro Cys Ala Met Met Leu Leu Gly
    130                 135                 140

Ser Ala His Met Ile Ala Ser Ile Ala Asp Arg Arg Leu Glu Arg Ala
145                 150                 155                 160

Glu Thr Glu Ser Pro Ala Ala Ala Gly Gln Gly Arg Pro Ala Ala Ala
                165                 170                 175

Pro Thr Phe Glu Val Ala Arg Met Lys Leu Ile Arg Thr Lys Gly Ser
            180                 185                 190

Ser Gly Met Ser Leu Ala Glu Arg Phe Ser Leu Thr Leu Ser Arg Ser
        195                 200                 205

Ser Leu Val Val Gly Arg Ser Cys Val Glu Phe Glu Pro Glu Thr Val
    210                 215                 220

Pro Leu Leu Ser Thr Leu Arg Gly Lys Pro Ile Thr Phe Leu Gly Leu
225                 230                 235                 240

Leu Pro Pro Glu Ile Pro Gly Asp Glu Lys Asp Glu Thr Trp Val Ser
                245                 250                 255

Ile Lys Lys Trp Leu Asp Gly Lys Gln Lys Gly Ser Val Val Tyr Val
            260                 265                 270

Ala Leu Gly Ser Glu Ala Leu Val Ser Gln Thr Glu Val Val Glu Leu
        275                 280                 285

Ala Leu Gly Leu Glu Leu Ser Gly Leu Pro Phe Val Trp Ala Tyr Arg
    290                 295                 300
```

```
Lys Pro Lys Gly Pro Ala Lys Ser Asp Ser Val Glu Leu Pro Asp Gly
305                 310                 315                 320

Phe Val Glu Arg Thr Arg Asp Arg Gly Leu Val Trp Thr Ser Trp Ala
                325                 330                 335

Pro Gln Leu Arg Ile Leu Ser His Glu Ser Val Cys Gly Phe Leu Thr
            340                 345                 350

His Cys Gly Ser Gly Ser Ile Val Glu Gly Leu Met Phe Gly His Pro
        355                 360                 365

Leu Ile Met Leu Pro Ile Phe Gly Asp Gln Pro Leu Asn Ala Arg Leu
    370                 375                 380

Leu Glu Asp Lys Gln Val Gly Ile Glu Ile Pro Arg Asn Glu Glu Asp
385                 390                 395                 400

Gly Cys Leu Thr Lys Glu Ser Val Ala Arg Ser Leu Arg Ser Val Val
                405                 410                 415

Val Glu Lys Glu Gly Glu Ile Tyr Lys Ala Asn Ala Arg Glu Leu Ser
            420                 425                 430

Lys Ile Tyr Asn Asp Thr Lys Val Glu Lys Glu Tyr Val Ser Gln Phe
        435                 440                 445

Val Asp Tyr Leu Glu Lys Asn Ala Arg Ala Val Ala Ile Asp His Glu
    450                 455                 460

Ser
465
```

<210> 129
<211> 480
<212> PRT
<213> Artificial Sequence

<220>

<223> UGT91D2e-b-EUGT11 chimera 9

<400> 129

```
Met Asp Ser Gly Tyr Ser Ser Ser Tyr Ala Ala Ala Ala Gly Met His
1               5                  10                  15


Val Val Ile Cys Pro Trp Leu Ala Phe Gly His Leu Leu Pro Cys Leu
            20                  25                  30


Asp Leu Ala Gln Arg Leu Ala Ser Arg Gly His Arg Val Ser Phe Val
        35                  40                  45


Ser Thr Pro Arg Asn Ile Ser Arg Leu Pro Pro Val Arg Pro Ala Leu
    50                  55                  60


Ala Pro Leu Val Ala Phe Val Ala Leu Pro Leu Pro Arg Val Glu Gly
65                  70                  75                  80


Leu Pro Asp Gly Ala Glu Ser Thr Asn Asp Val Pro His Asp Arg Pro
                85                  90                  95


Asp Met Val Glu Leu His Arg Arg Ala Phe Asp Gly Leu Ala Ala Pro
            100                 105                 110


Phe Ser Glu Phe Leu Gly Thr Ala Cys Ala Asp Trp Val Ile Val Asp
        115                 120                 125


Val Phe His His Trp Leu Pro Ser Ile Ala Ala Ser Leu Gly Ile Ser
    130                 135                 140


Arg Ala His Phe Ser Val Thr Thr Pro Trp Ala Ile Ala Tyr Met Gly
145                 150                 155                 160


Pro Ser Ala Asp Ala Met Ile Asn Gly Ser Asp Gly Arg Thr Thr Val
                165                 170                 175


Glu Asp Leu Thr Thr Pro Pro Lys Trp Phe Pro Phe Pro Thr Lys Val
            180                 185                 190
```

```
Cys Trp Arg Lys His Asp Leu Ala Arg Leu Val Pro Tyr Lys Ala Pro
        195                 200                 205

Gly Ile Ser Asp Gly Tyr Arg Met Gly Met Val Leu Lys Gly Ser Asp
    210                 215                 220

Cys Leu Leu Ser Lys Cys Tyr His Glu Phe Gly Thr Gln Trp Leu Pro
225                 230                 235                 240

Leu Leu Glu Thr Leu His Gln Val Pro Val Val Pro Val Gly Leu Leu
                245                 250                 255

Pro Pro Glu Ile Pro Gly Asp Glu Lys Asp Glu Thr Trp Val Ser Ile
            260                 265                 270

Lys Lys Trp Leu Asp Gly Lys Gln Lys Gly Ser Val Val Tyr Val Ala
        275                 280                 285

Leu Gly Ser Glu Ala Leu Val Ser Gln Thr Glu Val Val Glu Leu Ala
    290                 295                 300

Leu Gly Leu Glu Leu Ser Gly Leu Pro Phe Val Trp Ala Tyr Arg Lys
305                 310                 315                 320

Pro Lys Gly Pro Ala Lys Ser Asp Ser Val Glu Leu Pro Asp Gly Phe
                325                 330                 335

Val Glu Arg Thr Arg Asp Arg Gly Leu Val Trp Thr Ser Trp Ala Pro
            340                 345                 350

Gln Leu Arg Ile Leu Ser His Glu Ser Val Cys Gly Phe Leu Thr His
        355                 360                 365

Cys Gly Ser Gly Ser Ile Val Glu Gly Leu Met Phe Gly His Pro Leu
    370                 375                 380
```

```
Ile Met Leu Pro Ile Phe Gly Asp Gln Pro Leu Asn Ala Arg Leu Leu
385                 390                 395                 400


Glu Asp Lys Gln Val Gly Ile Glu Ile Pro Arg Asn Glu Glu Asp Gly
                405                 410                 415


Cys Leu Thr Lys Glu Ser Val Ala Arg Ser Leu Arg Ser Val Val Val
            420                 425                 430


Glu Lys Glu Gly Glu Ile Tyr Lys Ala Asn Ala Arg Glu Leu Ser Lys
        435                 440                 445


Ile Tyr Asn Asp Thr Lys Val Glu Lys Glu Tyr Val Ser Gln Phe Val
    450                 455                 460


Asp Tyr Leu Glu Lys Asn Ala Arg Ala Val Ala Ile Asp His Glu Ser
465                 470                 475                 480


<210>  130
<211>  472
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  UGT91D2e-b-EUGT11 chimera 10

<400>  130

Met Asp Ser Gly Tyr Ser Ser Ser Tyr Ala Ala Ala Ala Gly Met His
1               5                   10                  15


Val Val Ile Cys Pro Trp Leu Ala Phe Gly His Leu Leu Pro Cys Leu
            20                  25                  30


Asp Leu Ala Gln Arg Leu Ala Ser Arg Gly His Arg Val Ser Phe Val
        35                  40                  45


Ser Thr Pro Arg Asn Ile Ser Arg Leu Pro Pro Val Arg Pro Ala Leu
    50                  55                  60
```

```
Ala Pro Leu Val Ala Phe Val Ala Leu Pro Leu Pro Arg Val Glu Gly
65                  70                  75                  80

Leu Pro Asp Gly Ala Glu Ser Thr Asn Asp Val Pro His Asp Arg Pro
                85                  90                  95

Asp Met Val Glu Leu His Arg Arg Ala Phe Asp Gly Leu Ala Ala Pro
            100                 105                 110

Phe Ser Glu Phe Leu Gly Thr Ala Cys Ala Asp Trp Val Ile Val Asp
        115                 120                 125

Val Phe His His Trp Ala Ala Ala Ala Ala Leu Glu His Lys Val Pro
    130                 135                 140

Cys Ala Met Met Leu Leu Gly Ser Ala His Met Ile Ala Ser Ile Ala
145                 150                 155                 160

Asp Arg Arg Leu Glu Arg Ala Glu Thr Glu Ser Pro Ala Ala Ala Gly
                165                 170                 175

Gln Gly Arg Pro Ala Ala Ala Pro Thr Phe Glu Val Ala Arg Met Lys
            180                 185                 190

Leu Ile Arg Thr Lys Gly Ser Ser Gly Met Ser Leu Ala Glu Arg Phe
        195                 200                 205

Ser Leu Thr Leu Ser Arg Ser Ser Leu Val Val Gly Arg Ser Cys Val
    210                 215                 220

Glu Phe Glu Pro Glu Thr Val Pro Leu Leu Ser Thr Leu Arg Gly Lys
225                 230                 235                 240

Pro Ile Thr Phe Leu Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp Glu
                245                 250                 255

Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys Gln
            260                 265                 270
```

```
Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Ala Leu Val Ser
        275                 280                 285

Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly Leu
    290                 295                 300

Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser Asp
305                 310                 315                 320

Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg Gly
                325                 330                 335

Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His Glu
            340                 345                 350

Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val Glu
        355                 360                 365

Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly Asp
    370                 375                 380

Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile Glu
385                 390                 395                 400

Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val Ala
                405                 410                 415

Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr Lys
            420                 425                 430

Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val Glu
        435                 440                 445

Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala Arg
    450                 455                 460
```

Ala Val Ala Ile Asp His Glu Ser
465 470

<210> 131
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e-b-EUGT11 chimera 11

<400> 131

Met Asp Ser Gly Tyr Ser Ser Ser Tyr Ala Ala Ala Ala Gly Met His
1 5 10 15

Val Val Ile Cys Pro Trp Leu Ala Phe Gly His Leu Leu Pro Cys Leu
20 25 30

Asp Leu Ala Gln Arg Leu Ala Ser Arg Gly His Arg Val Ser Phe Val
35 40 45

Ser Thr Pro Arg Asn Ile Ser Arg Leu Pro Pro Val Arg Pro Ala Leu
50 55 60

Ala Pro Leu Val Ala Phe Val Ala Leu Pro Leu Pro Arg Val Glu Gly
65 70 75 80

Leu Pro Asp Gly Ala Glu Ser Thr Asn Asp Val Pro His Asp Arg Pro
85 90 95

Asp Met Val Glu Leu His Arg Arg Ala Phe Asp Gly Leu Ala Ala Pro
100 105 110

Phe Ser Glu Phe Leu Gly Thr Ala Cys Ala Asp Trp Val Ile Val Asp
115 120 125

Val Phe His His Trp Leu Pro Ser Ile Ala Ala Ser Leu Gly Ile Ser
130 135 140

```
Arg Ala His Phe Ser Val Thr Thr Pro Trp Ala Ile Ala Tyr Met Gly
145                 150                 155                 160

Pro Ser Ala Asp Ala Met Ile Asn Gly Ser Asp Gly Arg Thr Thr Val
                165                 170                 175

Glu Asp Leu Thr Thr Pro Pro Lys Trp Phe Pro Phe Pro Thr Lys Val
            180                 185                 190

Cys Trp Arg Lys His Asp Leu Ala Arg Leu Val Pro Tyr Lys Ala Pro
        195                 200                 205

Gly Ile Ser Asp Gly Tyr Arg Met Gly Met Val Leu Lys Gly Ser Asp
    210                 215                 220

Cys Leu Leu Ser Lys Cys Tyr His Glu Phe Gly Thr Gln Trp Leu Pro
225                 230                 235                 240

Leu Leu Glu Thr Leu His Gln Val Pro Val Val Pro Val Gly Leu Leu
                245                 250                 255

Pro Pro Glu Ile Pro Gly Asp Glu Lys Asp Glu Thr Trp Val Ser Ile
            260                 265                 270

Lys Lys Trp Leu Asp Gly Lys Gln Lys Gly Ser Val Val Tyr Val Ala
        275                 280                 285

Leu Gly Ser Glu Ala Leu Val Ser Gln Thr Glu Val Val Glu Leu Ala
    290                 295                 300

Leu Gly Leu Glu Leu Ser Gly Leu Pro Phe Val Trp Ala Tyr Arg Lys
305                 310                 315                 320

Pro Lys Gly Pro Ala Lys Ser Asp Ser Val Glu Leu Pro Asp Gly Phe
                325                 330                 335

Val Glu Arg Thr Arg Asp Arg Gly Leu Val Trp Thr Ser Trp Ala Pro
            340                 345                 350
```

```
Gln Leu Arg Ile Leu Ser His Glu Ser Val Cys Gly Phe Leu Thr His
        355                 360                 365


Cys Gly Ser Gly Ser Ile Val Glu Gly Leu Met Phe Gly His Pro Leu
    370                 375                 380


Ile Met Leu Pro Ile Phe Gly Asp Gln Pro Leu Asn Ala Arg Leu Leu
385                 390                 395                 400


Glu Asp Lys Gln Val Gly Ile Glu Ile 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>  132
<211>  463
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  UGT91D2e-b-EUGT11 chimera 12

<400>  132

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15


Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30
```

```
Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110

His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Met Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220
```

```
His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Met Pro Pro Leu His Glu Gly Arg
                245                 250                 255

Arg Glu Asp Gly Glu Asp Ala Thr Val Arg Trp Leu Asp Ala Gln Pro
            260                 265                 270

Ala Lys Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Pro Leu Gly
        275                 280                 285

Val Glu Lys Val His Glu Leu Ala Leu Gly Leu Glu Leu Ala Gly Thr
    290                 295                 300

Arg Phe Leu Trp Ala Leu Arg Lys Pro Thr Gly Val Ser Asp Ala Asp
305                 310                 315                 320

Leu Leu Pro Ala Gly Phe Glu Glu Arg Thr Arg Gly Arg Gly Val Val
                325                 330                 335

Ala Thr Arg Trp Val Pro Gln Met Ser Ile Leu Ala His Ala Ala Val
            340                 345                 350

Gly Ala Phe Leu Thr His Cys Gly Trp Asn Ser Thr Ile Glu Gly Leu
        355                 360                 365

Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly Asp Gln Gly
    370                 375                 380

Pro Asn Ala Arg Leu Ile Glu Ala Lys Asn Ala Gly Leu Gln Val Ala
385                 390                 395                 400

Arg Asn Asp Gly Asp Gly Ser Phe Asp Arg Glu Gly Val Ala Ala Ala
                405                 410                 415

Ile Arg Ala Val Ala Val Glu Glu Glu Ser Ser Lys Val Phe Gln Ala
            420                 425                 430
```

Lys Ala Lys Lys Leu Gln Glu Ile Val Ala Asp Met Ala Cys His Glu
        435   440   445

Arg Tyr Ile Asp Gly Phe Ile Gln Gln Leu Arg Ser Tyr Lys Asp
    450   455   460

<210> 133
<211> 462
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e-b-EUGT11 chimera 13

<400> 133

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1   5   10   15

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20   25   30

Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35   40   45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50   55   60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65   70   75   80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85   90   95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100   105   110

His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Ala Ala
        115   120   125

```
Ala Ala Ala Leu Glu His Lys Val Pro Cys Ala Met Met Leu Leu Gly
    130                 135                 140

Ser Ala His Met Ile Ala Ser Ile Ala Asp Arg Arg Leu Glu Arg Ala
145                 150                 155                 160

Glu Thr Glu Ser Pro Ala Ala Ala Gly Gln Gly Arg Pro Ala Ala Ala
                165                 170                 175

Pro Thr Phe Glu Val Ala Arg Met Lys Leu Ile Arg Thr Lys Gly Ser
            180                 185                 190

Ser Gly Met Ser Leu Ala Glu Arg Phe Ser Leu Thr Leu Ser Arg Ser
        195                 200                 205

Ser Leu Val Val Gly Arg Ser Cys Val Glu Phe Glu Pro Glu Thr Val
    210                 215                 220

Pro Leu Leu Ser Thr Leu Arg Gly Lys Pro Ile Thr Phe Leu Gly Leu
225                 230                 235                 240

Met Pro Pro Leu His Glu Gly Arg Arg Glu Asp Gly Glu Asp Ala Thr
                245                 250                 255

Val Arg Trp Leu Asp Ala Gln Pro Ala Lys Ser Val Val Tyr Val Ala
            260                 265                 270

Leu Gly Ser Glu Val Pro Leu Gly Val Glu Lys Val His Glu Leu Ala
        275                 280                 285

Leu Gly Leu Glu Leu Ala Gly Thr Arg Phe Leu Trp Ala Leu Arg Lys
    290                 295                 300

Pro Thr Gly Val Ser Asp Ala Asp Leu Leu Pro Ala Gly Phe Glu Glu
305                 310                 315                 320
```

```
Arg Thr Arg Gly Arg Gly Val Val Ala Thr Arg Trp Val Pro Gln Met
                325                 330                 335

Ser Ile Leu Ala His Ala Ala Val Gly Ala Phe Leu Thr His Cys Gly
            340                 345                 350

Trp Asn Ser Thr Ile Glu Gly Leu Met Phe Gly His Pro Leu Ile Met
        355                 360                 365

Leu Pro Ile Phe Gly Asp Gln Gly Pro Asn Ala Arg Leu Ile Glu Ala
    370                 375                 380

Lys Asn Ala Gly Leu Gln Val Pro Arg Asn Glu Glu Asp Gly Cys Leu
385                 390                 395                 400

Thr Lys Glu Ser Val Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys
                405                 410                 415

Glu Gly Glu Ile Tyr Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr
            420                 425                 430

Asn Asp Thr Lys Val Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr
        435                 440                 445

Leu Glu Lys Asn Ala Arg Ala Val Ala Ile Asp His Glu Ser
    450                 455                 460
```

<210> 134
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e-b-EUGT11 chimera 14

<400> 134

```
Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                  10                  15
```

```
Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30

Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110

His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Ala Ala
        115                 120                 125

Ala Ala Ala Leu Glu His Lys Val Pro Cys Ala Met Met Leu Leu Gly
    130                 135                 140

Ser Ala His Met Ile Ala Ser Ile Ala Asp Arg Arg Leu Glu Arg Ala
145                 150                 155                 160

Glu Thr Glu Ser Pro Ala Ala Ala Gly Gln Gly Arg Pro Ala Ala Ala
                165                 170                 175

Pro Thr Phe Glu Val Ala Arg Met Lys Leu Ile Arg Thr Lys Gly Ser
            180                 185                 190

Ser Gly Met Ser Leu Ala Glu Arg Phe Ser Leu Thr Leu Ser Arg Ser
        195                 200                 205

Ser Leu Val Val Gly Arg Ser Cys Val Glu Phe Glu Pro Glu Thr Val
    210                 215                 220
```

```
Pro Leu Leu Ser Thr Leu Arg Gly Lys Pro Ile Thr Phe Leu Gly Leu
225                 230                 235                 240

Leu Pro Pro Glu Ile Pro Gly Asp Glu Lys Asp Glu Thr Trp Val Ser
                245                 250                 255

Ile Lys Lys Trp Leu Asp Gly Lys Gln Lys Gly Ser Val Val Tyr Val
            260                 265                 270

Ala Leu Gly Ser Glu Ala Leu Val Ser Gln Thr Glu Val Val Glu Leu
        275                 280                 285

Ala Leu Gly Leu Glu Leu Ser Gly Leu Pro Phe Val Trp Ala Tyr Arg
    290                 295                 300

Lys Pro Lys Gly Pro Ala Lys Ser Asp Ser Val Glu Leu Pro Asp Gly
305                 310                 315                 320

Phe Val Glu Arg Thr Arg Asp Arg Gly Leu Val Trp Thr Ser Trp Ala
                325                 330                 335

Pro Gln Leu Arg Ile Leu Ser His Glu Ser Val Cys Gly Phe Leu Thr
            340                 345                 350

His Cys Gly Ser Gly Ser Ile Val Glu Gly Leu Met Phe Gly His Pro
        355                 360                 365

Leu Ile Met Leu Pro Ile Phe Gly Asp Gln Pro Leu Asn Ala Arg Leu
    370                 375                 380

Leu Glu Asp Lys Gln Val Gly Ile Glu Ile Ala Arg Asn Asp Gly Asp
385                 390                 395                 400

Gly Ser Phe Asp Arg Glu Gly Val Ala Ala Ala Ile Arg Ala Val Ala
                405                 410                 415
```

Val Glu Glu Glu Ser Ser Lys Val Phe Gln Ala Lys Ala Lys Lys Leu
420 425 430

Gln Glu Ile Val Ala Asp Met Ala Cys His Glu Arg Tyr Ile Asp Gly
435 440 445

Phe Ile Gln Gln Leu Arg Ser Tyr Lys Asp
450 455

<210> 135
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector (forward)

<400> 135
ggcaagccac gtttggtg 18

<210> 136
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector (reverse)

<400> 136
ggagctgcat gtgtcagagg 20

<210> 137
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> EUGT11 fragment 1 / UGT91D2e-b fragment 2 (forward)

<400> 137
cgatgtattt catcactggt tgccatccat cgcggct 37

<210> 138
<211> 37

<212> DNA
<213> Artificial Sequence

<220>
<223> EUGT11 / UGT91D2e-b fragment 2 (reverse)

<400> 138
agccgcgatg gatggcaacc agtgatgaaa tacatcg 37

<210> 139
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT91D2e-b fragment 1 / EUGT11 fragment 2 (forward)

<400> 139
ttatgattat actcactact gggctgctgc agccgcattg 40

<210> 140
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT91D2e-b fragment 1 / EUGT11 fragment 2 (reverse)

<400> 140
agccgcgatg gatggcaacc agtgatgaaa tacatcg 37

<210> 141
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> EUGT11 fragment 2 / UGT91D2e-b fragment 3 (forward)

<400> 141
caaacctatt actttccttg gtttactgcc accggaaata c 41

<210> 142
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> EUGT11 fragment 2 / UGT91D2e-b fragment 3 (reverse)

<400> 142
gtatttccgg tggcagtaaa ccaaggaaag taataggttt g 41

<210> 143
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT91D2e-b fragment 2 / EUGT11 fragment 3 (forward)

<400> 143
ccggtggttc cggtgggact aatgcctcca ttacatga 38

<210> 144
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT91D2e-b fragment 2 / EUGT11 fragment 3 (reverse)

<400> 144
tcatgtaatg gaggcattag tcccaccgga accaccgg 38

<210> 145
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> EUGT11 fragment 3 / UGT91D2e-b fragment 4 (forward)

<400> 145
gaacgcaggt ctgcaggttc caagaaatga ggaagatgg 39

<210> 146
<211> 39
<212> DNA
<213> Artificial Sequence

<220>

<223> EUGT11 fragment 3 / UGT91D2e-b fragment 4 (reverse)

<400> 146
ccatcttcct catttcttgg aacctgcaga cctgcgttc 39

<210> 147
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 Q21L

<400> 147

Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1 5 10 15

Pro Phe Pro Ala Leu Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20 25 30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35 40 45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50 55 60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65 70 75 80

Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85 90 95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100 105 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115 120 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130 135 140

```
Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335
```

```
Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480

Asn
```

<210> 148
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT8C2 Q21T

<400> 148

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                  10                  15

Pro Phe Pro Ala Thr Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35                  40                  45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80

Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205
```

```
Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400
```

```
Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480

Asn
```

<210> 149
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 Q21V

<400> 149

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                   10                  15

Pro Phe Pro Ala Val Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35                  40                  45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60
```

```
Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80


Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95


Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110


Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125


Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140


Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160


Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175


Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190


Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205


Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220


Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240


Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255


Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270
```

```
His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460
```

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465 470 475 480

Asn

<210> 150
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 F48S

<400> 150

Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1 5 10 15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
20 25 30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Ser
35 40 45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
50 55 60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65 70 75 80

Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
85 90 95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
100 105 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
115 120 125

```
Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335
```

```
Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480

Asn
```

<210> 151
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 F48H

<400> 151

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                  10                  15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp His
        35                  40                  45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80

Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190
```

```
Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400
```

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
405 410 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
420 425 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
435 440 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
450 455 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465 470 475 480

Asn

<210> 152
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 F48Y

<400> 152

Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1 5 10 15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
20 25 30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Tyr
35 40 45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
50 55 60

```
Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80

Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255
```

```
Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460
```

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465 470 475 480

Asn

<210> 153
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 F48R

<400> 153

Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1 5 10 15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
20 25 30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Arg
35 40 45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
50 55 60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65 70 75 80

Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
85 90 95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
100 105 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
115 120 125

```
Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320
```

```
Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480

Asn
```

<210> 154
<211> 481
<212> PRT
<213> Artificial Sequence

<220>

<223> UGT85C2 F48Q

<400> 154

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                  10                  15


Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30


Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Gln
        35                  40                  45


Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60


Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80


Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95


Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110


Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125


Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140


Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160


Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175


Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190
```

```
Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380
```

```
Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400


Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415


Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430


Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445


Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460


Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480


Asn
```

<210> 155
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 F48W

<400> 155

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                   10                  15


Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30


Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Trp
        35                  40                  45
```

```
Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80

Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255
```

```
Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445
```

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450   455   460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465   470   475   480

Asn

<210> 156
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 F48T

<400> 156

Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1   5   10   15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20   25   30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Thr
        35   40   45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50   55   60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65   70   75   80

Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85   90   95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100   105   110

```
Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320
```

```
Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480

Asn
```

<210> 157
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 I49V

<400> 157

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                  10                  15


Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30


Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35                  40                  45


Val His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60


Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80


Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95


Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110


Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125


Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140


Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160


Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175
```

```
Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380
```

```
Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400


Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415


Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430


Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445


Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460


Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480


Asn
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<210> 158
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 S84G

<400> 158

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                   10                  15


Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30


Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35                  40                  45
```

```
Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80

Pro Glu Ala Gly Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240
```

```
Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445
```

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450   455   460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465   470   475   480

Asn

<210> 159
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 S84A

<400> 159

Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1   5   10   15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20   25   30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35   40   45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50   55   60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65   70   75   80

Pro Glu Ala Ala Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85   90   95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100   105   110

```
Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300
```

```
Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480

Asn
```

<210> 160
<211> 481

<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 S84T

<400> 160

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                  10                  15


Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30


Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35                  40                  45


Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60


Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80


Pro Glu Ala Thr Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95


Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110


Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125


Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140


Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160


Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175
```

```
Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365
```

```
Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480

Asn
```

<210> 161
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 S84C

<400> 161

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                   10                  15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30
```

```
Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35                  40                  45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80

Pro Glu Ala Cys Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240
```

```
Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430
```

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435   440   445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450   455   460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465   470   475   480

Asn

<210> 162
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 S84P

<400> 162

Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1   5   10   15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20   25   30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35   40   45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50   55   60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65   70   75   80

Pro Glu Ala Pro Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85   90   95

```
Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300
```

```
Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480

Asn
```

<210> 163
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 S84N

<400> 163

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                   10                  15


Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30


Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35                  40                  45


Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60


Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80


Pro Glu Ala Asn Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95


Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110


Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125


Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140


Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160
```

```
Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365
```

```
Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480

Asn
```

<210> 164
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 S84V

<400> 164

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                   10                  15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30
```

```
Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35                  40                  45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80

Pro Glu Ala Val Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220
```

```
Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430
```

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
435 440 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
450 455 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465 470 475 480

Asn

<210> 165
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 P86R

<400> 165

Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1 5 10 15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
20 25 30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
35 40 45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
50 55 60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65 70 75 80

Pro Glu Ala Ser Ile Arg Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
85 90 95

```
Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285
```

```
Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480

Asn
```

<210> 166
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 P86G

<400> 166

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                   10                  15


Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30


Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35                  40                  45


Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60


Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80


Pro Glu Ala Ser Ile Gly Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95


Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110


Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125


Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140


Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160
```

```
Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350
```

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355   360   365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370   375   380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385   390   395   400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405   410   415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420   425   430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435   440   445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450   455   460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465   470   475   480

Asn

<210> 167
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 I87H

<400> 167

Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1   5   10   15

```
Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35                  40                  45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80

Pro Glu Ala Ser Ile Pro His Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220
```

```
Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415
```

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
420 425 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
435 440 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
450 455 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465 470 475 480

Asn

<210> 168
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 I87P

<400> 168

Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1 5 10 15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
20 25 30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
35 40 45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
50 55 60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65 70 75 80

```
Pro Glu Ala Ser Ile Pro Pro Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285
```

```
Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480
```

Asn

<210> 169
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 I87M

<400> 169

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                   10                  15


Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30


Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35                  40                  45


Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60


Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80


Pro Glu Ala Ser Ile Pro Met Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95


Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110


Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125


Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140
```

```
Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160


Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175


Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190


Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205


Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220


Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240


Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255


Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270


His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285


Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300


Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320


Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335


Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350
```

```
Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365


Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380


Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400


Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415


Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430


Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445


Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460


Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480


Asn
```

<210> 170
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 I87Y

<400> 170

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                   10                  15
```

```
Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35                  40                  45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80

Pro Glu Ala Ser Ile Pro Tyr Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205
```

```
Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415
```

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420   425   430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435   440   445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450   455   460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465   470   475   480

Asn

<210> 171
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 L91K

<400> 171

Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1   5   10   15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20   25   30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35   40   45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50   55   60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65   70   75   80

```
Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Lys Leu Arg Ser Ile Glu
                85                  90                  95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270
```

```
His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480
```

Asn

<210> 172
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 L91R

<400> 172

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                   10                  15


Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30


Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35                  40                  45


Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60


Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80


Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Arg Leu Arg Ser Ile Glu
                85                  90                  95


Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110


Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125


Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140
```

```
Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335
```

```
Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480

Asn
```

<210> 173
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 L91T

<400> 173

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                   10                  15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35                  40                  45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80

Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Thr Leu Arg Ser Ile Glu
                85                  90                  95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205
```

```
Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400
```

```
Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480

Asn
```

<210> 174
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 L92F

<400> 174

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                   10                  15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35                  40                  45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60
```

```
Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80

Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Phe Arg Ser Ile Glu
                85                  90                  95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270
```

```
His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460
```

```
Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480


Asn



<210>  175
<211>  481
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  UGT85C2 L92I

<400>  175

Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                   10                  15


Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30


Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35                  40                  45


Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60


Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80


Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Ile Arg Ser Ile Glu
                85                  90                  95


Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110


Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125
```

```
Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335
```

```
Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480

Asn
```

<210> 176
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 L92M

<400> 176

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                  10                  15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35                  40                  45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80

Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Met Arg Ser Ile Glu
                85                  90                  95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190
```

```
Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400
```

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
405 410 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
420 425 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
435 440 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
450 455 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465 470 475 480

Asn

<210> 177
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 I95K

<400> 177

Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1 5 10 15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
20 25 30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
35 40 45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
50 55 60

```
Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80

Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Lys Glu
                85                  90                  95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255
```

```
Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460
```

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465 470 475 480

Asn

<210> 178
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 F122S

<400> 178

Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1 5 10 15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
20 25 30

Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
35 40 45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
50 55 60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65 70 75 80

Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
85 90 95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
100 105 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Ser Leu Ser Val Phe Thr Ile
115 120 125

```
Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320
```

```
Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Leu Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480

Asn
```

<210> 179
<211> 481
<212> PRT
<213> Artificial Sequence

<220>

<223> UGT85C2 L334S

<400> 179

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                  10                  15


Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30


Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35                  40                  45


Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60


Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80


Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95


Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110


Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125


Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140


Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160


Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175


Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190
```

```
Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255

Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Ser Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380
```

```
Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400


Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415


Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430


Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445


Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450                 455                 460


Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480


Asn
```

<210> 180
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85C2 L334M

<400> 180

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                   10                  15


Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30


Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
        35                  40                  45
```

```
Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
    50                  55                  60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
65                  70                  75                  80

Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Leu Arg Ser Ile Glu
                85                  90                  95

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
            100                 105                 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
        115                 120                 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
    130                 135                 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu Gly Ile Arg Leu
            180                 185                 190

Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn Asp Lys Val Leu
        195                 200                 205

Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys Val Ser His His
    210                 215                 220

Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile Ile Lys Thr Leu
225                 230                 235                 240

Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro Leu Gln Leu Leu
                245                 250                 255
```

```
Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly Ile Thr Ser Leu
            260                 265                 270

His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys Phe Gln Trp Leu
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly Trp Gly Leu Ala
305                 310                 315                 320

Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser Asn Met Val Ile
                325                 330                 335

Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu His Ile Lys Lys
            340                 345                 350

Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys Val Leu Lys His
        355                 360                 365

Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp Gly Ser Thr Ile
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
                405                 410                 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
            420                 425                 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
        435                 440                 445
```

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
    450   455   460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465   470   475   480

Asn

<210> 181
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 Q23H

<400> 181

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 His 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 Lys 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> 182
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 I26W

<400> 182

```
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 Trp 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 Lys 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>  183
<211>  458
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  UGT76G1 T146G

<400>  183

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 Gly 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 Lys 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> 184
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 H155L

<400> 184

```
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 Leu 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 Lys 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> 185
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 L257G

<400> 185

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 Lys 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

Gly 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> 186
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 S253W

<400> 186

```
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 Lys 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 Trp 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>  187
<211>  458
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  UGT76G1 T284G

<400>  187

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 Lys 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 Gly 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> 188
<211> 458
<212> PRT
<213> Artificial Sequence

<220>

<223> UGT76G1 S283N

<400> 188

```
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 Lys 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 Asn 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>  189
<211>  458
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  UGT76G1 K337P

<400>  189

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 Lys 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

Pro 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> 190
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 T55K

<400> 190

```
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 Lys 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 Lys 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>  191
<211>  473
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  UGT91D2e L213E

<400>  191

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15


Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30


Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45


Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60


Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80
```

```
Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110

His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Glu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270
```

```
Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460

Arg Ala Val Ala Ile Asp His Glu Ser
465                 470
```

<210> 192
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e S221Y

<400> 192

```
Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15


Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30


Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45


Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60


Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80


Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95


Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110


His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125


Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140


Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160
```

```
Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Tyr Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350
```

```
Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460

Arg Ala Val Ala Ile Asp His Glu Ser
465                 470
```

<210> 193
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e E438H

<400> 193

```
Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30
```

```
Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110

His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240
```

```
Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430
```

Lys Ala Asn Ala Arg His Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435   440   445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450   455   460

Arg Ala Val Ala Ile Asp His Glu Ser
465   470

<210> 194
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e M152T

<400> 194

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1   5   10   15

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20   25   30

Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35   40   45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50   55   60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65   70   75   80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85   90   95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100   105   110

```
His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Thr Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320
```

```
Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460

Arg Ala Val Ala Ile Asp His Glu Ser
465                 470
```

<210> 195
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e L211C

<400> 195

```
Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15


Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30


Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45


Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60


Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80


Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95


Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110


His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125


Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140


Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160


Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175


Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190
```

```
Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Cys Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400
```

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
405 410 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
420 425 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
435 440 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
450 455 460

Arg Ala Val Ala Ile Asp His Glu Ser
465 470

<210> 196
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e L195S

<400> 196

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1 5 10 15

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
20 25 30

Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
35 40 45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
50 55 60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65 70 75 80

```
Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110

His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Ser Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270
```

```
Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460

Arg Ala Val Ala Ile Asp His Glu Ser
465                 470
```

<210> 197
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e L195V

<400> 197

```
Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15


Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30


Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45


Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60


Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80


Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95


Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110


His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125


Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140


Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160
```

```
Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Val Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350
```

```
Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460

Arg Ala Val Ala Ile Asp His Glu Ser
465                 470


<210>  198
<211>  473
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  UGT91D2e V286S

<400>  198

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30
```

```
Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110

His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240
```

```
Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Ser Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430
```

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435   440   445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450   455   460

Arg Ala Val Ala Ile Asp His Glu Ser
465   470

<210> 199
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e S221S

<400> 199

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1   5   10   15

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20   25   30

Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35   40   45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50   55   60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65   70   75   80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85   90   95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100   105   110

```
His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320
```

```
Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460

Arg Ala Val Ala Ile Asp His Glu Ser
465                 470
```

<210> 200
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e P93V M152G

<400> 200

```
Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15


Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30


Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45


Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60


Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80


Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Val Tyr Leu Lys
                85                  90                  95


Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110


His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125


Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140


Thr Pro Trp Ala Ile Ala Tyr Gly Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160


Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175


Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190
```

```
Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400
```

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
405 410 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
420 425 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
435 440 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
450 455 460

Arg Ala Val Ala Ile Asp His Glu Ser
465 470

<210> 201
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e S99I

<400> 201

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1 5 10 15

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
20 25 30

Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
35 40 45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
50 55 60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65 70 75 80

```
Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95

Lys Ala Ile Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110

His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270
```

```
Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460

Arg Ala Val Ala Ile Asp His Glu Ser
465                 470
```

<210> 202
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e T144K P201P

<400> 202

```
Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15


Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30


Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45


Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60


Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80


Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95


Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110


His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125


Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Lys
    130                 135                 140


Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160
```

```
Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350
```

```
Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460

Arg Ala Val Ala Ile Asp His Glu Ser
465                 470
```

<210> 203
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e T144L

<400> 203

```
Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30
```

```
Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110

His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Leu
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240
```

```
Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430
```

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435   440   445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450   455   460

Arg Ala Val Ala Ile Asp His Glu Ser
465   470

<210> 204
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e T144M

<400> 204

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1   5   10   15

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20   25   30

Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35   40   45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50   55   60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65   70   75   80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85   90   95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100   105   110

```
His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Met
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320
```

```
Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460

Arg Ala Val Ala Ile Asp His Glu Ser
465                 470
```

<210> 205
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e A148K L211I

<400> 205

```
Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15


Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30


Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45


Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60


Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80


Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95


Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110


His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125


Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140


Thr Pro Trp Lys Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160


Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175


Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190
```

```
Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Ile Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400
```

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
405 410 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
420 425 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
435 440 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
450 455 460

Arg Ala Val Ala Ile Asp His Glu Ser
465 470

<210> 206
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e L195N

<400> 206

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1 5 10 15

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
20 25 30

Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
35 40 45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
50 55 60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65 70 75 80

```
Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110

His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Asn Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270
```

```
Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460

Arg Ala Val Ala Ile Asp His Glu Ser
465                 470
```

<210> 207
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e K199C

<400> 207

```
Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15


Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30


Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45


Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60


Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80


Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95


Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110


His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125


Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140


Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160
```

```
Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Cys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350
```

```
Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365


Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380


Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400


Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415


Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430


Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445


Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460


Arg Ala Val Ala Ile Asp His Glu Ser
465                 470


<210>  208
<211>  473
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  UGT91D2e L211M E426G A466V

<400>  208

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15


Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30
```

```
Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110

His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Met Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240
```

```
Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Gly Lys Glu Gly Glu Ile Tyr
            420                 425                 430
```

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435   440   445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450   455   460

Arg Val Val Ala Ile Asp His Glu Ser
465   470

<210> 209
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e L211T I303I

<400> 209

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1   5   10   15

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20   25   30

Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35   40   45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50   55   60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65   70   75   80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85   90   95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100   105   110

```
His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Thr Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320
```

```
Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460

Arg Ala Val Ala Ile Asp His Glu Ser
465                 470
```

<210> 210
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e V286N

<400> 210

```
Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15


Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30


Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45


Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60


Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80


Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95


Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110


His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125


Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140


Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160


Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175


Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190
```

```
Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Asn Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400
```

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
405 410 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
420 425 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
435 440 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
450 455 460

Arg Ala Val Ala Ile Asp His Glu Ser
465 470

<210> 211
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e S114F V286S

<400> 211

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1 5 10 15

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
20 25 30

Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
35 40 45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
50 55 60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65 70 75 80

```
Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110

His Phe Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270
```

```
Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Ser Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460

Arg Ala Val Ala Ile Asp His Glu Ser
465                 470
```

<210> 212
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e G384K

<400> 212

```
Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15


Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30


Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45


Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60


Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80


Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95


Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110


His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125


Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140


Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160
```

```
Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350
```

```
Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Lys
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460

Arg Ala Val Ala Ile Asp His Glu Ser
465                 470
```

<210> 213
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e G384Y

<400> 213

```
Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1               5                   10                  15

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20                  25                  30
```

```
Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35                  40                  45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50                  55                  60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65                  70                  75                  80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85                  90                  95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100                 105                 110

His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240
```

```
Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Tyr
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430
```

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435   440   445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450   455   460

Arg Ala Val Ala Ile Asp His Glu Ser
465   470

<210> 214
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT91D2e E438M

<400> 214

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1   5   10   15

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
            20   25   30

Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
        35   40   45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
    50   55   60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65   70   75   80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
                85   90   95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
            100   105   110

```
His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
        115                 120                 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
    130                 135                 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
145                 150                 155                 160

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
                165                 170                 175

Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
            180                 185                 190

Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
        195                 200                 205

Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
    210                 215                 220

His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
225                 230                 235                 240

Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
                245                 250                 255

Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
            260                 265                 270

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
        275                 280                 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
    290                 295                 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305                 310                 315                 320
```

```
Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
                325                 330                 335

Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
            340                 345                 350

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
        355                 360                 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
    370                 375                 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385                 390                 395                 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
                405                 410                 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
            420                 425                 430

Lys Ala Asn Ala Arg Met Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
        435                 440                 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
    450                 455                 460

Arg Ala Val Ala Ile Asp His Glu Ser
465                 470
```

<210> 215
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward USER primer

<400> 215
atcaacgggu aaaatggatg ctatggctac caccg 35

<210> 216
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse USER primer

<400> 216
cgtgcgautc agtttctggc caaaacggtg att 33

<210> 217
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 Q23H H155L

<400> 217

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 His 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 Leu 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 Lys 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
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<210> 218
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 T146G H155L

<400> 218

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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 Gly Ser Ser Leu Phe Asn Phe His Ala Leu 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 Lys 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> 219
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT76G1 L257G H155L

<400> 219

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 Leu 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 Lys 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

Gly 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> 220
<211> 458
<212> PRT
<213> Artificial Sequence

<220>

<223> UGT76G1 S283N H155L

<400> 220

```
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 Leu 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 Lys 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 Asn 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
```