SEQUENCE LISTING

<110> Senomyx, Inc.

<120> METHODS FOR MAKING HIGH INTENSITY
SWEETENERS

<130> SNMX.044WO

<150> 62/501018
<151> 2017-05-03

<150> 62/551750
<151> 2017-08-29

<160> 1023

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 694
<212> PRT
<213> Artificial Sequence

<220>
<223> Cyclomaltodextrin glucanotransferase (CGTase;
Bacillus)

<400> 1

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

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Val Tyr Arg Asn Leu Phe Asp Leu Ala Asp Leu Asn His Gln Asn Ile
        195                 200                 205
Ala Ile Asp Leu Tyr Phe Lys Glu Ala Ile Lys Leu Trp Leu Asp Gln
    210                 215                 220
Gly Ile Asp Gly Ile Arg Val Asp Ala Val Lys His Met Ser Tyr Gly
225                 230                 235                 240
Trp Gln Lys Ser Trp Leu Asn Ser Ile Tyr Asn Tyr Arg Pro Val Phe
                245                 250                 255
Ile Phe Gly Glu Trp Tyr Ile Asn Pro Asn Glu Tyr Asp His Arg Asn
            260                 265                 270
Val His Phe Ala Asn Asn Ser Gly Met Ser Leu Leu Asp Phe Ser Phe
        275                 280                 285
Ala His Lys Val Arg Glu Val Phe Arg Asp Gly Met Asp Ser Met His
    290                 295                 300
Gly Leu His Lys Met Ile Glu Glu Thr Tyr Gln Ile Tyr Asn Asp Val
305                 310                 315                 320
Asn Asn Leu Val Thr Phe Ile Asp Asn His Asp Met Asp Arg Phe His
                325                 330                 335
Ile Asn Gly Gln Ser Lys Arg Arg Ile Glu Gln Ser Leu Val Phe Leu
            340                 345                 350
Leu Thr Ser Arg Gly Ile Pro Ser Val Tyr Tyr Gly Thr Glu Gln Tyr
        355                 360                 365
Met Val Gly Asn Gly Asp Pro Asn Asn Arg Gly Gln Met Glu Ser Phe
    370                 375                 380
Asp Val Asn Thr Asp Asn Phe Lys Ile Ile Gln Ser Leu Ser Ser Leu
385                 390                 395                 400
Arg Ser Leu Asn Tyr Ala Leu Pro Tyr Gly Asn Thr Lys Glu Arg Tyr
                405                 410                 415
Ile Thr Asn Asp Ile Tyr Val Tyr Glu Arg Tyr Phe Gly Ser Asp Val
            420                 425                 430
Val Leu Ile Ala Leu Asn Arg Asn Leu Thr Glu Gly Tyr Glu Ile Lys
        435                 440                 445
Asp Val Lys Thr Ile Leu Pro Ser Arg Lys Tyr Lys Asp Ile Leu Asp
    450                 455                 460
Gly Leu Leu Asp Gly Glu Ala Ile Arg Val Glu Asn Asn Asn Ile Asp
465                 470                 475                 480
Ser Leu Trp Leu Gly Pro Gly Ser Gly Gln Val Trp His His Lys Gly
                485                 490                 495
Val Asn Ser Ile Pro Leu Ile Gly Thr Val Gly His Lys Met Thr Thr
            500                 505                 510
Val Gly Gln Ile Ile Cys Ile Glu Gly Cys Gly Phe Thr Ser Lys Lys
        515                 520                 525
Gly Ser Val Leu Phe Glu Glu Lys Glu Ala Glu Val Val Ser Trp Ser
    530                 535                 540
His Thr Ser Ile Lys Val Lys Val Pro Ala Val Asn Asp Gly Lys Tyr
545                 550                 555                 560
Glu Ile Thr Val Val Thr Asp Thr Gly Thr Arg Ser Asn Ile Tyr Lys
                565                 570                 575
His Ile Glu Val Leu Asn Thr Lys Gln Val Cys Ile Arg Phe Val Ile
            580                 585                 590
Glu Asn Gly Tyr Glu Ile Pro Glu Ser Glu Val Phe Ile Met Gly Asn
        595                 600                 605
Thr Tyr Ser Leu Gly Asn Met Asn Pro Cys Lys Ala Val Gly Pro Phe
    610                 615                 620
```

Phe Asn Gln Ile Met Tyr Gln Phe Pro Thr Gly Tyr Phe Asp Ile Ser
625 630 635 640
Val Pro Ala Asp Thr Leu Leu Glu Phe Lys Phe Ile Arg Lys Ile Asn
645 650 655
Asn Thr Leu Leu Ile Glu Gly Gly Glu Asn His Lys Tyr Arg Thr Pro
660 665 670
Ser Phe Gly Thr Gly Glu Val Val Val Lys Trp Gln Thr Ala Glu Lys
675 680 685
Thr Ile Leu Val Glu Ser
690

<210> 2
<211> 1381
<212> PRT
<213> Artificial Sequence

<220>
<223> DexT Protein

<400> 2
Met Pro Ala Asn Ala Pro Asp Lys Gln Ser Val Thr Asn Ala Pro Val
1 5 10 15
Val Pro Pro Lys His Asp Thr Asp Gln Gln Asp Asp Ser Leu Glu Lys
20 25 30
Gln Gln Val Leu Glu Pro Ser Val Asn Ser Asn Ile Pro Lys Lys Gln
35 40 45
Thr Asn Gln Gln Leu Ala Val Val Thr Ala Pro Ala Asn Ser Ala Pro
50 55 60
Gln Thr Lys Thr Thr Ala Glu Ile Ser Ala Gly Thr Glu Leu Asp Thr
65 70 75 80
Met Pro Asn Val Lys His Val Asp Gly Lys Val Tyr Phe Tyr Gly Asp
85 90 95
Asp Gly Gln Pro Lys Lys Asn Phe Thr Thr Ile Ile Asp Gly Lys Pro
100 105 110
Tyr Tyr Phe Asp Lys Asp Thr Gly Ala Leu Ser Asn Asn Asp Lys Gln
115 120 125
Tyr Val Ser Glu Leu Phe Ser Ile Gly Asn Lys His Asn Ala Val Tyr
130 135 140
Asn Thr Ser Ser Asp Asn Phe Thr Gln Leu Glu Gly His Leu Thr Ala
145 150 155 160
Ser Ser Trp Tyr Arg Pro Lys Asp Ile Leu Lys Asn Gly Lys Arg Trp
165 170 175
Ala Pro Ser Thr Val Thr Asp Phe Arg Pro Leu Leu Met Ala Trp Trp
180 185 190
Pro Asp Lys Ser Thr Gln Val Thr Tyr Leu Asn Tyr Met Lys Asp Gln
195 200 205
Gly Leu Leu Ser Gly Thr His His Phe Ser Asp Asn Glu Asn Met Arg
210 215 220
Thr Leu Thr Ala Ala Ala Met Gln Ala Gln Val Asn Ile Glu Lys Lys
225 230 235 240
Ile Gly Gln Leu Gly Asn Thr Asp Trp Leu Lys Thr Ala Met Thr Gln
245 250 255
Tyr Ile Asp Ala Gln Pro Asn Trp Asn Ile Asp Ser Glu Ala Lys Gly

```
            260                 265                 270
Asp Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Thr Asn Ser Asp Met
        275                 280                 285
Ser Pro Lys Ala Asn Ser Asp Tyr Arg Lys Leu Ser Arg Thr Pro Lys
    290                 295                 300
Asn Gln Lys Gly Gln Ile Ala Asp Lys Tyr Lys Gln Gly Gly Phe Glu
305                 310                 315                 320
Leu Leu Leu Ala Asn Asp Val Asp Asn Ser Asn Pro Val Val Gln Ala
                325                 330                 335
Glu Gln Leu Asn Trp Leu His Tyr Met Met Asn Ile Gly Ser Ile Leu
            340                 345                 350
Gln Asn Asp Asp Gln Ala Asn Phe Asp Gly Tyr Arg Val Asp Ala Val
        355                 360                 365
Asp Asn Val Asp Ala Asp Leu Leu Gln Ile Ala Gly Glu Tyr Ala Lys
    370                 375                 380
Ala Ala Tyr Gly Val Asp Lys Asn Asp Ala Arg Ala Asn Gln His Leu
385                 390                 395                 400
Ser Ile Leu Glu Asp Trp Gly Asp Glu Asp Pro Asp Tyr Val Lys Ala
                405                 410                 415
His Gly Asn Gln Gln Ile Thr Met Asp Phe Pro Leu His Leu Ala Ile
            420                 425                 430
Lys Tyr Ala Leu Asn Met Pro Asn Asp Lys Arg Ser Gly Leu Glu Pro
        435                 440                 445
Thr Arg Glu His Ser Leu Val Lys Arg Ile Thr Asp Asp Lys Glu Asn
    450                 455                 460
Val Ala Gln Pro Asn Tyr Ser Phe Ile Arg Ala His Asp Ser Glu Val
465                 470                 475                 480
Gln Thr Ile Ile Ala Asp Ile Ile Lys Asp Lys Ile Asn Pro Ala Ser
                485                 490                 495
Thr Gly Leu Asp Ser Thr Val Thr Leu Asp Gln Ile Lys Gln Ala Phe
            500                 505                 510
Asp Ile Tyr Asn Ala Asp Glu Leu Lys Ala Asp Lys Val Tyr Thr Pro
        515                 520                 525
Tyr Asn Ile Pro Ala Ser Tyr Ala Leu Leu Leu Thr Asn Lys Asp Thr
    530                 535                 540
Ile Pro Arg Val Tyr Tyr Gly Asp Met Phe Thr Asp Asp Gly Gln Tyr
545                 550                 555                 560
Met Ala Lys Gln Ser Pro Tyr Tyr Gln Ala Ile Asp Ala Leu Leu Lys
                565                 570                 575
Ala Arg Ile Lys Tyr Ala Ala Gly Gly Gln Thr Met Lys Met Asn Tyr
            580                 585                 590
Phe Pro Asp Glu Gln Ser Val Met Thr Ser Val Arg Tyr Gly Lys Gly
        595                 600                 605
Ala Met Thr Ala Ser Asp Ser Gly Asn Gln Glu Thr Arg Tyr Gln Gly
    610                 615                 620
Ile Gly Leu Val Val Asn Asn Arg Pro Asp Leu Lys Leu Ser Asp Lys
625                 630                 635                 640
Asp Glu Val Lys Met Asp Met Gly Ala Ala His Lys Asn Gln Asp Tyr
                645                 650                 655
Arg Pro Val Leu Leu Thr Thr Lys Ser Gly Leu Lys Val Tyr Ser Thr
            660                 665                 670
Asp Ala Asn Ala Pro Val Val Arg Thr Asp Ala Asn Gly Gln Leu Thr
        675                 680                 685
Phe Lys Ala Asp Met Val Tyr Gly Val Asn Asp Pro Gln Val Ser Gly
```

```
    690                 695                 700
Tyr Ile Ala Ala Trp Val Pro Val Gly Ala Ser Glu Asn Gln Asp Ala
705                 710                 715                 720
Arg Thr Lys Ser Glu Thr Thr Gln Ser Thr Asp Gly Ser Val Tyr His
                725                 730                 735
Ser Asn Ala Ala Leu Asp Ser Gln Val Ile Tyr Glu Gly Phe Ser Asn
            740                 745                 750
Phe Gln Asp Phe Pro Thr Thr Pro Asp Glu Phe Thr Asn Ile Lys Ile
        755                 760                 765
Ala Gln Asn Val Asn Leu Phe Lys Asp Trp Gly Ile Thr Ser Phe Glu
    770                 775                 780
Met Ala Pro Gln Tyr Arg Ala Ser Ser Asp Lys Ser Phe Leu Asp Ala
785                 790                 795                 800
Ile Val Gln Asn Gly Tyr Ala Phe Thr Asp Arg Tyr Asp Ile Gly Tyr
                805                 810                 815
Asn Thr Pro Thr Lys Tyr Gly Thr Ala Asp Asn Leu Leu Asp Ala Leu
            820                 825                 830
Arg Ala Leu His Gly Gln Gly Ile Gln Ala Ile Asn Asp Trp Val Pro
        835                 840                 845
Asp Gln Ile Tyr Asn Leu Pro Asp Glu Gln Leu Val Thr Ala Ile Arg
    850                 855                 860
Thr Asp Gly Ser Gly Asp His Thr Tyr Gly Ser Val Ile Asp His Thr
865                 870                 875                 880
Leu Tyr Ala Ser Lys Thr Val Gly Gly Gly Ile Tyr Gln Gln Gln Tyr
                885                 890                 895
Gly Gly Ala Phe Leu Glu Gln Leu Lys Thr Gln Tyr Pro Gln Leu Phe
            900                 905                 910
Gln Gln Lys Gln Ile Ser Thr Asp Gln Pro Met Asn Pro Asp Ile Gln
        915                 920                 925
Ile Lys Ser Trp Glu Ala Lys Tyr Phe Asn Gly Ser Asn Ile Gln Gly
    930                 935                 940
Arg Gly Ala Trp Tyr Val Leu Lys Asp Trp Gly Thr Gln Gln Tyr Phe
945                 950                 955                 960
Asn Val Ser Asp Ala Gln Thr Phe Leu Pro Lys Gln Leu Leu Gly Glu
                965                 970                 975
Lys Ala Lys Thr Gly Phe Val Thr Arg Gly Lys Glu Thr Ser Phe Tyr
            980                 985                 990
Ser Thr Ser Gly Tyr Gln Ala Lys Ser Ala Phe Ile Cys Asp Asn Gly
        995                 1000                1005
Asn Trp Tyr Tyr Phe Asp Asp Lys Gly Lys Met Val Val Gly Asn Gln
    1010                1015                1020
Val Ile Asn Gly Ile Asn Tyr Tyr Phe Leu Pro Asn Gly Ile Glu Leu
1025                1030                1035                1040
Gln Asp Ala Tyr Leu Val His Asp Gly Met Tyr Tyr Tyr Tyr Asn Asn
                1045                1050                1055
Ile Gly Lys Gln Leu His Asn Thr Tyr Tyr Gln Asp Lys Gln Lys Asn
            1060                1065                1070
Phe His Tyr Phe Phe Glu Asp Gly His Met Ala Gln Gly Ile Val Thr
        1075                1080                1085
Ile Ile Gln Ser Asp Gly Thr Pro Val Thr Gln Tyr Phe Asp Glu Asn
    1090                1095                1100
Gly Lys Gln Gln Lys Gly Val Ala Val Lys Gly Ser Asp Gly His Leu
1105                1110                1115                1120
His Tyr Phe Asp Gly Ala Ser Gly Asn Met Leu Phe Lys Ser Trp Gly
```

```
                1125                1130                1135
Arg Leu Ala Asp Gly Ser Trp Leu Tyr Val Asp Glu Lys Gly Asn Ala
            1140                1145                1150
Val Thr Gly Lys Gln Thr Ile Asn Asn Gln Thr Val Tyr Phe Asn Asp
        1155                1160                1165
Asp Gly Arg Gln Ile Lys Asn Asn Phe Lys Glu Leu Ala Asp Gly Ser
    1170                1175                1180
Trp Leu Tyr Leu Asn Asn Lys Gly Val Ala Val Thr Gly Glu Gln Ile
1185                1190                1195                1200
Ile Asn Gly Gln Thr Leu Tyr Phe Gly Asn Asp Gly Arg Gln Phe Lys
                1205                1210                1215
Gly Thr Thr His Ile Asn Ala Thr Gly Glu Ser Arg Tyr Tyr Asp Pro
            1220                1225                1230
Asp Ser Gly Asn Met Ile Thr Asp Arg Phe Glu Arg Val Gly Asp Asn
        1235                1240                1245
Gln Trp Ala Tyr Phe Gly Tyr Asp Gly Val Ala Val Thr Gly Asp Arg
    1250                1255                1260
Ile Ile Lys Gly Gln Lys Leu Tyr Phe Asn Gln Asn Gly Ile Gln Met
1265                1270                1275                1280
Lys Gly His Leu Arg Leu Glu Asn Gly Ile Met Arg Tyr Tyr Asp Ala
                1285                1290                1295
Asp Thr Gly Glu Leu Val Arg Asn Arg Phe Val Leu Leu Ser Asp Gly
            1300                1305                1310
Ser Trp Val Tyr Phe Gly Gln Asp Gly Val Pro Val Thr Gly Val Gln
        1315                1320                1325
Val Ile Asn Gly Gln Thr Leu Tyr Phe Asp Ala Asp Gly Arg Gln Val
    1330                1335                1340
Lys Gly Gln Gln Arg Val Ile Gly Asn Gln Arg Tyr Trp Met Asp Lys
1345                1350                1355                1360
Asp Asn Gly Glu Met Lys Lys Ile Thr Tyr Ala Ala Ala Leu Glu His
                1365                1370                1375
His His His His His
            1380
```

<210> 3
<211> 711
<212> PRT
<213> Artificial Sequence

<220>
<223> CGTase CGT-SL

<400> 3

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

```
Asp Trp Gln Gly Ile Ile Asn Lys Ile Asn Asp Gly Tyr Leu Thr Glu
                85                  90                  95
Met Gly Val Thr Ala Ile Trp Ile Ser Gln Pro Val Glu Asn Val Phe
            100                 105                 110
Ala Val Met Asn Asp Ala Asp Gly Ser Thr Ser Tyr His Gly Tyr Trp
        115                 120                 125
Ala Arg Asp Phe Lys Lys Thr Asn Pro Phe Phe Gly Thr Leu Ser Asp
    130                 135                 140
Phe Gln Arg Leu Val Asp Ala Ala His Ala Lys Gly Ile Lys Val Ile
145                 150                 155                 160
Ile Asp Phe Ala Pro Asn His Thr Ser Pro Ala Ser Glu Thr Asn Pro
                165                 170                 175
Ser Tyr Met Glu Asn Gly Arg Leu Tyr Asp Asn Gly Thr Leu Ile Gly
            180                 185                 190
Gly Tyr Thr Asn Asp Thr Asn Ser Tyr Phe His His Asn Gly Gly Thr
        195                 200                 205
Thr Phe Ser Asn Leu Glu Asp Gly Ile Tyr Arg Asn Leu Phe Asp Leu
    210                 215                 220
Ala Asp Phe Asn His Gln Asn Gln Phe Ile Asp Lys Tyr Leu Lys Asp
225                 230                 235                 240
Ala Ile Lys Leu Trp Leu Asp Met Gly Ile Asp Gly Ile Arg Met Asp
                245                 250                 255
Ala Val Lys His Met Pro Phe Gly Trp Gln Lys Ser Phe Met Asp Glu
            260                 265                 270
Val Tyr Asp Tyr Arg Pro Val Phe Thr Phe Gly Glu Trp Phe Leu Ser
        275                 280                 285
Glu Asn Glu Val Asp Ser Asn Asn His Phe Phe Ala Asn Glu Ser Gly
    290                 295                 300
Met Ser Leu Leu Asp Phe Arg Phe Gly Gln Lys Leu Arg Gln Val Leu
305                 310                 315                 320
Arg Asn Asn Ser Asp Asp Trp Tyr Gly Phe Asn Gln Met Ile Gln Asp
                325                 330                 335
Thr Ala Ser Ala Tyr Asp Glu Val Ile Asp Gln Val Thr Phe Ile Asp
            340                 345                 350
Asn His Asp Met Asp Arg Phe Met Ala Asp Glu Gly Asp Pro Arg Lys
        355                 360                 365
Val Asp Ile Ala Leu Ala Val Leu Leu Thr Ser Arg Gly Val Pro Asn
    370                 375                 380
Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asn Gly Asp Pro Asn
385                 390                 395                 400
Asn Arg Lys Met Met Thr Ser Phe Asn Lys Asn Thr Arg Ala Tyr Gln
                405                 410                 415
Val Ile Gln Lys Leu Ser Ser Leu Arg Arg Ser Asn Pro Ala Leu Ser
            420                 425                 430
Tyr Gly Asp Thr Glu Gln Arg Trp Ile Asn Ser Asp Val Tyr Ile Tyr
        435                 440                 445
Glu Arg Gln Phe Gly Lys Asp Val Val Leu Val Ala Val Asn Arg Ser
    450                 455                 460
Leu Ser Lys Ser Tyr Ser Ile Thr Gly Leu Phe Thr Ala Leu Pro Ser
465                 470                 475                 480
Gly Thr Tyr Thr Asp Gln Leu Gly Ala Leu Leu Asp Gly Asn Thr Ile
                485                 490                 495
Gln Val Gly Ser Asn Gly Ala Val Asn Ala Phe Asn Leu Gly Pro Gly
            500                 505                 510
```

Glu Val Gly Val Trp Thr Tyr Ser Ala Ala Glu Ser Val Pro Ile Ile
515 520 525
Gly His Ile Gly Pro Met Met Gly Gln Val Gly His Lys Leu Thr Ile
530 535 540
Asp Gly Glu Gly Phe Gly Thr Asn Val Gly Thr Val Lys Phe Gly Asn
545 550 555 560
Thr Val Ala Ser Val Val Ser Trp Ser Asn Asn Gln Ile Thr Val Thr
565 570 575
Val Pro Asn Ile Pro Ala Gly Lys Tyr Asn Ile Thr Val Gln Thr Ser
580 585 590
Gly Gly Gln Val Ser Ala Ala Tyr Asp Asn Phe Glu Val Leu Thr Asn
595 600 605
Asp Gln Val Ser Val Arg Phe Val Val Asn Asn Ala Asn Thr Asn Trp
610 615 620
Gly Glu Asn Ile Tyr Leu Val Gly Asn Val His Glu Leu Gly Asn Trp
625 630 635 640
Asn Thr Ser Lys Ala Ile Gly Pro Leu Phe Asn Gln Val Ile Tyr Ser
645 650 655
Tyr Pro Thr Trp Tyr Val Asp Val Ser Val Pro Glu Gly Lys Thr Ile
660 665 670
Glu Phe Lys Phe Ile Lys Lys Asp Gly Ser Gly Asn Val Ile Trp Glu
675 680 685
Ser Gly Ser Asn His Val Tyr Thr Thr Pro Thr Ser Thr Thr Gly Thr
690 695 700
Val Asn Val Asn Trp Gln Tyr
705 710

<210> 4
<211> 496
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT73C3

<400> 4
Met Ala Thr Glu Lys Thr His Gln Phe His Pro Ser Leu His Phe Val
1 5 10 15
Leu Phe Pro Phe Met Ala Gln Gly His Met Ile Pro Met Ile Asp Ile
20 25 30
Ala Arg Leu Leu Ala Gln Arg Gly Val Thr Ile Thr Ile Val Thr Thr
35 40 45
Pro His Asn Ala Ala Arg Phe Lys Asn Val Leu Asn Arg Ala Ile Glu
50 55 60
Ser Gly Leu Ala Ile Asn Ile Leu His Val Lys Phe Pro Tyr Gln Glu
65 70 75 80
Phe Gly Leu Pro Glu Gly Lys Glu Asn Ile Asp Ser Leu Asp Ser Thr
85 90 95
Glu Leu Met Val Pro Phe Phe Lys Ala Val Asn Leu Leu Glu Asp Pro
100 105 110
Val Met Lys Leu Met Glu Glu Met Lys Pro Arg Pro Ser Cys Leu Ile
115 120 125
Ser Asp Trp Cys Leu Pro Tyr Thr Ser Ile Ile Ala Lys Asn Phe Asn

```
    130                 135                 140
Ile Pro Lys Ile Val Phe His Gly Met Gly Cys Phe Asn Leu Leu Cys
145                 150                 155                 160
Met His Val Leu Arg Arg Asn Leu Glu Ile Leu Glu Asn Val Lys Ser
                165                 170                 175
Asp Glu Glu Tyr Phe Leu Val Pro Ser Phe Pro Asp Arg Val Glu Phe
            180                 185                 190
Thr Lys Leu Gln Leu Pro Val Lys Ala Asn Ala Ser Gly Asp Trp Lys
        195                 200                 205
Glu Ile Met Asp Glu Met Val Lys Ala Glu Tyr Thr Ser Tyr Gly Val
    210                 215                 220
Ile Val Asn Thr Phe Gln Glu Leu Glu Pro Pro Tyr Val Lys Asp Tyr
225                 230                 235                 240
Lys Glu Ala Met Asp Gly Lys Val Trp Ser Ile Gly Pro Val Ser Leu
                245                 250                 255
Cys Asn Lys Ala Gly Ala Asp Lys Ala Glu Arg Gly Ser Lys Ala Ala
            260                 265                 270
Ile Asp Gln Asp Glu Cys Leu Gln Trp Leu Asp Ser Lys Glu Glu Gly
        275                 280                 285
Ser Val Leu Tyr Val Cys Leu Gly Ser Ile Cys Asn Leu Pro Leu Ser
    290                 295                 300
Gln Leu Lys Glu Leu Gly Leu Gly Leu Glu Glu Ser Arg Arg Ser Phe
305                 310                 315                 320
Ile Trp Val Ile Arg Gly Ser Glu Lys Tyr Lys Glu Leu Phe Glu Trp
                325                 330                 335
Met Leu Glu Ser Gly Phe Glu Glu Arg Ile Lys Glu Arg Gly Leu Leu
            340                 345                 350
Ile Lys Gly Trp Ala Pro Gln Val Leu Ile Leu Ser His Pro Ser Val
        355                 360                 365
Gly Gly Phe Leu Thr His Cys Gly Trp Asn Ser Thr Leu Glu Gly Ile
    370                 375                 380
Thr Ser Gly Ile Pro Leu Ile Thr Trp Pro Leu Phe Gly Asp Gln Phe
385                 390                 395                 400
Cys Asn Gln Lys Leu Val Val Gln Val Leu Lys Ala Gly Val Ser Ala
                405                 410                 415
Gly Val Glu Glu Val Met Lys Trp Gly Glu Glu Asp Lys Ile Gly Val
            420                 425                 430
Leu Val Asp Lys Glu Gly Val Lys Lys Ala Val Glu Glu Leu Met Gly
        435                 440                 445
Asp Ser Asp Asp Ala Lys Glu Arg Arg Arg Arg Val Lys Glu Leu Gly
    450                 455                 460
Glu Leu Ala His Lys Ala Val Glu Lys Gly Gly Ser Ser His Ser Asn
465                 470                 475                 480
Ile Thr Leu Leu Leu Gln Asp Ile Met Gln Leu Ala Gln Phe Lys Asn
                485                 490                 495
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<210> 5
<211> 495
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT73C6

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

```
Val Lys Glu Val Met Lys Trp Gly Glu Glu Glu Lys Ile Gly Val Leu
            420                 425                 430
Val Asp Lys Glu Gly Val Lys Lys Ala Val Glu Glu Leu Met Gly Glu
        435                 440                 445
Ser Asp Asp Ala Lys Glu Arg Arg Arg Arg Ala Lys Glu Leu Gly Glu
    450                 455                 460
Ser Ala His Lys Ala Val Glu Glu Gly Gly Ser Ser His Ser Asn Ile
465                 470                 475                 480
Thr Phe Leu Leu Gln Asp Ile Met Gln Leu Ala Gln Ser Asn Asn
                485                 490                 495


<210> 6
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> rf85C2

<400> 6
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
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            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> 7
<211> 495
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT73C5

<400> 7

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Pro Phe Met Ala Gln Gly His Met Ile Pro Met Val Asp Ile Ala Arg
            20                  25                  30
Leu Leu Ala Gln Arg Gly Val Ile Ile Thr Ile Val Thr Thr Pro His
        35                  40                  45
Asn Ala Ala Arg Phe Lys Asn Val Leu Asn Arg Ala Ile Glu Ser Gly
    50                  55                  60
Leu Pro Ile Asn Leu Val Gln Val Lys Phe Pro Tyr Leu Glu Ala Gly
65                  70                  75                  80
Leu Gln Glu Gly Gln Glu Asn Ile Asp Ser Leu Asp Thr Met Glu Arg
                85                  90                  95
Met Ile Pro Phe Phe Lys Ala Val Asn Phe Leu Glu Glu Pro Val Gln
            100                 105                 110
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Lys Leu Ile Glu Glu Met Asn Pro Arg Pro Ser Cys Leu Ile Ser Asp
        115                 120                 125
Phe Cys Leu Pro Tyr Thr Ser Lys Ile Ala Lys Lys Phe Asn Ile Pro
    130                 135                 140
Lys Ile Leu Phe His Gly Met Gly Cys Phe Cys Leu Leu Cys Met His
145                 150                 155                 160
Val Leu Arg Lys Asn Arg Glu Ile Leu Asp Asn Leu Lys Ser Asp Lys
                165                 170                 175
Glu Leu Phe Thr Val Pro Asp Phe Pro Asp Arg Val Glu Phe Thr Arg
            180                 185                 190
Thr Gln Val Pro Val Glu Thr Tyr Val Pro Ala Gly Asp Trp Lys Asp
        195                 200                 205
Ile Phe Asp Gly Met Val Glu Ala Asn Glu Thr Ser Tyr Gly Val Ile
    210                 215                 220
Val Asn Ser Phe Gln Glu Leu Glu Pro Ala Tyr Ala Lys Asp Tyr Lys
225                 230                 235                 240
Glu Val Arg Ser Gly Lys Ala Trp Thr Ile Gly Pro Val Ser Leu Cys
                245                 250                 255
Asn Lys Val Gly Ala Asp Lys Ala Glu Arg Gly Asn Lys Ser Asp Ile
            260                 265                 270
Asp Gln Asp Glu Cys Leu Lys Trp Leu Asp Ser Lys Lys His Gly Ser
        275                 280                 285
Val Leu Tyr Val Cys Leu Gly Ser Ile Cys Asn Leu Pro Leu Ser Gln
    290                 295                 300
Leu Lys Glu Leu Gly Leu Gly Leu Glu Glu Ser Gln Arg Pro Phe Ile
305                 310                 315                 320
Trp Val Ile Arg Gly Trp Glu Lys Tyr Lys Glu Leu Val Glu Trp Phe
                325                 330                 335
Ser Glu Ser Gly Phe Glu Asp Arg Ile Gln Asp Arg Gly Leu Leu Ile
            340                 345                 350
Lys Gly Trp Ser Pro Gln Met Leu Ile Leu Ser His Pro Ser Val Gly
        355                 360                 365
Gly Phe Leu Thr His Cys Gly Trp Asn Ser Thr Leu Glu Gly Ile Thr
    370                 375                 380
Ala Gly Leu Pro Leu Leu Thr Trp Pro Leu Phe Ala Asp Gln Phe Cys
385                 390                 395                 400
Asn Glu Lys Leu Val Val Glu Val Leu Lys Ala Gly Val Arg Ser Gly
                405                 410                 415
Val Glu Gln Pro Met Lys Trp Gly Glu Glu Glu Lys Ile Gly Val Leu
            420                 425                 430
Val Asp Lys Glu Gly Val Lys Lys Ala Val Glu Glu Leu Met Gly Glu
        435                 440                 445
Ser Asp Asp Ala Lys Glu Arg Arg Arg Arg Ala Lys Glu Leu Gly Asp
    450                 455                 460
Ser Ala His Lys Ala Val Glu Glu Gly Gly Ser Ser His Ser Asn Ile
465                 470                 475                 480
Ser Phe Leu Leu Gln Asp Ile Met Glu Leu Ala Glu Pro Asn Asn
                485                 490                 495
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<210> 8
<211> 495
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT73E1

<400> 8
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Phe Pro Leu Met Ala Gln Gly His Leu Val Pro Met Val Asp Ile Ala
            20                  25                  30
Arg Ile Leu Ala Gln Arg Gly Ala Thr Val Thr Ile Ile Thr Thr Pro
        35                  40                  45
Tyr His Ala Asn Arg Val Arg Pro Val Ile Ser Arg Ala Ile Ala Thr
    50                  55                  60
Asn Leu Lys Ile Gln Leu Leu Glu Leu Gln Leu Arg Ser Thr Glu Ala
65                  70                  75                  80
Gly Leu Pro Glu Gly Cys Glu Ser Phe Asp Gln Leu Pro Ser Phe Glu
                85                  90                  95
Tyr Trp Lys Asn Ile Ser Thr Ala Ile Asp Leu Leu Gln Gln Pro Ala
            100                 105                 110
Glu Asp Leu Leu Arg Glu Leu Ser Pro Pro Pro Asp Cys Ile Ile Ser
        115                 120                 125
Asp Phe Leu Phe Pro Trp Thr Thr Asp Val Ala Arg Arg Leu Asn Ile
    130                 135                 140
Pro Arg Leu Val Phe Asn Gly Pro Gly Cys Phe Tyr Leu Leu Cys Ile
145                 150                 155                 160
His Val Ala Ile Thr Ser Asn Ile Leu Gly Glu Asn Glu Pro Val Ser
                165                 170                 175
Ser Asn Thr Glu Arg Val Val Leu Pro Gly Leu Pro Asp Arg Ile Glu
            180                 185                 190
Val Thr Lys Leu Gln Ile Val Gly Ser Ser Arg Pro Ala Asn Val Asp
        195                 200                 205
Glu Met Gly Ser Trp Leu Arg Ala Val Glu Ala Glu Lys Ala Ser Phe
    210                 215                 220
Gly Ile Val Val Asn Thr Phe Glu Glu Leu Glu Pro Glu Tyr Val Glu
225                 230                 235                 240
Glu Tyr Lys Thr Val Lys Asp Lys Lys Met Trp Cys Ile Gly Pro Val
                245                 250                 255
Ser Leu Cys Asn Lys Thr Gly Pro Asp Leu Ala Glu Arg Gly Asn Lys
            260                 265                 270
Ala Ala Ile Thr Glu His Asn Cys Leu Lys Trp Leu Asp Glu Arg Lys
        275                 280                 285
Leu Gly Ser Val Leu Tyr Val Cys Leu Gly Ser Leu Ala Arg Ile Ser
    290                 295                 300
Ala Ala Gln Ala Ile Glu Leu Gly Leu Gly Leu Glu Ser Ile Asn Arg
305                 310                 315                 320
Pro Phe Ile Trp Cys Val Arg Asn Glu Thr Asp Glu Leu Lys Thr Trp
                325                 330                 335
Phe Leu Asp Gly Phe Glu Glu Arg Val Arg Asp Arg Gly Leu Ile Val
            340                 345                 350
His Gly Trp Ala Pro Gln Val Leu Ile Leu Ser His Pro Thr Ile Gly
        355                 360                 365
Gly Phe Leu Thr His Cys Gly Trp Asn Ser Thr Ile Glu Ser Ile Thr
    370                 375                 380
Ala Gly Val Pro Met Ile Thr Trp Pro Phe Phe Ala Asp Gln Phe Leu

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

<210> 9
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT98

<400> 9
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Leu Gly Tyr Gly His Leu Ser Ala Phe Leu Glu Leu Ala Lys Ser Leu
20 25 30
Ser Arg Arg Asn Phe His Ile Tyr Phe Cys Ser Thr Ser Val Asn Leu
35 40 45
Asp Ala Ile Lys Pro Lys Leu Pro Ser Ser Ser Ser Ser Asp Ser Ile
50 55 60
Gln Leu Val Glu Leu Cys Leu Pro Ser Ser Pro Asp Gln Leu Pro Pro
65 70 75 80
His Leu His Thr Thr Asn Ala Leu Pro Pro His Leu Met Pro Thr Leu
85 90 95
His Gln Ala Phe Ser Met Ala Ala Gln His Phe Ala Ala Ile Leu His
100 105 110
Thr Leu Ala Pro His Leu Leu Ile Tyr Asp Ser Phe Gln Pro Trp Ala
115 120 125
Pro Gln Leu Ala Ser Ser Leu Asn Ile Pro Ala Ile Asn Phe Asn Thr
130 135 140
Thr Gly Ala Ser Val Leu Thr Arg Met Leu His Ala Thr His Tyr Pro
145 150 155 160
Ser Ser Lys Phe Pro Ile Ser Glu Phe Val Leu His Asp Tyr Trp Lys
165 170 175
Ala Met Tyr Ser Ala Ala Gly Gly Ala Val Thr Lys Lys Asp His Lys
180 185 190
Ile Gly Glu Thr Leu Ala Asn Cys Leu His Ala Ser Cys Ser Val Ile
195 200 205
Leu Ile Asn Ser Phe Arg Glu Leu Glu Glu Lys Tyr Met Asp Tyr Leu
210 215 220
Ser Val Leu Leu Asn Lys Lys Val Val Pro Val Gly Pro Leu Val Tyr
225 230 235 240

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Glu Pro Asn Gln Asp Gly Glu Asp Glu Gly Tyr Ser Ser Ile Lys Asn
                245                 250                 255
Trp Leu Asp Lys Lys Glu Pro Ser Ser Thr Val Phe Val Ser Phe Gly
            260                 265                 270
Ser Glu Tyr Phe Pro Ser Lys Glu Glu Met Glu Glu Ile Ala His Gly
        275                 280                 285
Leu Glu Ala Ser Glu Val His Phe Ile Trp Val Val Arg Phe Pro Gln
    290                 295                 300
Gly Asp Asn Thr Ser Ala Ile Glu Asp Ala Leu Pro Lys Gly Phe Leu
305                 310                 315                 320
Glu Arg Val Gly Glu Arg Gly Met Val Val Lys Gly Trp Ala Pro Gln
                325                 330                 335
Ala Lys Ile Leu Lys His Trp Ser Thr Gly Gly Phe Val Ser His Cys
            340                 345                 350
Gly Trp Asn Ser Val Met Glu Ser Met Met Phe Gly Val Pro Ile Ile
        355                 360                 365
Gly Val Pro Met His Leu Asp Gln Pro Phe Asn Ala Gly Leu Ala Glu
    370                 375                 380
Glu Ala Gly Val Gly Val Glu Ala Lys Arg Asp Ser Asp Gly Lys Ile
385                 390                 395                 400
Gln Arg Glu Glu Val Ala Lys Ser Ile Lys Glu Val Val Ile Glu Lys
                405                 410                 415
Thr Arg Glu Asp Val Arg Lys Lys Ala Arg Glu Met Gly Glu Ile Leu
            420                 425                 430
Arg Ser Lys Gly Asp Glu Lys Ile Asp Glu Leu Val Ala Glu Ile Ser
        435                 440                 445
Leu Leu Arg Lys Lys Ala Pro Cys Ser Ile
    450                 455
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<210> 10
<211> 1434
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT1495 gene sequence

<400> 10
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ccaaaactct ctcagaagct ctcctcccac gtggagctgg tggagctcaa cctaccgccc 180
tcgccggagc tccctccgca ccgccacacc accgccggcc ttccaccgca cctcatgttc 240
tcgctcaagc gagctttcga catggccgct cccgccttcg ccgccatcct ccgcgacctg 300
aacccggact tgctcatcta cgacttcctg cagccgtggg cggcggcgga ggctctgtcg 360
gcggatattc cggccgtgat gttcaaaagc acgggtgcgc tcatggcggc catggtcgcg 420
tacgagctga cgtttccgaa ctctgatttt ttctcgcttt tccctgagat tcgtctctcc 480
gagtgcgaga ttaaacagct gaagaacttg tttcaatgtt ctgtgaatga tgcgaaagac 540
aagcaaagga ttaagggatg ttatgagaga tcttgcggca tgattttggt gaaatctttc 600
agagaaatcg aaggcaaata tattgatttt ctctctactc tgctgggcaa gaaggttgtt 660
ccagttggtc cacttgttca acaaacagaa gacgacgtcg tatcaggaag ttttgacgaa 720
tggctaaatg gaaaagatag atcgtcttcc atactcgtgt ctttcggaag cgagttctac 780
ctgtccagag aagacatgga agagatcgcg catggcttag agctgagcca ggtgaacttc 840
atatgggtcg tcaggtttcc ggcgggagga gagagaaaca cgacaaaggt ggaagaagaa 900
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ctgccaaaag ggtttctaga gagagttaga gagagaggga tggtggtgga gggctgggcg 960
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gaccagccgc tgaattcccg gctggtcgag cggctcggcg tcggcgtagt ggtggagaga 1140
gacggccgcc tccggggaga ggtggagaga gttgtcagag aggtggtggt ggagaaaagt 1200
ggagagagag tgaggaagaa ggtggaggag tttgcagaga tcatgaagaa gaaaaaagac 1260
aatgaagaga tggacgtagt cgtggaagag ttggtgacgc tctgcaggaa gaagaagaag 1320
gaggaggatt tacagagtaa ttattggtgc agaaccgcca ttgatgacca ttgttctgaa 1380
gtcgtgaaga ttgaagatgc tgcagcagcc gacgaggagc ctctttgcaa ataa 1434

<210> 11
<211> 1383
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT1817 gene sequence

<400> 11
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atcccaacga aaacgctaac caaattgcag cctttcaatc tctttccaga tctcattacc 180
tttgtcccca tcactgttcc tcatgttgat ggtctccctc ttggagctga gactactgct 240
gatgtttctc acccttcaca gctcagtctc atcatgactg ctatggattg cacccaaccc 300
gaaatcgagt gtcttcttcg agacataaaa cctgatgcca tcttcttcga tttcgcgcac 360
tgggtgccaa aattggcatg tggattgggc attaagtcga ttgattacag tgtctgttct 420
gcagtatcaa ttggttatgt tttgccccta ttaaggaaag tttgtggaca agatttatta 480
actgaagatg attttatgca gccatctcct ggctacccga gttccaccat caatcttcaa 540
gctcatgagg ctcgatattt tgcatctctg agccgctgga ggtttggcag tgatgtccct 600
ttctttagtc gccatcttac tgcacttaat gaatgcaatg ctttagcatt caggtcatgt 660
agggagattg aagggccttt tatagactat ccagaaagtg aattaaaaaa gcctgtgttg 720
ctttccggag cagtggatct acaaccgcca accacaactg tagaagaaag atgggcaaaa 780
tggctatcag ggttcaacac cgactcggtc gtatattgtg catttggaag tgagtgtacc 840
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tttgctgcac ttaaaccacc ttttggtgtt gactcggttg aagcagcctt gcctgaaggt 960
tttgaacaga gagttcaggg aagaggggtg gtctatgggg gatgggtcca acagcagctc 1020
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gatggatctt ttacaaagga aagtgtgtgg aaggcagtga agacagtgat ggatgaagag 1260
aatgaaactg ggaaagagtt cagagcgaac cgtgccaaga taagagagct attgctcgac 1320
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<210> 12
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT5914

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tcttcccctg caaatcttca aaacgtcaag ccaaaactcc cccatcacta ctctgattcc 180
attgaactcg tggagctcaa ccttccatcg tcgccggagc ttccccctca tatgcacacc 240
accaatggcc tccctttgca tttagttccc accctcgttg acgccttgga catggccgct 300
ccgcacttct ccgccatttt acaggaactg aatccagatt ttctcatatt cgacatcttc 360
caaccctggg cggctgaaat cgcttcctcc ttcggcgttc ctgctatttt gttgcttatc 420
gttggatctg ctataaccgc tttaggggtt cattttgtcc ggagctccgg tacggaattc 480
ccctttcccg agcttactaa atcattcaag aaggaggacg accgaaaacc tccaggagat 540
tccggcaacg atagaggaaa acggctattc aaatgtctgc tggacctgga acattcttca 600
gagactattt tggtgaacag ttttacagag atagagggca aatatatgga ctatctctcg 660
gtcttactga agaagaagat ccttccgatt ggtcctttgg ttcagaaaat tggctccgat 720
gacgatgaat cgggaatcct ccggtggctt gacaagaaga aaccgaattc aactgtgtac 780
gtttcgttcg ggagtgagta ctatttgagc aaagaagaca tagcagagct tgcgcatggt 840
ctggaaatca gcggcgtcaa tttcatctgg attgttcggt ttccaaaggg agagaaaatc 900
gccattgaag aggcattacc agatgaattt cttgaaagag tcggagagag aggcgtcgtc 960
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tctcactgcg gatggaactc tgtgctggag agtctggtgc tcggcgtgcc gatcatatcc 1080
ctgccgatac acctcgaaca gccgtggaac gccttggtag cggagcacgt cggcgtttgt 1140
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aaagaagtgg tggttgagga aacaggagcg gaactgagaa gcaaagcaag agtaattagt 1260
gaaatcttga aaaataaaga agctgaaaca atacaagatt tggtggctga gcttcaccgg 1320
ctttctgacg caagaagagc ttgttga 1347

<210> 13
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT8468 gene sequence

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ccaagaaata ttcagagact yccccaaatc ccgccggact tagcttcttt catagatttg 180
gtggccattc ccttgccgag actcgacgac gatctgttgc tagaatctgc agaggccact 240
tctgatattc cgatcgacaa gattcagtat ttgaagcgag ccgtcgacct cctccgccac 300
cccttcaaga agtttgtcgc cgaacaatcg ccggactggg tcgtcgttga ttttcatgct 360
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tcggccatct gtttgcttta tcttggacct ccagacgtgt attcgaagga tcctcagatc 480
atggcacgaa tatctcccgt taccatgacg gtgccgccgg agtgggtcgg ttttccgtcc 540
gccgtagcct acaacttgca tgaggcgacg gtcatgtact ctgctctcta tgaaacaaat 600
gggtctggaa taagcgactg cgagaggatt cgccggctcg tcctttcctg tcaagccgtg 660
gccattcgaa gctgcgagga gattgaaggc gaatacctta ggttatgtaa gaaactgatt 720
ccaccgcagg ggattgccgt cggcttgctt ccgccggaaa agccaccaaa atcagatcac 780
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gaccagccgc tgaactcaaa gcttttggtg gagaaaggga tggcgcttga gatcagaagg 1200
aacggttctg atggatggtt tagtagagaa gacatcgccg gaactttgag agaagctatg 1260
cggtcgtctg aggaaggcgg gcagctgagg agccgtgcaa aagaggcggc ggccatcgtt 1320

ggagatgaga agctgcagtg ggaacaatac ttcggcgcgt tcgtacagtt tctgagggac 1380
aagtcttga 1389

<210> 14
<211> 1395
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT10391 gene sequence

<400> 14
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atgaacgccg agaaacgaag caccaaaatc ttgatgctcc catggctggc tcacggccac 120
atatctccat acttcgagct cgccaagagg ctcaccaaga aaaactgcca cgtttacttg 180
tgttcttcgc ctgtaaatct ccaaggcatc aagccgaaac tctctgaaaa ttactcttcc 240
tccattgaac ttgtggagct tcatcttcca tctctccccg accttcctcc ccatatgcac 300
acgaccaaag gcatccctct acatctacaa tccaccctca tcaaagcctt cgacatggcc 360
gcccctgatt tttccgacct gttgcagaaa ctcgagccgg atctcgtcat ttccgatctc 420
ttccagccat gggcagttca attagcgtcg tctcggaaca ttcccgtcgt caatttcgtt 480
gtcaccggag tcgctgttct tagtcgtttg gctcacgtgt tttgcaactc cgttaaggaa 540
ttccctttcc cggaactcga tctaaccgac cattggatct ccaagagccg ccgcaaaacg 600
tccgacgaat taggtcgcga gtgcgcgatg cgatttttca actgcatgaa acaatcttca 660
aacatcactc tagccaacac tttccccgag ttcgaagaaa aatacatcga ttatctctct 720
tcctcgttta agaaaaagat tcttccggtt gctcctctag ttcctgaaat cgacgcagac 780
gacgagaaat cggaaattat cgagtggctt gacaagaaga aaccgaaatc gactgtttac 840
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accattgaag aggctttacc agaaggattt ctcgagagag taggggacag gggagtgatt 1020
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gcggaggcga agagagacgt tgaagggagc gttcagagag aagaggtggc gaaggccatt 1260
aaagaggtgg tgtttgagaa gaaggggggg gttctgagtg gaaaagcaag agagatcagc 1320
gaggccttga gaaagaggga aggggaaatc atagaggaat tggttgctga gtttcaccag 1380
ctctgtgaag cttga 1395

<210> 15
<211> 496
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT1576 amino acid sequence

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

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His Val Leu Gln Leu Gln Phe Pro Cys Lys Glu Gly Gly Leu Pro Glu
65                  70                  75                  80
Gly Cys Glu Asn Val Asp Leu Leu Pro Ser Leu Ala Ser Ile Pro Arg
                85                  90                  95
Phe Tyr Arg Ala Ala Ser Asp Leu Leu Tyr Glu Pro Ser Glu Lys Leu
            100                 105                 110
Phe Glu Glu Leu Ile Pro Arg Pro Thr Cys Ile Ile Ser Asp Met Cys
        115                 120                 125
Leu Pro Trp Thr Met Arg Ile Ala Leu Lys Tyr His Val Pro Arg Leu
    130                 135                 140
Val Phe Tyr Ser Leu Ser Cys Phe Phe Leu Leu Cys Met Arg Ser Leu
145                 150                 155                 160
Lys Asn Asn Leu Ala Leu Ile Ser Ser Lys Ser Asp Ser Glu Phe Val
                165                 170                 175
Thr Phe Ser Asp Leu Pro Asp Pro Val Glu Phe Leu Lys Ser Glu Leu
            180                 185                 190
Pro Lys Ser Thr Asp Glu Asp Leu Val Lys Phe Ser Tyr Glu Met Gly
        195                 200                 205
Glu Ala Asp Arg Gln Ser Tyr Gly Val Ile Leu Asn Leu Phe Glu Glu
    210                 215                 220
Met Glu Pro Lys Tyr Leu Ala Glu Tyr Glu Lys Glu Arg Glu Ser Pro
225                 230                 235                 240
Glu Arg Val Trp Cys Val Gly Pro Val Ser Leu Cys Asn Asp Asn Lys
                245                 250                 255
Leu Asp Lys Ala Glu Arg Gly Asn Lys Ala Ser Ile Asp Glu Tyr Lys
            260                 265                 270
Cys Ile Arg Trp Leu Asp Gly Gln Gln Pro Ser Ser Val Val Tyr Val
        275                 280                 285
Ser Leu Gly Ser Leu Cys Asn Leu Val Thr Ala Gln Ile Ile Glu Leu
    290                 295                 300
Gly Leu Gly Leu Glu Ala Ser Lys Lys Pro Phe Ile Trp Val Ile Arg
305                 310                 315                 320
Arg Gly Asn Ile Thr Glu Glu Leu Gln Lys Trp Leu Val Glu Tyr Asp
                325                 330                 335
Phe Glu Glu Lys Ile Lys Gly Arg Gly Leu Val Ile Leu Gly Trp Ala
            340                 345                 350
Pro Gln Val Leu Ile Leu Ser His Pro Ala Ile Gly Cys Phe Leu Thr
        355                 360                 365
His Cys Gly Trp Asn Ser Ser Ile Glu Gly Ile Ser Ala Gly Val Pro
    370                 375                 380
Met Val Thr Trp Pro Leu Phe Ala Asp Gln Val Phe Asn Glu Lys Leu
385                 390                 395                 400
Ile Val Gln Ile Leu Arg Ile Gly Val Ser Val Gly Thr Glu Thr Thr
                405                 410                 415
Met Asn Trp Gly Glu Glu Glu Glu Lys Gly Val Val Val Lys Arg Glu
            420                 425                 430
Lys Val Arg Glu Ala Ile Glu Ile Val Met Asp Gly Asp Glu Arg Glu
        435                 440                 445
Glu Arg Arg Glu Arg Cys Lys Glu Leu Ala Glu Thr Ala Lys Arg Ala
    450                 455                 460
Ile Glu Glu Gly Gly Ser Ser His Arg Asn Leu Thr Met Leu Ile Glu
465                 470                 475                 480
Asp Ile Ile His Gly Gly Gly Leu Ser Tyr Glu Lys Gly Ser Cys Arg
                485                 490                 495
```

<210> 16
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT SK98

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

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


<210> 17
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT430 amino acid sequence

<400> 17
Met Glu Gln Ala His Asp Leu Leu His Val Leu Leu Phe Pro Tyr Pro
 1               5                  10                  15
Ala Lys Gly His Ile Lys Pro Phe Leu Cys Leu Ala Glu Leu Leu Cys
            20                  25                  30
Asn Ala Gly Leu Asn Val Thr Phe Leu Asn Thr Asp Tyr Asn His Arg
        35                  40                  45
Arg Leu His Asn Leu His Leu Leu Ala Ala Cys Phe Pro Ser Leu His
    50                  55                  60
Phe Glu Ser Ile Ser Asp Gly Leu Gln Pro Asp Gln Pro Arg Asp Ile
65                  70                  75                  80
Leu Asp Pro Lys Phe Tyr Ile Ser Ile Cys Gln Val Thr Lys Pro Leu
                85                  90                  95
Phe Arg Glu Leu Leu Leu Ser Tyr Lys Arg Thr Ser Ser Val Gln Thr
            100                 105                 110
Gly Arg Pro Pro Ile Thr Cys Val Ile Thr Asp Val Ile Phe Arg Phe
        115                 120                 125
Pro Ile Asp Val Ala Glu Glu Leu Asp Ile Pro Val Phe Ser Phe Cys
    130                 135                 140
Thr Phe Ser Ala Arg Phe Met Phe Leu Tyr Phe Trp Ile Pro Lys Leu
145                 150                 155                 160
Ile Glu Asp Gly Gln Leu Pro Tyr Pro Asn Gly Asn Ile Asn Gln Lys
                165                 170                 175
Leu Tyr Gly Val Ala Pro Glu Ala Glu Gly Leu Leu Arg Cys Lys Asp
            180                 185                 190
Leu Pro Gly His Trp Ala Phe Ala Asp Glu Leu Lys Asp Asp Gln Leu
        195                 200                 205
Asn Phe Val Asp Gln Thr Thr Ala Ser Leu Arg Ser Ser Gly Leu Ile
    210                 215                 220
```

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

<210> 18
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT1697

<400> 18

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

```
                85                  90                  95
Ile Gln Ser Leu Asn Asp Gly Arg Trp Pro Ile Thr Cys Ile Ile Thr
            100                 105                 110
Asp Ile Met Leu Ser Ser Pro Ile Glu Val Ala Glu Glu Phe Gly Ile
        115                 120                 125
Pro Val Ile Ala Phe Cys Pro Cys Ser Ala Arg Tyr Leu Ser Ile His
    130                 135                 140
Phe Phe Ile Pro Lys Leu Val Glu Glu Gly Gln Ile Pro Tyr Ala Asp
145                 150                 155                 160
Asp Asp Pro Ile Gly Glu Ile Gln Gly Val Pro Leu Phe Glu Gly Leu
                165                 170                 175
Leu Arg Arg Asn His Leu Pro Gly Ser Trp Ser Asp Lys Ser Ala Asp
            180                 185                 190
Ile Ser Phe Ser His Gly Leu Ile Asn Gln Thr Leu Ala Ala Gly Arg
        195                 200                 205
Ala Ser Ala Leu Ile Leu Asn Thr Phe Asp Glu Leu Glu Ala Pro Phe
    210                 215                 220
Leu Thr His Leu Ser Ser Ile Phe Asn Lys Ile Tyr Thr Ile Gly Pro
225                 230                 235                 240
Leu His Ala Leu Ser Lys Ser Arg Leu Gly Asp Ser Ser Ser Ser Ala
                245                 250                 255
Ser Ala Leu Ser Gly Phe Trp Lys Glu Asp Arg Ala Cys Met Ser Trp
            260                 265                 270
Leu Asp Cys Gln Pro Pro Arg Ser Val Val Phe Val Ser Phe Gly Ser
        275                 280                 285
Thr Met Lys Met Lys Ala Asp Glu Leu Arg Glu Phe Trp Tyr Gly Leu
    290                 295                 300
Val Ser Ser Gly Lys Pro Phe Leu Cys Val Leu Arg Ser Asp Val Val
305                 310                 315                 320
Ser Gly Gly Glu Ala Ala Glu Leu Ile Glu Gln Met Ala Glu Glu Glu
                325                 330                 335
Gly Ala Gly Gly Lys Leu Gly Met Val Val Glu Trp Ala Ala Gln Glu
            340                 345                 350
Lys Val Leu Ser His Pro Ala Val Gly Gly Phe Leu Thr His Cys Gly
        355                 360                 365
Trp Asn Ser Thr Val Glu Ser Ile Ala Ala Gly Val Pro Met Met Cys
    370                 375                 380
Trp Pro Ile Leu Gly Asp Gln Pro Ser Asn Ala Thr Trp Ile Asp Arg
385                 390                 395                 400
Val Trp Lys Ile Gly Val Glu Arg Asn Asn Arg Glu Trp Asp Arg Leu
                405                 410                 415
Thr Val Glu Lys Met Val Arg Ala Leu Met Glu Gly Gln Lys Arg Val
            420                 425                 430
Glu Ile Gln Arg Ser Met Glu Lys Leu Ser Lys Leu Ala Asn Glu Lys
        435                 440                 445
Val Val Arg Gly Gly Leu Ser Phe Asp Asn Leu Glu Val Leu Val Glu
    450                 455                 460
Asp Ile Lys Lys Leu Lys Pro Tyr Lys Phe
465                 470


<210> 19
<211> 452
<212> PRT
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<213> Artificial Sequence

<220>
<223> UGT11789

<400> 19
Met Asp Ala Lys Glu Glu Ser Leu Lys Val Phe Met Leu Pro Trp Leu
 1               5                  10                  15
Ala His Gly His Ile Ser Pro Tyr Leu Glu Leu Ala Lys Arg Leu Ala
            20                  25                  30
Lys Arg Lys Phe Leu Val Tyr Phe Cys Ser Thr Pro Val Asn Leu Glu
        35                  40                  45
Ala Ile Lys Pro Lys Leu Ser Lys Ser Tyr Ser Asp Ser Ile Gln Leu
    50                  55                  60
Met Glu Val Pro Leu Glu Ser Thr Pro Glu Leu Pro Pro His Tyr His
65                  70                  75                  80
Thr Ala Lys Gly Leu Pro Pro His Leu Met Pro Lys Leu Met Asn Ala
                85                  90                  95
Phe Lys Met Val Ala Pro Asn Leu Glu Ser Ile Leu Lys Thr Leu Asn
            100                 105                 110
Pro Asp Leu Leu Ile Val Asp Ile Leu Leu Pro Trp Met Leu Pro Leu
        115                 120                 125
Ala Ser Ser Leu Lys Ile Pro Met Val Phe Phe Thr Ile Phe Gly Ala
    130                 135                 140
Met Ala Ile Ser Phe Met Ile Tyr Asn Arg Thr Val Ser Asn Glu Leu
145                 150                 155                 160
Pro Phe Pro Glu Phe Glu Leu His Glu Cys Trp Lys Ser Lys Cys Pro
                165                 170                 175
Tyr Leu Phe Lys Asp Gln Ala Glu Ser Gln Ser Phe Leu Glu Tyr Leu
            180                 185                 190
Asp Gln Ser Ser Gly Val Ile Leu Ile Lys Thr Ser Arg Glu Ile Glu
        195                 200                 205
Ala Lys Tyr Val Asp Phe Leu Thr Ser Ser Phe Thr Lys Lys Val Val
    210                 215                 220
Thr Thr Gly Pro Leu Val Gln Gln Pro Ser Ser Gly Glu Asp Glu Lys
225                 230                 235                 240
Gln Tyr Ser Asp Ile Ile Glu Trp Leu Asp Lys Lys Glu Pro Leu Ser
                245                 250                 255
Thr Val Leu Val Ser Phe Gly Ser Glu Tyr Tyr Leu Ser Lys Glu Glu
            260                 265                 270
Met Glu Glu Ile Ala Tyr Gly Leu Glu Ser Ala Ser Glu Val Asn Phe
        275                 280                 285
Ile Trp Ile Val Arg Phe Pro Met Gly Gln Glu Thr Glu Val Glu Ala
    290                 295                 300
Ala Leu Pro Glu Gly Phe Ile Gln Arg Ala Gly Glu Arg Gly Lys Val
305                 310                 315                 320
Val Glu Gly Trp Ala Pro Gln Ala Lys Ile Leu Ala His Pro Ser Thr
                325                 330                 335
Gly Gly His Val Ser His Asn Gly Trp Ser Ser Ile Val Glu Cys Leu
            340                 345                 350
Met Ser Gly Val Pro Val Ile Gly Ala Pro Met Gln Leu Asp Gly Pro
        355                 360                 365
Ile Val Ala Arg Leu Val Glu Glu Ile Gly Val Gly Leu Glu Ile Lys
    370                 375                 380

```
Arg Asp Glu Glu Gly Arg Ile Thr Arg Gly Glu Val Ala Asp Ala Ile
385                 390                 395                 400
Lys Thr Val Ala Val Gly Lys Thr Gly Glu Asp Phe Arg Arg Lys Ala
                405                 410                 415
Lys Lys Ile Ser Ser Ile Leu Lys Met Lys Asp Glu Glu Glu Val Asp
            420                 425                 430
Thr Leu Ala Met Glu Leu Val Arg Leu Cys Gln Met Lys Arg Gly Gln
        435                 440                 445
Glu Ser Gln Asp
    450
```

<210> 20
<211> 520
<212> PRT
<213> Artificial Sequence

<220>
<223> CYP1798 amino acid sequence

<400> 20

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

```
            260                 265                 270
Gly Ile Ile Asn Lys Arg Gln Lys Ala Met Glu Glu Gly Glu Ala Gly
        275                 280                 285
Gln Ser Asp Leu Leu Gly Ile Leu Met Glu Ser Asn Ser Asn Glu Ile
    290                 295                 300
Gln Gly Glu Gly Asn Asn Lys Glu Asp Gly Met Ser Ile Glu Asp Val
305                 310                 315                 320
Ile Glu Glu Cys Lys Val Phe Tyr Ile Gly Gly Gln Glu Thr Thr Ala
                325                 330                 335
Arg Leu Leu Ile Trp Thr Met Ile Leu Leu Ser Ser His Thr Glu Trp
            340                 345                 350
Gln Glu Arg Ala Arg Thr Glu Val Leu Lys Val Phe Gly Asn Lys Lys
        355                 360                 365
Pro Asp Phe Asp Gly Leu Ser Arg Leu Lys Val Val Thr Met Ile Leu
    370                 375                 380
Asn Glu Val Leu Arg Leu Tyr Pro Pro Ala Ser Met Leu Thr Arg Ile
385                 390                 395                 400
Ile Gln Lys Glu Thr Arg Val Gly Lys Leu Thr Leu Pro Ala Gly Val
                405                 410                 415
Ile Leu Ile Met Pro Ile Ile Leu Ile His Arg Asp His Asp Leu Trp
            420                 425                 430
Gly Glu Asp Ala Asn Glu Phe Lys Pro Glu Arg Phe Ser Lys Gly Val
        435                 440                 445
Ser Lys Ala Ala Lys Val Gln Pro Ala Phe Phe Pro Phe Gly Trp Gly
    450                 455                 460
Pro Arg Ile Cys Met Gly Gln Asn Phe Ala Met Ile Glu Ala Lys Met
465                 470                 475                 480
Ala Leu Ser Leu Ile Leu Gln Arg Phe Ser Phe Glu Leu Ser Ser Ser
                485                 490                 495
Tyr Val His Ala Pro Thr Val Val Phe Thr Thr Gln Pro Gln His Gly
            500                 505                 510
Ala His Ile Val Leu Arg Lys Leu
        515                 520
```

<210> 21
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> EPH1 epoxide hydrolase

<400> 21

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

Gly Asp Leu Val Gly Leu Leu Asp Gln Leu Gly Val Asp Gln Val Phe
                85                  90                  95
Leu Val Gly Asp Trp Gly Ala Met Met Ala Trp Tyr Phe Cys Leu Phe
            100                 105                 110
Arg Pro Asp Arg Val Lys Ala Leu Val Asn Leu Ser Val His Phe Thr
        115                 120                 125
Pro Arg Asn Pro Ala Ile Ser Pro Leu Asp Gly Phe Arg Leu Met Leu
    130                 135                 140
Gly Asp Asp Phe Tyr Val Cys Lys Phe Gln Glu Pro Gly Val Ala Glu
145                 150                 155                 160
Ala Asp Phe Gly Ser Val Asp Thr Ala Thr Met Phe Lys Lys Phe Leu
                165                 170                 175
Thr Met Arg Asp Pro Arg Pro Pro Ile Ile Pro Asn Gly Phe Arg Ser
            180                 185                 190
Leu Ala Thr Pro Glu Ala Leu Pro Ser Trp Leu Thr Glu Glu Asp Ile
        195                 200                 205
Asp Tyr Phe Ala Ala Lys Phe Ala Lys Thr Gly Phe Thr Gly Gly Phe
    210                 215                 220
Asn Tyr Tyr Arg Ala Ile Asp Leu Thr Trp Glu Leu Thr Ala Pro Trp
225                 230                 235                 240
Ser Gly Ser Glu Ile Lys Val Pro Thr Lys Phe Ile Val Gly Asp Leu
                245                 250                 255
Asp Leu Val Tyr His Phe Pro Gly Val Lys Glu Tyr Ile His Gly Gly
            260                 265                 270
Gly Phe Lys Lys Asp Val Pro Phe Leu Glu Glu Val Val Val Met Glu
        275                 280                 285
Gly Ala Ala His Phe Ile Asn Gln Glu Lys Ala Asp Glu Ile Asn Ser
    290                 295                 300
Leu Ile Tyr Asp Phe Ile Lys Gln Phe
305                 310


<210> 22
<211> 316
<212> PRT
<213> Artificial Sequence

<220>
<223> EPH2 epoxide hydrolase

<400> 22
Met Glu Lys Ile Glu His Thr Thr Ile Ser Thr Asn Gly Ile Asn Met
 1               5                  10                  15
His Val Ala Ser Ile Gly Ser Gly Pro Ala Val Leu Phe Leu His Gly
            20                  25                  30
Phe Pro Glu Leu Trp Tyr Ser Trp Arg His Gln Leu Leu Phe Leu Ser
        35                  40                  45
Ser Met Gly Tyr Arg Ala Ile Ala Pro Asp Leu Arg Gly Phe Gly Asp
    50                  55                  60
Thr Asp Ala Pro Pro Ser Pro Ser Ser Tyr Thr Ala His His Ile Val
65                  70                  75                  80
Gly Asp Leu Val Gly Leu Leu Asp Gln Leu Gly Ile Asp Gln Val Phe
                85                  90                  95
Leu Val Gly His Asp Trp Gly Ala Met Met Ala Trp Tyr Phe Cys Leu

```
            100                 105                 110
Phe Arg Pro Asp Arg Val Lys Ala Leu Val Asn Leu Ser Val His Phe
        115                 120                 125
Leu Arg Arg His Pro Ser Ile Lys Phe Val Asp Gly Phe Arg Ala Leu
    130                 135                 140
Leu Gly Asp Asp Phe Tyr Phe Cys Gln Phe Gln Glu Pro Gly Val Ala
145                 150                 155                 160
Glu Ala Asp Phe Gly Ser Val Asp Val Ala Thr Met Leu Lys Lys Phe
                165                 170                 175
Leu Thr Met Arg Asp Pro Arg Pro Pro Met Ile Pro Lys Glu Lys Gly
            180                 185                 190
Phe Arg Ala Leu Glu Thr Pro Asp Pro Leu Pro Ala Trp Leu Thr Glu
        195                 200                 205
Glu Asp Ile Asp Tyr Phe Ala Gly Lys Phe Arg Lys Thr Gly Phe Thr
    210                 215                 220
Gly Gly Phe Asn Tyr Tyr Arg Ala Phe Asn Leu Thr Trp Glu Leu Thr
225                 230                 235                 240
Ala Pro Trp Ser Gly Ser Glu Ile Lys Val Ala Ala Lys Phe Ile Val
                245                 250                 255
Gly Asp Leu Asp Leu Val Tyr His Phe Pro Gly Ala Lys Glu Tyr Ile
            260                 265                 270
His Gly Gly Gly Phe Lys Lys Asp Val Pro Leu Leu Glu Glu Val Val
        275                 280                 285
Val Val Asp Gly Ala Ala His Phe Ile Asn Gln Glu Arg Pro Ala Glu
    290                 295                 300
Ile Ser Ser Leu Ile Tyr Asp Phe Ile Lys Lys Phe
305                 310                 315


<210> 23
<211> 316
<212> PRT
<213> Artificial Sequence

<220>
<223> EPH3 epoxide hydrolase

<400> 23
Met Asp Gln Ile Glu His Ile Thr Ile Asn Thr Asn Gly Ile Lys Met
 1               5                  10                  15
His Ile Ala Ser Val Gly Thr Gly Pro Val Val Leu Leu Leu His Gly
            20                  25                  30
Phe Pro Glu Leu Trp Tyr Ser Trp Arg His Gln Leu Leu Tyr Leu Ser
        35                  40                  45
Ser Val Gly Tyr Arg Ala Ile Ala Pro Asp Leu Arg Gly Tyr Gly Asp
    50                  55                  60
Thr Asp Ser Pro Ala Ser Pro Thr Ser Tyr Thr Ala Leu His Ile Val
65                  70                  75                  80
Gly Asp Leu Val Gly Ala Leu Asp Glu Leu Gly Ile Glu Lys Val Phe
                85                  90                  95
Leu Val Gly His Asp Trp Gly Ala Ile Ile Ala Trp Tyr Phe Cys Leu
            100                 105                 110
Phe Arg Pro Asp Arg Ile Lys Ala Leu Val Asn Leu Ser Val Gln Phe
        115                 120                 125
```

```
Ile Pro Arg Asn Pro Ala Ile Pro Phe Ile Glu Gly Phe Arg Thr Ala
    130                 135                 140
Phe Gly Asp Asp Phe Tyr Met Cys Arg Phe Gln Val Pro Gly Glu Ala
145                 150                 155                 160
Glu Glu Asp Phe Ala Ser Ile Asp Thr Ala Gln Leu Phe Lys Thr Ser
                165                 170                 175
Leu Cys Asn Arg Ser Ser Ala Pro Pro Cys Leu Pro Lys Glu Ile Gly
            180                 185                 190
Phe Arg Ala Ile Pro Pro Pro Glu Asn Leu Pro Ser Trp Leu Thr Glu
        195                 200                 205
Glu Asp Ile Asn Tyr Tyr Ala Ala Lys Phe Lys Gln Thr Gly Phe Thr
    210                 215                 220
Gly Ala Leu Asn Tyr Tyr Arg Ala Phe Asp Leu Thr Trp Glu Leu Thr
225                 230                 235                 240
Ala Pro Trp Thr Gly Ala Gln Ile Gln Val Pro Val Lys Phe Ile Val
                245                 250                 255
Gly Asp Ser Asp Leu Thr Tyr His Phe Pro Gly Ala Lys Glu Tyr Ile
            260                 265                 270
His Asn Gly Gly Phe Lys Lys Asp Val Pro Leu Leu Glu Glu Val Val
        275                 280                 285
Val Val Lys Asp Ala Cys His Phe Ile Asn Gln Glu Arg Pro Gln Glu
    290                 295                 300
Ile Asn Ala His Ile His Asp Phe Ile Asn Lys Phe
305                 310                 315


<210> 24
<211> 316
<212> PRT
<213> Artificial Sequence

<220>
<223> EPH4 epoxide hydrolase

<400> 24
Met Glu Asn Ile Glu His Thr Thr Val Gln Thr Asn Gly Ile Lys Met
 1               5                  10                  15
His Val Ala Ala Ile Gly Thr Gly Pro Pro Val Leu Leu Leu His Gly
            20                  25                  30
Phe Pro Glu Leu Trp Tyr Ser Trp Arg His Gln Leu Leu Tyr Leu Ser
        35                  40                  45
Ser Ala Gly Tyr Arg Ala Ile Ala Pro Asp Leu Arg Gly Tyr Gly Asp
    50                  55                  60
Thr Asp Ala Pro Pro Ser Pro Ser Ser Tyr Thr Ala Leu His Ile Val
65                  70                  75                  80
Gly Asp Leu Val Gly Leu Leu Asp Val Leu Gly Ile Glu Lys Val Phe
                85                  90                  95
Leu Ile Gly His Asp Trp Gly Ala Ile Ile Ala Trp Tyr Phe Cys Leu
            100                 105                 110
Phe Arg Pro Asp Arg Ile Lys Ala Leu Val Asn Leu Ser Val Gln Phe
        115                 120                 125
Phe Pro Arg Asn Pro Thr Thr Pro Phe Val Lys Gly Phe Arg Ala Val
    130                 135                 140
Leu Gly Asp Gln Phe Tyr Met Val Arg Phe Gln Glu Pro Gly Lys Ala
```

```
145                 150                 155                 160
Glu Glu Glu Phe Ala Ser Val Asp Ile Arg Glu Phe Phe Lys Asn Val
                165                 170                 175
Leu Ser Asn Arg Asp Pro Gln Ala Pro Tyr Leu Pro Asn Glu Val Lys
            180                 185                 190
Phe Glu Gly Val Pro Pro Pro Ala Leu Ala Pro Trp Leu Thr Pro Glu
        195                 200                 205
Asp Ile Asp Val Tyr Ala Asp Lys Phe Ala Glu Thr Gly Phe Thr Gly
    210                 215                 220
Gly Leu Asn Tyr Tyr Arg Ala Phe Asp Arg Thr Trp Glu Leu Thr Ala
225                 230                 235                 240
Pro Trp Thr Gly Ala Arg Ile Gly Val Pro Val Lys Phe Ile Val Gly
                245                 250                 255
Asp Leu Asp Leu Thr Tyr His Phe Pro Gly Ala Gln Lys Tyr Ile His
            260                 265                 270
Gly Glu Gly Phe Lys Lys Ala Val Pro Gly Leu Glu Glu Val Val Val
        275                 280                 285
Met Glu Asp Thr Ser His Phe Ile Asn Gln Glu Arg Pro His Glu Ile
    290                 295                 300
Asn Ser His Ile His Asp Phe Phe Ser Lys Phe Cys
305                 310                 315


<210> 25
<211> 325
<212> PRT
<213> Artificial Sequence

<220>
<223> EPH5 epoxide hydrolase

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


<210> 26
<211> 316
<212> PRT
<213> Artificial Sequence

<220>
<223> EPH6 epoxide hydrolase

<400> 26
Met Glu Lys Ile Glu His Thr Ile Ile Thr Thr Asn Gly Ile Asn Met
 1               5                  10                  15
His Val Ala Ser Ile Gly Thr Gly Pro Ala Val Leu Phe Leu His Gly
            20                  25                  30
Phe Pro Glu Leu Trp Tyr Ser Trp Arg His Gln Leu Leu Ser Phe Ser
        35                  40                  45
Ser Leu Gly Tyr Arg Ala Ile Ala Pro Asp Leu Arg Gly Tyr Gly Asp
    50                  55                  60
Ser Asp Ala Pro Pro Ser Pro Ser Ser Tyr Thr Val Phe His Ile Val
65                  70                  75                  80
Gly Asp Leu Val Gly Leu Leu Asp Gln Leu Gly Ile Asp Gln Val Phe
                85                  90                  95
Leu Val Gly His Asp Trp Gly Ala Ser Ile Ala Trp Tyr Phe Ser Leu
            100                 105                 110
Leu Arg Pro Asp Arg Ile Lys Ala Leu Val Asn Leu Ser Val Gln Tyr
        115                 120                 125
Phe Pro Arg Asn Pro Ala Arg Asn Thr Val Glu Ala Leu Arg Ala Leu
    130                 135                 140
Phe Gly Asp Asp Tyr Tyr Val Cys Arg Phe Gln Glu Pro Gly Glu Met
145                 150                 155                 160
Glu Glu Asp Phe Ala Ser Ile Asp Thr Ala Val Ile Phe Lys Ile Phe
                165                 170                 175
Leu Ser Ser Arg Asp Pro Arg Pro Pro Cys Ile Pro Lys Ala Val Gly
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            180                 185                 190
Phe Arg Ala Phe Pro Val Pro Asp Ser Leu Pro Ser Trp Leu Ser Glu
        195                 200                 205
Glu Asp Ile Ser Tyr Tyr Ala Ser Lys Phe Ser Lys Lys Gly Phe Thr
    210                 215                 220
Gly Gly Leu Asn Tyr Tyr Arg Ala Leu Ala Leu Asn Trp Glu Leu Thr
225                 230                 235                 240
Ala Pro Trp Thr Gly Thr Gln Ile Lys Val Pro Thr Lys Phe Ile Val
                245                 250                 255
Gly Asp Leu Asp Leu Thr Tyr His Ile Pro Gly Ser Lys Glu Tyr Ile
            260                 265                 270
His Lys Gly Gly Phe Glu Arg Asp Val Pro Ser Leu Glu Glu Val Val
        275                 280                 285
Val Ile Glu Gly Ala Ala His Phe Val Asn Gln Glu Arg Pro Glu Glu
    290                 295                 300
Ile Ser Lys His Ile Tyr Asp Phe Ile Lys Lys Phe
305                 310                 315


<210> 27
<211> 316
<212> PRT
<213> Artificial Sequence

<220>
<223> EPH7 epoxide hydrolase

<400> 27
Met Asp Ala Ile Glu His Arg Thr Val Ser Val Asn Gly Ile Asn Met
 1               5                  10                  15
His Val Ala Glu Lys Gly Glu Gly Pro Val Val Leu Leu Leu His Gly
            20                  25                  30
Phe Pro Glu Leu Trp Tyr Ser Trp Arg His Gln Ile Leu Ala Leu Ser
        35                  40                  45
Ser Leu Gly Tyr Arg Ala Val Ala Pro Asp Leu Arg Gly Tyr Gly Asp
    50                  55                  60
Thr Asp Ala Pro Gly Ser Ile Ser Ser Tyr Thr Cys Phe His Ile Val
65                  70                  75                  80
Gly Leu Val Ala Leu Val Glu Ser Leu Gly Val Asp Arg Val Phe Val
                85                  90                  95
Val Ala His Asp Trp Gly Ala Met Ile Ala Trp Cys Leu Cys Leu Phe
            100                 105                 110
Arg Pro Glu Met Val Lys Ala Phe Val Cys Leu Ser Val Pro Phe Arg
        115                 120                 125
Gln Arg Asn Pro Lys Met Lys Pro Val Gln Ser Met Arg Ala Phe Phe
    130                 135                 140
Gly Asp Asp Tyr Tyr Ile Cys Arg Phe Gln Asn Pro Gly Glu Ile Glu
145                 150                 155                 160
Glu Glu Met Ala Gln Val Gly Ala Arg Glu Val Leu Arg Gly Ile Leu
                165                 170                 175
Thr Ser Arg Arg Pro Gly Pro Pro Ile Leu Pro Lys Gly Gln Ala Phe
            180                 185                 190
Arg Ala Arg Pro Gly Ala Ser Thr Ala Leu Pro Ser Trp Leu Ser Glu
        195                 200                 205
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Lys Asp Leu Ser Phe Phe Ala Ser Lys Tyr Asp Gln Lys Gly Phe Thr
    210                 215                 220
Gly Pro Leu Asn Tyr Tyr Arg Ala Met Asp Leu Asn Trp Glu Leu Thr
225                 230                 235                 240
Ala Ser Trp Thr Gly Val Gln Val Lys Val Pro Val Lys Tyr Ile Val
                245                 250                 255
Gly Asp Val Asp Met Val Phe Thr Thr Pro Gly Val Lys Glu Tyr Val
            260                 265                 270
Asn Gly Gly Gly Phe Lys Lys Asp Val Pro Phe Leu Gln Glu Val Val
        275                 280                 285
Ile Met Glu Gly Val Gly His Phe Ile Asn Gln Glu Lys Pro Glu Glu
    290                 295                 300
Ile Ser Ser His Ile His Asp Phe Ile Ser Arg Phe
305                 310                 315


<210> 28
<211> 311
<212> PRT
<213> Artificial Sequence

<220>
<223> EPH8 epoxide hydrolase

<400> 28
Met Asp Gln Ile Gln His Lys Phe Ile Asp Ile Arg Gly Leu Lys Leu
 1               5                  10                  15
His Ile Ala Glu Ile Gly Thr Gly Ser Pro Ala Val Val Phe Leu His
            20                  25                  30
Gly Phe Pro Glu Ile Trp Tyr Ser Trp Arg His Gln Met Val Ala Ala
        35                  40                  45
Ala Ala Val Gly Tyr Arg Ala Ile Ser Pro Asp Leu Arg Gly Tyr Gly
    50                  55                  60
Phe Ser Asp Pro His Pro Gln Pro Gln Asn Ala Ser Phe Asp Asp Phe
65                  70                  75                  80
Val Glu Asp Thr Leu Ala Ile Leu Asp Phe Leu His Ile Pro Lys Ala
                85                  90                  95
Phe Leu Val Gly Lys Asp Phe Gly Ser Trp Pro Val Tyr Leu Phe Ser
            100                 105                 110
Leu Val His Pro Thr Arg Val Ala Gly Ile Val Ser Leu Gly Val Pro
        115                 120                 125
Phe Leu Pro Pro Asn Pro Lys Arg Tyr Arg Asp Leu Pro Glu Gly Phe
    130                 135                 140
Tyr Ile Phe Arg Trp Lys Glu Ser Gly Arg Ala Glu Ala Asp Phe Gly
145                 150                 155                 160
Arg Phe Asp Val Lys Thr Val Leu Arg Arg Ile Tyr Thr Leu Phe Ser
                165                 170                 175
Arg Ser Glu Ile Pro Ile Ala Glu Lys Asp Gln Glu Ile Met Asp Met
            180                 185                 190
Val Asp Glu Ser Thr Pro Pro Pro Pro Trp Leu Thr Asp Glu Asp Leu
        195                 200                 205
Ala Ala Tyr Ala Thr Ala Tyr Glu His Ser Gly Phe Glu Ser Ala Leu
    210                 215                 220
Gln Val Pro Tyr Arg Arg Arg His Gln Glu Leu Gly Met Ser Asn Pro
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225 230 235 240
Arg Val Asp Val Pro Val Leu Leu Ile Ile Gly Gly Lys Asp Tyr Phe
245 250 255
Leu Lys Phe Pro Gly Ile Glu Asp Tyr Ile Lys Ser Glu Lys Met Arg
260 265 270
Glu Ile Val Pro Asp Leu Glu Val Ala Asp Leu Ala Asp Gly Thr His
275 280 285
Phe Met Gln Glu Gln Phe Pro Ala Gln Val Asn His Leu Leu Ile Ser
290 295 300
Phe Leu Gly Lys Arg Asn Thr
305 310

<210> 29
<211> 317
<212> PRT
<213> Artificial Sequence

<220>
<223> EH1 epoxide hydrolase 1

<400> 29
Met Asp Ala Ile Glu His Arg Thr Val Ser Val Asn Gly Ile Asn Met
1 5 10 15
His Val Ala Glu Lys Gly Glu Gly Pro Val Val Leu Leu Leu His Gly
20 25 30
Phe Pro Glu Leu Trp Tyr Ser Trp Arg His Gln Ile Leu Ala Leu Ser
35 40 45
Ser Leu Gly Tyr Arg Ala Val Ala Pro Asp Leu Arg Gly Tyr Gly Asp
50 55 60
Thr Asp Ala Pro Gly Ser Ile Ser Ser Tyr Thr Cys Phe His Ile Val
65 70 75 80
Gly Asp Leu Val Ala Leu Val Glu Ser Leu Gly Met Asp Arg Val Phe
85 90 95
Val Val Ala His Asp Trp Gly Ala Met Ile Ala Trp Cys Leu Cys Leu
100 105 110
Phe Arg Pro Glu Met Val Lys Ala Phe Val Cys Leu Ser Val Pro Phe
115 120 125
Arg Gln Arg Asn Pro Lys Met Lys Pro Val Gln Ser Met Arg Ala Phe
130 135 140
Phe Gly Asp Asp Tyr Tyr Ile Cys Arg Phe Gln Asn Pro Gly Glu Ile
145 150 155 160
Glu Glu Glu Met Ala Gln Val Gly Ala Arg Glu Val Leu Arg Gly Ile
165 170 175
Leu Thr Ser Arg Arg Pro Gly Pro Pro Ile Leu Pro Lys Gly Gln Ala
180 185 190
Phe Arg Ala Arg Pro Gly Ala Ser Thr Ala Leu Pro Ser Trp Leu Ser
195 200 205
Glu Lys Asp Leu Ser Phe Phe Ala Ser Lys Tyr Asp Gln Lys Gly Phe
210 215 220
Thr Gly Pro Leu Asn Tyr Tyr Arg Ala Met Asp Leu Asn Trp Glu Leu
225 230 235 240
Thr Ala Ser Trp Thr Gly Val Gln Val Lys Val Pro Val Lys Tyr Ile
245 250 255

Val Gly Asp Val Asp Met Val Phe Thr Thr Pro Gly Val Lys Glu Tyr
            260                 265                 270
Val Asn Gly Gly Gly Phe Lys Lys Asp Val Pro Phe Leu Gln Glu Val
        275                 280                 285
Val Ile Met Glu Gly Val Gly His Phe Ile Asn Gln Glu Lys Pro Glu
    290                 295                 300
Glu Ile Ser Ser His Ile His Asp Phe Ile Ser Lys Phe
305                 310                 315


<210> 30
<211> 316
<212> PRT
<213> Artificial Sequence

<220>
<223> EH2 epoxide hydrolase

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

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        275                 280                 285
Val Val Lys Asp Ala Cys His Phe Ile Asn Gln Glu Arg Pro Gln Glu
    290                 295                 300
Ile Asn Ala His Ile His Asp Phe Ile Asn Lys Phe
305                 310                 315
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<210> 31
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> CYP533 (sequence) 3

<400> 31
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gctctcatcc ggctattatc tggaagattc agctctcaac agaagagact gccacctgaa 120
gccggtggcg cctggccact gatcggccat ctccatctcc taggtgggtc ggaacctgca 180
cataaaacct tggcgaacat ggcggacgcc tacggaccag tttttacgtt gaaactgggc 240
atgcatacag ctttggttat gagcagttgg gaaatagcga gagagtgctt tactaaaaac 300
gacagaatct ttgcctcccg ccccatagtc actgcctcaa agcttctcac ctataaccat 360
accatgtttg ggttcagcca atatggtcca ttctggcgcc atatgcgcaa aatagccacg 420
cttcaactcc tctcaaacca ccgcctcgag cagctccaac acatcagaat atcggaggtc 480
cagacttcga ttaagaaact gtacgagttg tgggtcaaca gcagaaataa tggaggcgag 540
aaagtgttgg tggagatgaa gacgtggttc ggaggcataa ccttgaacac catattcagg 600
atggtggtcg gaaagcgatt ctcgactgct ttcgaaggca gtggtggcga acggtatcgg 660
aaggcgttga gggattctct tgaatggttt ggggcattcg ttccgtcaga ttcattcccg 720
tttttaagat ggttggattt gggaggatat gagaaggcga tgaagaagac ggcgagtgtg 780
ctggacgagg tgcttgataa atggctcaaa gagcatcagc agaggagaaa ctccggtgaa 840
ctggagacgg aggagcacga cttcatgcac gtgatgctgt ctattgttaa ggatgatgaa 900
gaactatccg gctacgatgc cgatacagtc acaaaagcta catgtttgaa tttaatagtt 960
ggtggattcg acactacaca agtaactatg acatgggctc tttctttgct tctcaacaat 1020
gaagaggtat taaaaaaggc ccaacttgaa ctagacgaac aagttggaag agagaggttt 1080
gtggaagagt ccgatgttaa aaatctgtta tatctccagg ccatcgtgaa ggaaactttg 1140
cgtttgtacc cttcagcgcc aatctcgaca tttcatgagg ccatggaaga ttgcactgtt 1200
tctggctacc acatcttttc agggacgcgt ttgatggtga atcttcaaaa gcttcaaaga 1260
gatccacttg catgggagga tccatgtgac tttcgaccgg agagatttct gacaactcat 1320
aaggatttcg atcttagagg acatagtcct caattgatac catttgggag tggtcgaaga 1380
atatgccctg gcatctcgtt tgccattcaa gttttgcatc ttacgcttgc aaatctactt 1440
catgggtttg acattggaag gccatctcat gaaccaatcg atatgcagga gagtaaagga 1500
ctaacgagta ttaaaacaac tccacttgag gttgttttag ctccacgcct tgctgctcaa 1560
gtttatgagt ga                                                    1572

<210> 32
<211> 1497
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CYP937 4

<400> 32
atgccgatcg cagaaggtgc agtctctgat ttgtttggtc gcccactctt ctttgcacta 60

tatgattggt tcttagagca tggatctgtt tataaacttg cctttggacc aaaagccttt 120
gttgttgtat cagatcccat tgtggcaaga tatattcttc gagaaaatgc atttggttat 180
gacaagggag tgcttgctga tattttagaa ccgataatgg gtaaaggact aataccagct 240
gaccttggca cttggaagca gaggagacga gttattgctc caggattcca tgccttgtac 300
ttggaagcta tgaccaaagt atttgccaat tgttcagaac gatcaatatt gaaattggag 360
aagcttctag gagaaggtga actacaggag aataaaacca ttgagttgga tatggaagca 420
gagttttcaa gtttggctct tgatatcatt ggactcggtg ttttcaacta tgattttggt 480
tctgtaacca aagaatctcc ggtgattaag gctgtatatg ggactctttt tgaagcagag 540
catagatcga ctttctatat cccatattgg aaagtacctt tggcaaggtg gatagtccca 600
aggcagcgta aattccatgg tgaccttaag gttattaatg agtgtcttga tggcctaata 660
cgcaacgcaa gagaaacccg agacgaaacg gatgttgaga aattgcagca aagggactac 720
ttaaatctca aggatgccag tcttttgcgt ttcttagttg atatgcgggg agctgatgtt 780
gatgatcgcc agcttaggga cgatctgatg acgatgctta ttgctggcca tgaaacaact 840
gctgctgtgc ttacatgggc tgtttttttg cttgcacaaa atccttcaaa aatgaaaaaa 900
gcgcaagcag agattgattt ggttcttggc atggggaggc caacttttga atcatttaaa 960
gcattgaagt acatcagact tatcgttgca gagactcttc gtttgtttcc tcagcctcca 1020
ttgctgataa gacgagctct caaatcagat atattaccag gaggatacaa tggtgacaaa 1080
actggatatg caattcctgc agggactgac atcttcatct ctgtttacaa tctccacaga 1140
tctccctact tctgggataa tcctcaagaa tttgaaccag agagatttca agtaaagagg 1200
gcaagcgagg gaattgaagg atgggatggt ttcgacccat ctagaagccc tggagctcta 1260
tacccgaatg agattgtagc agacttttcc ttcttaccat ttggtggagg ccctagaaaa 1320
tgtgtgggag atcaatttgc tctaatggag tcaactatag cattggccat gttactgcag 1380
aagtttgatg tggagctaaa aggaagtcca gaatctgtag aactagttac tggagccaca 1440
atacatacca aaagtgggtt gtggtgcaaa ctgagaagaa gatcacaagt aaactga 1497

<210> 33
<211> 1563
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized DNA sequence encoding CYP17985

<400> 33
atggaaatgt cctcaagtgt cgcagccaca atcagtatct ggatggtcgt cgtatgtatc 60
gtaggtgtag gttggagagt cgtaaattgg gtttggttga gaccaaagaa attggaaaag 120
agattgagag aacaaggttt ggccggtaat tcttacagat tgttgttcgg tgacttgaag 180
gaaagagctg caatggaaga acaagcaaat tcaaagccta taaacttctc ccatgacatc 240
ggtccaagag ttttcccttc aatgtacaag accatccaaa actacggtaa aaactcctac 300
atgtggttag gtccataccc tagagtccac atcatggatc cacaacaatt gaagaccgtt 360
tttactttgg tctacgacat tcaaaagcca aatttgaacc ctttgattaa attcttgtta 420
gatggtatcg ttacacatga aggtgaaaag tgggctaagc acagaaagat tattaaccca 480
gcattccatt tggaaaagtt gaaggatatg atacctgctt tctttcactc atgtaatgaa 540
atcgtcaacg aatgggaaag attgatttca aaagaaggtt cctgcgaatt ggatgtaatg 600
ccttatttgc aaaatttggc cgctgacgcc atttcaagaa ccgcttttgg ttcttcatac 660
gaagaaggta aaatgatctt ccaattgttg aaggaattga ctgatttggt tgtcaaggta 720
gcttttggtg tttatattcc aggttggaga ttcttgccta caaagagtaa caacaaaatg 780
aaggaaatta atagaaaaat caagtctttg ttgttgggta tcattaacaa gagacaaaag 840
gcaatggaag aaggtgaagc cggtcaatct gatttgttgg gtatattaat ggaaagtaat 900
tctaacgaaa tccaaggtga aggtaataac aaggaagatg gcatgtctat tgaagacgtc 960
atcgaagagt gtaaggtatt ttatataggt ggtcaagaaa ctacagcaag attattgatc 1020
tggactatga tattgttgtc cagtcataca gaatggcaag aaagagccag aaccgaagtc 1080
ttgaaggtat ttggtaataa gaaaccagat ttcgacggtt tgtcaagatt gaaggtagtt 1140
actatgatct tgaacgaagt tttaagattg tacccacctg cttccatgtt gacaagaatc 1200

atccaaaagg aaacaagagt tggtaaatta accttgccag caggtgttat cttgataatg 1260
cctatcatct tgatacatag agatcacgac ttgtggggtg aagatgctaa cgagtttaaa 1320
ccagaaagat tcagtaaagg tgtttctaag gcagccaaag tccaaccagc ctttttccct 1380
tttggttggg gtcctagaat ttgcatgggt caaaacttcg ctatgatcga agctaagatg 1440
gcattgagtt tgatcttgca aagattttct ttcgaattgt cttcatccta cgttcatgca 1500
ccaactgtcg tcttcactac acaaccacaa cacggtgccc acatcgtttt gagaaagtta 1560
tga 1563

<210> 34
<211> 1602
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CYP1994

<400> 34
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ggtgtcattg ccattatttt cttccgtttt ctcgtcaaaa gagtcaccgg cgccggtgag 120
cgaaagggtc cgaagccgcc aaaagtagcc ggagggtggc ctctaattgg ccacctccct 180
ctcctcggag gacctgaact gccccatgtc aaactgggtg gtttggctga taaatatggt 240
ccaatcttct cgatccggct gggtgtccac tccgccgtcg tgataaacag ttgggaggcg 300
gcgaaacagt tattaaccaa ccatgacgtc gccgtctctt cccgccccca aatgctcggc 360
ggaaaactcc tgggctacaa ctacgccgtg tttggtttcg gaccctacgg ctcttactgg 420
cgcaacatgc gcaagataac cacgcaagag cttctatcca atagcagaat ccagctccta 480
agagacgttc gagcgtcaga agtgaaccaa ggcataaaag agctctacca gcactggaaa 540
gaaagaagag acggtcacga ccaagccttg gtggaactgc agcagtgggt cggggacttg 600
actatgaatc tgattctcgg agtcatcgcc gggaaaaggt tctttggagc tgcagcaacg 660
gtagacgagg aagaggcgcg acggagccat aaagcattga aggagttgtt acattatatg 720
gggctttttc tactgggtga tgctgttcca tatctaggat ggttggacgt cggcggccat 780
gtgaaggcga tgaagaaaac ttcaaaagaa ttggaccgta tgttaacaca gtggttggag 840
gagcacaaga aggaaggacc caagaaagat cataaagact tcatggacgt gatgctttca 900
gttctcaatg aaacatccga tgttctttca gataagaccc atggcttcga tgctgatacc 960
atcatcaaag ctacatgtat gacgatggtt ttaggaggga gtgatacgac ggcggtggtt 1020
gtgatatggg caatctcgct gctgctgaat aatcgccctg cgttgagaaa agtgcaagaa 1080
gaactggaag cccatatcgg ccgagacaga gaactggagg aatcggatct cggtaagcta 1140
gtgtatttgc aggcagtcgt gaaggagaca ttgcggctgt acggagccgg aggcctttc 1200
tttcgtgaaa ccacagagga tgtcaccatc gacggattcc atgtcgagaa agggacatgg 1260
ctgttcgtga acgtggggaa gatccacaga gatgggaagg tgtggccgga gccaacggag 1320
ttcaaaccgg agaggtttct gacgacccac aaagattttg atctgaaggg ccagcggttt 1380
gagctcatcc ctttcggggg aggaagaaga tcgtgccctg gaatgtcttt tgggctccaa 1440
atgctacagc ttattttggg taaactgctt caggcttttg atatatcgac gccgggggac 1500
gccgccgttg atatgaccgg atccattgga ctgacgaaca tgaaagccac tccattggaa 1560
gtgctcatca ccccgcgctt gcctctttcg ctttacgatt ga 1602

<210> 35
<211> 1236
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CYP20487

<400> 35

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tcatcagaag cctcaccccc ttctccacca aagcttccca tcttcggaca ccttctaaac 180
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ctcctccact tcggcagcaa gcccaccatc gtcgtctctt ctgccgaaat cgctcgcgat 300
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attctttacg gctccaaaga tttagccgca tctccttacg gcgaatactg gaggcagatg 420
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ctcgtcccca gagaatcaac ccaagacatc aggttgaggg ggtacgatat cagaggcggc 1200
acccgggtta tgatcaatgc atgggccatc ggaaga 1236

<210> 36
<211> 1614
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CYP27408

<400> 36
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gtttccattc tccactgggc ccatccgggc ggcccggctt ggggccgcta ctggtggcgc 180
cgccgccgca gcaattccac cgccgctgct attcccggcc cgagaggcct ccccctcgtc 240
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aaccccgacg tcgccaaaga gattctcaac agctccctct tcgccgaccg ccccgttaag 420
gagtccgctt actccttgat gttcaaccgc gccattgggt tcgccccta tggcctttac 480
tggcggaccc tccgccgcat cgcttcccac cacctcttct gccccaagca aatcaagtcc 540
tcccagtccc agcgccgcca aatcgcttcc caaatggtcg caatgttcgc aaaccgcgat 600
gccacacaga gcctctgcgt tcgcgactct ctcaagcggg cttctctcaa caacatgatg 660
ggctctgttt tcggccgagt ttacgacctc tctgactcgg ctaacaatga cgtccaagaa 720
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tcgccgtccg atcaaaacga cgccgtcgac ttgtcggagg tcctcaagct ctcctgcgag 1560
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<210> 37
<211> 1506
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CYP34049

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ggagtgagaa gggtgcctgg tccaccagct attccactgg tcggacatct tcccttgctg 180
gctaagtacg gcccagacgt tttctctgtc cttgccaccc aatatggccc tatcttcagg 240
ttccatatgg gtaggcagcc attgataatt atagcagacc ctgagctttg taaagaagct 300
ggtattaaga aattcaagga catcccaaat agaagtgtcc cttctccaat atcagcttcc 360
cctcttcatc agaagggtct tttcttcaca agggatgcaa gatggtcgac aatgcggaac 420
acgatattat cggtctatca gtcctcccat ctagcgagac taatacctac tatgcaatca 480
atcattgaaa ctgcaactca aaatctccat tcctctgtcc aggaagacat ccctttctcc 540
aatctctccc tcaaattgac caccgatgtg attggaacag cagccttcgg tgtcaacttt 600
gggctctcta atccacaggc aaccaaaact tgtgctacca acggccaaga caacaaaaat 660
gacgaagttt cagacttcat caatcaacac atctactcca caacgcagct caagatggat 720
ttatcaggtt ccttctcaat catacttgga ctgcttgtcc ctatactcca agaaccattt 780
agacaagtcc taaagagaat accattcacc atggactgga aagtggaccg gacaaatcag 840
aaattaagtg gtcggcttaa tgagattgtg gagaagagaa tgaagtgtaa cgatcaaggt 900
tcaaaagact tcttatcgct cattttgaga gcaagagagt cagagacagt atcaaggaat 960
gtcttcactc cagactacat cagtgcagtt acgtatgaac acctacttgc tgggtcggct 1020
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gatcttcatc agaagtttcc atatcttgat caggtgatta aagaggctat gaggttctac 1200
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cttccaaagg ggacatgggt ttggttagca cttggagttc ttgccaagga tccaaagaac 1320
tttccagaac cagataaatt caaaccagag aggtttgatc caaatgaaga agaggagaaa 1380
caaaggcatc cttatgcttt aatccccttt ggaattggtc ctcgagcatg cattggtaaa 1440
aaattcgccc ttcaggagtt gaagctctcg ttgattcatt tgtacaggaa gtttgtattt 1500
cggcat 1506

<210> 38
<211> 1566
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CYP396810

<400> 38
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gccggcggat ggccgatcat cggccacctg agactgctcg ggggttcgca acttccccat 180
gaaaccttgg gagccatggc cgacaagtat ggaccaatct tcagcatccg agttggtgtc 240

cacccatctc ttgttataag cagttgggaa gtggctaaag agtgctacac caccctcgac 300
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gcttttgggt tcaggcctta tgattccttt taccggagta tccgcaaaac catagcctcc 420
gaggtgctgt cgaaccgccg tctggagttg cagagacaca ttcgagtttc tgaggtgaag 480
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cttattgatg cggatgaatg gattggtaat attaatttga acgtgattct gatgatggtt 600
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cctggggcgg ggcttggggt tcagatgacg cagttggtgc tggcgagtct gattcattcg 1440
gtggaacttg gaactcgctc cgatgaagcg gtggacatgg ctgctaagtt tggactcaca 1500
atgtacagag ccacccctct tcaggctctc gtcaagccac gcctccaagc cggtgcttat 1560
tcatga 1566

<210> 39
<211> 1425
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CYP4112

<400> 39
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ggtcacgatc aaagaagtac cacagatagt ccacctggtt caagaggttt gccattgata 120
ggtgaaactt tgcaattcat ggctgctatt aattctttga acggtgtata cgatttcgtt 180
agaataagat gtttgagata cggtagatgc tttaagacaa gaatcttcgg tgaaacccat 240
gtttttgtct caactacaga atccgctaag ttgatcttga aggatggtgg tgaaaaattc 300
accaaaaagt acatcagatc aatcgctgaa ttggttggtg acagaagttt gttatgtgca 360
tctcatttgc aacacaagag attgagaggt ttgttgacta atttgttttc tgccacattc 420
ttggcttctt tcgtaactca attcgatgaa caaatcgttg aagcttttag atcatgggaa 480
tccggtagta ccataatcgt tttgaacgaa gcattgaaga tcacttgtaa ggccatgtgc 540
aaaatggtca tgtccttaga aagagaaaac gaattggaag ctttgcaaaa ggaattgggt 600
catgtttgtg aagctatgtt ggcatttcca tgcagattcc ctggtacaag atttcacaat 660
ggtttgaagg caagaagaag aatcattaaa gttgtcgaaa tggccattag agaaagaaga 720
agatctgaag ctcctagaga agatttcttg caaagattgt tgacagaaga aaaggaagaa 780
gaagacggtg gtggtgtttt aagtgatgcc gaaattggtg acaacatatt gacaatgatg 840
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ttcagatgga aggttataga ttccgactct tcaatcgaaa aatgggcttt gttctctaag 1380
ttgaagtcag gttgccctat cgtagttacc cacatcggtt cctaa 1425

<210> 40
<211> 1509
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CYP414912

<400> 40
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cttcactcga gaacaaacag cagcggcact tccaaacttc ctcccggacc gaaacccttg 120
ccgatcatcg gaagcctttt ggctctcggc cacgagcccc acaagtcttt ggctaatctc 180
gctaaatctc atggccctct tatgacctta aagctcggcc aaatcaccac cgtcgtagtt 240
tcctccgctg ccatggctaa gcaagttctc caaacgcacg accagtttct gtccagcagg 300
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ggggattatt tccctctgct gaagaagata gatcttcaag gaataaagag gagacagacc 720
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atggacgaaa agcttggcct cactctggag ttggcttttc ccctcacagc cttgcctgtc 1500
cttgtctaa 1509

<210> 41
<211> 1734
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CYP449113

<400> 41
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tcctccagag cctgcaactc agacgaaaac tcaagaattt tgagagattt cgtaacaaga 120
gaagttaacg ctttcttatg gttgtccttg atcactatca cagcagtttt gatcagtaaa 180
gttgtcggtt tgtttagatt gtggtctaag gcaaagcaat tgagaggtcc accttgtcca 240
tcattctacg gtcattctaa gatcatctca agacaaaatt tgactgattt gttatatgac 300

tcccacaaaa agtacggtcc agtagttaaa ttgtggttag gtcctatgca attgttagtc 360
tccgtaaagg aaccaagttt gttgaaggaa atattggtta aagctgagga taagttgcct 420
ttaacaggta gagcctttag attggctttc ggtagatctt cattatttgc atccagtttc 480
gaaaaggttc aaaacagaag acaaagattg gccgaaaagt tgaataagat cgcattccaa 540
agagccaaca tcattccaga aaaggccgta gcttgtttca tgggtagagt tcaagatttg 600
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ggttgcacat tgtttggtga cgccttctta ggttggtcta aggctacaat ctatgaagaa 720
ttgttgatga tgatcgctaa ggacgcatcc ttttgggcta gttatagagt taccccaatc 780
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tacgaaatta aattgcaatc cgagagtaag aatgattcta aaccatccag taacacctct 1680
gccagtcaaa tcgtcccaaa ctcaaaaatc gtattcgtaa gaagaaactc ataa 1734

<210> 42
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CYP549114

<400> 42
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ctcatcggag agacgattca actgagtcga cccagtgact ccctcgacgt tcacccttc 180
atccagaaaa aagttgaaag atacgggccg atcttcaaaa catgtctggc cggaaggccg 240
gtggtggtgt cggcggacgc agagttcaac aactacataa tgctgcagga aggaagagca 300
gtggaaatgt ggtatttgga tacgctctcc aaatttttcg gcctcgacac cgagtggctc 360
aaagctctgg gcctcatcca caagtacatc agaagcatta ctctcaatca cttcggcgcc 420
gaggccctgc gggagagatt tcttcctttt attgaagcat cctccatgga agcccttcac 480
tcctggtcta ctcaacctag cgtcgaagtc aaaaatgcct ccgctctcat ggtttttagg 540
acctcggtga ataagatgtt cggtgaggat gcgaagaagc tatcgggaaa tatccctggg 600
aagttcacga agcttctagg aggatttctc agtttaccac tgaattttcc cggcaccacc 660
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gatagattgg ctaatgtggg ccctgatgtg gaagatttct tggggcaagc ccttaaagat 780
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gatccagatg gaccaattac ttgggaagaa tacaaatcca tgacttttac attacaagtc 1020
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gatcttcaag taaaaggata cataatcccg gaaggatgga caataatgct tgtcaccgct 1140
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aaggacttgg actcaattac catccaaaag aacttcatgc cttttggggg aggcttaagg 1260
cattgtgctg gtgctgagta ctctaaagtc tacttgtgca ccttcttgca catcctctgt 1320
accaaatacc gatggaccaa acttggggga ggaaggattg caagagctca tatattgagt 1380
tttgaagatg ggttacatgt gaagttcaca cccaaggaat ga 1422

<210> 43
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CYP647915

<400> 43
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ccaagggttt atcctcatgt tcacctatgg atcaacaaat atgggaaaaa cttcattcag 120
tggaatggca acgtagctca gttgattgtt tcggatcctg acacgatcaa ggagatactc 180
caaaaccgag aacaagctgt tcccaaaata gatctcagcg gagatgcacg gaggatattc 240
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tacgctttcc acggggatct cctaagaaat atggggccaa ccatggtttc ctgtgctgag 360
gcaatggtgg aaaagtggaa gcatcatcaa ggcaaagagc ttgatttgtt cgaagagttt 420
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ataagtggtg aagcagataa ctatggtaat gattttcttg gattactttt gaaggcaaag 720
aatgagcctg accagaggca gaggatttct gttgatgatg tagtggatga atgcaaaaca 780
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tctctaagat tatatcctcc agccccgccc atgtcaagga aggttaaaaa ggaagtcaga 1020
ttggggaagc tggttctccc ccccaacatt caagtaagca tctcaactat tgcagttcat 1080
catgatactg caatatgggg tgaagatgcc catgtattca aaccagaaag attttctgaa 1140
ggaacagcta aagatatccc atcagctgca tacatcccat ttggctttgg tcctcgaaac 1200
tgcatcggca atatcttggc catcaacgaa actaagattg cactgtcgat gattctacaa 1260
cgattttctt tcaccatctc cccggcctac gtccacgcac ctttccagtt cctcactatc 1320
tgcccccaac acggggttca ggtaaagctt cagtccctat taagtgaaag gtga 1374

<210> 44
<211> 1590
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CYP760416

<400> 44
atggaagctg aatttggtgc cggtgctact atggtattat ccgttgtcgc aatcgtcttc 60
tttttcacat ttttacactt gtttgaatct ttctttttga agccagatag attgagatct 120
aagttgagaa agcaaggtat tggtggtcca tctccttcat ttttgttggg taatttgtca 180
gaaattaaat ccatcagagc tttgtcttca caagctaaga acgcagaaga tgcctctgct 240
ggtggtggtg gtggttccgc cagtatagct catggttgga cttcaaattt gtttcctcac 300
ttagaacaat ggagaaacag atatggtcca attttcgtat actccagtgg tacaatccaa 360
atcttgtgta tcacagaaat ggaaaccgtt aaggaaatct ctttgtcaac ctccttgagt 420

ttaggtaaac ctgctcattt gtctaaggat agaggtccat tgttaggttt gggtatctta 480
gcctcttcag gtcctatttg ggttcaccaa agaaagatca tcgctccaca attgtatttg 540
gataaagtaa agggtatgac ctcattgatg gttgaaagtg caaattctat gttaagatcc 600
tgggaaacta aagttgaaaa tcatggtggt caagccgaaa ttaacgtcga tggtgacttg 660
agagcattaa gtgccgatat catttctaag gcttgctttg gttcaaacta ttccgaaggt 720
gaagaaattt tcttgaagtt gagagcattg caagttgtca tgagtaaggg ttctattggt 780
atacctggtt ttagatacat accaactaaa aataacagag aaatgtggaa gttggaaaag 840
gaaatcgaat caatgatctt gaaggttgcc aacgaaagaa cacaacattc cagtcacgaa 900
caagatttgt tgcaaatgat tttggaaggt gcaaagtctt tgggtgaaga caataagagt 960
atgaacatat caagagacaa gtttattgtt gacaattgta agaacatcta tttcgctggt 1020
catgaaacta cagctataac cgcatcttgg tgcttgatgt tgttagctgc acaccctgat 1080
tggcaagcaa gagccagatc tgaagtttta caatgttgcg atgacagacc aatcgatgca 1140
gacacagtca aaaatatgaa gaccttgact atggtaattc aagaaacttt gagattgtac 1200
ccacctgctg tattcgttac aagacaagca ttagaagata tcagattcaa aaacatcaca 1260
ataccaaagg gtatgaactt tcatatacca atccctatgt tgcaacaaga cttccactta 1320
tggggtcctg atgcttgttc atttgaccca caaagattct ccaatggtgt cttaggtgca 1380
tgcaaaaacc cacaagccta tatgcctttt ggtgttggtc caagagtctg tgccggtcaa 1440
catttcgcta tgatcgaatt gaaagtcatc gtatcattgg ttttgtccag attcgaattt 1500
tctttgtcac cttcctacaa gcattcacca gccttcagat tagttgtcga accagaaaac 1560
ggtgtcatat tgcatgtcag aaagttgtga 1590

<210> 45
<211> 1554
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CYP822417

<400> 45
atggaagtgg atatcaatat cttcaccgtc ttttccttcg tattatgcac agtcttcctc 60
ttctttctat ccttcttgat cctcctcctc ctccgaacgc tcgccggaaa atccataacg 120
agctccgagt acacgccagt gtacggcacc gtctacggtc aggctttcta tttcaacaac 180
ctgtacgatc atctaacgga ggtggccaag agacatcgaa ccttccggct gcttgcgccg 240
gcatacagcg agatatacac gaccgatccg agaaacatcg agcatatgtt gaagacgaaa 300
ttcgataagt attcgaaagg aagcaaggat caagaaatcg ttggggatct gtttggagag 360
gggatatttg cagtcgatgg agataagtgg aagcagcaga ggaagctggc tagctatgaa 420
ttctcgacga ggattcttag ggattttagc tgctcggttt tcagacgaag tgctgctaaa 480
cttgttggag ttgtttcgga gttttccagc atgggtcggg tttttgatat ccaggatttg 540
ctaatgcggt gcgctttgga ctccattttc aaagtggggt tcggggttga tttgaattgc 600
ttggaggaat caagcaaaga agggagcgat ttcatgaaag ccttcgatga ttctagcgct 660
cagatttttt ggcgctatat cgatcccttc tggaaattga agagattgct taacatcggt 720
tccgaagctt cgtttaggaa caacataaaa accatagatg cttttgtgca ccagttgatc 780
agagacaaga gaaaattgct tcagcaaccg aatcacaaga atgacaaaga ggacatactt 840
tggaggtttc tgatggaaag tgagaaggat ccaacaagaa tgaatgatca atatctaagg 900
gatatagtcc tcaatttcat gttggctggc aaagattcaa gtggaggaac tctgtcctgg 960
ttcttctaca tgctatgcaa gaacccttta atacaggaaa aagttgcaga agaagtgagg 1020
caaattgttg cgtttgaagg ggaagaagtt gacatcaatt tgttcataca aaacttaact 1080
gattcagctc ttgacaaaat gcattatctt catgcagcat tgaccgagac tctgaggcta 1140
tatcctgcag tccctttgga tggaaggact gcagaaatag atgacattct tcctgatggc 1200
tataaactaa gaaaagggga tggagtatac tacatggcct attccatggg caggatgtcc 1260
tccctttggg gagaagatgc tgaagatttt aaacccgaaa gatggcttga aagtggaact 1320
tttcaacccg aatcaccttt caaattcatc gcttttcatg cgggtcctcg aatgtgtttg 1380
ggaaaagagt ttgcttatcg acaaatgaag atagtatctg ctgctttgct tcaatttttt 1440

cgattcaaag tagctgatac aacgaggaat gtgacttata ggatcatgct tacccttcac 1500
attgatggag gtctccctct tcttgcaatt ccgagaatta gaaaatttac ctaa 1554

<210> 46
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CYP872818

<400> 46
ttggatagtg gagttaaaag agtgaaacgg ctagttgaag agaaacggcg agcagaattg 60
tctgcccgga ttgcctctgg agaattcaca gtcgaaaaag ctggttttcc atctgtattg 120
aggagtggct tatcaaagat gggtgttccc agtgagattc tggacatatt atttggtttc 180
gttgatgctc aagaagaata tcccaagatt cccgaagcaa aaggatcagt aaatgcaatt 240
cgtagtgagg ccttcttcat acctctctat gagctttatc tcacatatgg tggaatattt 300
aggttgactt ttgggccaaa gtcattcttg atagtttctg atccttccat tgctaaacat 360
atactgaagg ataatccgag gaattattct aagggtatct tagctgaaat tctagagttt 420
gtcatgggga agggacttat accagctgac gagaagatat ggcgtgtacg aaggcgggct 480
atagtcccat ctttgcatct gaagtatgta ggtgctatga ttaatctttt tggagaagct 540
gcagataggc tttgcaagaa gctagatgct gcagcatctg atggggttga tgtggaaatg 600
gagtccctgt tctcccgttt gactttagat atcattggca aggcagtttt taactatgac 660
tttgattcac ttacaaatga cactggcata gttgaggctg tttacactgt gctaagagaa 720
gcagaggatc gcagtgttgc accaattcca gtatgggaaa ttccaatttg gaaggatatt 780
tcaccacggc aaaaaaaggt ctctaaagcc ctcaaattga tcaacgacac cctcgatcaa 840
ctaattgcta tatgcaagag gatggttgat gaggaggagc tgcagtttca tgaggaatac 900
atgaatgagc aagatccaag catccttcat ttccttttgg catcaggaga tgatgtttca 960
agcaagcagc ttcgtgatga cttgatgact atgcttatag ctgggcatga aacatctgct 1020
gcagttttaa catggacctt ttatcttctt tccaaggagc cgaggatcat gtccaagctc 1080
caggaggagg ttgattcagt ccttggggat cggtttccaa ctattgaaga tatgaagaac 1140
ctcaaatatg ccacacgaat aattaacgaa tccttgaggc tttacccaca gccaccagtt 1200
ttaatacgtc gatctcttga caatgatatg ctcgggaagt accccattaa aaagggtgag 1260
gacatattca tttctgtttg gaacttgcat cgcagtccaa aactctggga tgatgcggat 1320
aaatttaatc ctgaaaggtg gcctctggat ggacccaatc caaatgagac aaatcaaaat 1380
ttcagatatt tacctttttgg tggcggacca cggaaatgtg tgggagacat gtttgcttcg 1440
tacgagactg ttgtagcact tgcaatgctt gttcggcgat ttgacttcca aatggcactt 1500
ggagcacctc ctgtaaaaat gacaactgga gctacaattc acacaacaga tggattgaaa 1560
atgacagtta cacgaagaat gagacctcca atcataccca cattagagat gcctgcagtg 1620
gtcgttgact cgtctgtcgt ggactcgtcc gtcgccattt tgaaagaaga aacacaaatt 1680
ggttag 1686

<210> 47
<211> 1299
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CY1002019

<400> 47
cagttcctct cctggtcctc ccagtttggc aagaggttca tcttctggaa tgggatcgag 60
cccagaatgt gcctcaccga gaccgatttg atcaaagagc ttctctctaa gtacagcgcc 120
gtctccggta agtcatggct tcagcaacag ggctccaagc acttcatcgg ccgcggtctc 180

ttaatggcca acggccaaaa ctggtaccac cagcgtcaca tcgtcgcgcc ggccttcatg 240
ggagacagac tcaagagtta cgccgggtac atggtggaat gcacaaagga gatgcttcag 300
tcaattgaaa acgaggtcaa ctcggggcga tccgagttcg aaatcggtga gtatatgacc 360
agactcaccg ccgatataat atcacgaacc gagttcgaaa gcagctacga aaagggaaag 420
caaattttcc atttgctcac cgttttacag catctctgcg ctcaggcgag ccgccacctc 480
tgccttcctg gaagccggtt ttttccgagt aaatacaaca gagagataaa ggcattgaag 540
acgaaggtgg aggggttgtt aatggagata atacagagca gaagagactg tgtggaggtg 600
gggaggagca gttcgtatgg aaatgatctg ttgggaatgt tgctgaatga gatgcagaag 660
aagaaagatg ggaatgggtt gagcttgaat ttgcagatta taatggatga atgcaagacc 720
ttcttcttcg ccggccatga aaccactgct cttttgctca cttggactgt aatgttattg 780
gccagcaacc cttcttggca acacaaggtt cgagccgaag ttatggccgt ctgcaatgga 840
ggaactctct ctcttgaaca tctctccaag ctctctctgt tgagtatggt gataaatgaa 900
tcgttgaggc tatacccgcc agcaagtatt cttccaagaa tggcatttga agatataaag 960
ctgggagatc ttgagatccc aaaagggctg tcgatatgga tcccagtgct tgcaattcac 1020
cacagtgaag agctatgggg caaagatgca aatgagttca acccagaaag atttgcaaat 1080
tcaaaagcct tcacttcggg gagattcatt ccctttgctt ctggccctcg caactgcgtt 1140
ggccaatcat ttgctctcat ggaaaccaag atcattttgg ctatgctcat ctccaagttt 1200
tccttcacca tctctgacaa ttatcgccat gcacccgtgg tcgtcctcac tataaaaccc 1260
aaatacggag tccaagtttg cttgaagcct ttcaattaa 1299

<210> 48
<211> 1506
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding CYP10285

<400> 48
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aagctcatcc gtcgatccgg aggagttcgc aggaacttac cgccgagtcc gccctctctt 120
ccggttatcg gccacctcca tctcttgaaa aagccactcc accggacttt ccagaaactt 180
tccgccaaat atggtcctgt tatgtccctc cgcctcgggt ctcgcctcgc agtcattgta 240
tcgtcgtcgt cggcggtgga cgagtgtttc actaaaaacg acgtcgtgct cgccaaccgt 300
cctcgtttgc taattggcaa acacctcggc tacaactaca ctaccatggt tggggctccc 360
tacggcgacc actggcgtag cctccgccgc atcggtgccc tcgaaatctt ctcttcatct 420
cgcctcaaca aattcgccga catccgaagg gatgaagtag agggattgct tcgcaaactc 480
tcacgcaatt cgctccatca attctcgaaa gtggaagttc aatcggcctt gtcggagctg 540
acgttcaaca tctcgatgag aatggcggca gggaaacggt attacggaga tgacgtgacg 600
gacgaggaag aggcgagaaa gttcagagag ttaattaaac agatagtggc gctgggcgga 660
gtatcaaatc caggggattt cgtcccgatt ctgaattgga ttccgaacgg tttcgagagg 720
aagttgatcg agtgtgggaa gaagacggat gcgttcttgc aggggctgat cgaggaccac 780
cggagaaaga aggaagaggg taggaacacg atgatcgatc acctgctctc tctgcaagaa 840
tcggagcctg ctcactacgg agaccaaata atcaaaggat ttatactggt gttactgacg 900
gcgggggaccg atacatcggc cgtgacaatg gagtgggcgc tatctcatct cctgaacaat 960
cctgaagtgc taaagaaggc aagagatgag gtcgacactg aaattggaca agaacgactt 1020
gtcgaagaat cagacgtagt atctaagtta ccctatcttc aagggatcat ctccgagact 1080
ctccggctga atcccgccgc tccgatgttg ttgccccatt acgcctcgga cgactgcacg 1140
atatgtggat acgacgtgcc acgtgacaca atcgtaatgg tcaatgcatg ggccatacat 1200
agggatccaa acgaatggga ggagcccacg tgtttcagac cagaacgata tgaaaagtcg 1260
tcgtcggaag cggaggtaca caagtcggtg agtttcgggg tgggaaggcg agcttgtcct 1320
gggtctggca tggcgcagag ggtgatgggc ttgactttgg cggcactggt tcagtgcttc 1380
gagtgggaga gagttggaga agaagaagtg gacatgaacg aaggctcagg tgccacaatg 1440
cccaagatgg tgccattgga ggccatgtgc agagctcgtc ccatcgtcca caaccttctt 1500

tactga 1506

<210> 49
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of CYP5491

<400> 49
Met Trp Thr Val Val Leu Gly Leu Ala Thr Leu Phe Val Ala Tyr Tyr
 1               5                  10                  15
Ile His Trp Ile Asn Lys Trp Arg Asp Ser Lys Phe Asn Gly Val Leu
            20                  25                  30
Pro Pro Gly Thr Met Gly Leu Pro Leu Ile Gly Glu Thr Ile Gln Leu
        35                  40                  45
Ser Arg Pro Ser Asp Ser Leu Asp Val His Pro Phe Ile Gln Lys Lys
    50                  55                  60
Val Glu Arg Tyr Gly Pro Ile Phe Lys Thr Cys Leu Ala Gly Arg Pro
65                  70                  75                  80
Val Val Val Ser Ala Asp Ala Glu Phe Asn Asn Tyr Ile Met Leu Gln
                85                  90                  95
Glu Gly Arg Ala Val Glu Met Trp Tyr Leu Asp Thr Leu Ser Lys Phe
            100                 105                 110
Phe Gly Leu Asp Thr Glu Trp Leu Lys Ala Leu Gly Leu Ile His Lys
        115                 120                 125
Tyr Ile Arg Ser Ile Thr Leu Asn His Phe Gly Ala Glu Ala Leu Arg
    130                 135                 140
Glu Arg Phe Leu Pro Phe Ile Glu Ala Ser Ser Met Glu Ala Leu His
145                 150                 155                 160
Ser Trp Ser Thr Gln Pro Ser Val Glu Val Lys Asn Ala Ser Ala Leu
                165                 170                 175
Met Val Phe Arg Thr Ser Val Asn Lys Met Phe Gly Glu Asp Ala Lys
            180                 185                 190
Lys Leu Ser Gly Asn Ile Pro Gly Lys Phe Thr Lys Leu Leu Gly Gly
        195                 200                 205
Phe Leu Ser Leu Pro Leu Asn Phe Pro Gly Thr Thr Tyr His Lys Cys
    210                 215                 220
Leu Lys Asp Met Lys Glu Ile Gln Lys Lys Leu Arg Glu Val Val Asp
225                 230                 235                 240
Asp Arg Leu Ala Asn Val Gly Pro Asp Val Glu Asp Phe Leu Gly Gln
                245                 250                 255
Ala Leu Lys Asp Lys Glu Ser Glu Lys Phe Ile Ser Glu Glu Phe Ile
            260                 265                 270
Ile Gln Leu Leu Phe Ser Ile Ser Phe Ala Ser Phe Glu Ser Ile Ser
        275                 280                 285
Thr Thr Leu Thr Leu Ile Leu Lys Leu Leu Asp Glu His Pro Glu Val
    290                 295                 300
Val Lys Glu Leu Glu Ala Glu His Glu Ala Ile Arg Lys Ala Arg Ala
305                 310                 315                 320
Asp Pro Asp Gly Pro Ile Thr Trp Glu Glu Tyr Lys Ser Met Thr Phe
                325                 330                 335
Thr Leu Gln Val Ile Asn Glu Thr Leu Arg Leu Gly Ser Val Thr Pro

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


<210> 50
<211> 496
<212> PRT
<213> Artificial Sequence

<220>
<223> Saccharomyces cerevisiae protein sequence of
      squalene epoxidase

<400> 50
Met Ser Ala Val Asn Val Ala Pro Glu Leu Ile Asn Ala Asp Asn Thr
 1               5                  10                  15
Ile Thr Tyr Asp Ala Ile Val Ile Gly Ala Gly Val Ile Gly Pro Cys
            20                  25                  30
Val Ala Thr Gly Leu Ala Arg Lys Gly Lys Lys Val Leu Ile Val Glu
        35                  40                  45
Arg Asp Trp Ala Met Pro Asp Arg Ile Val Gly Glu Leu Met Gln Pro
    50                  55                  60
Gly Gly Val Arg Ala Leu Arg Ser Leu Gly Met Ile Gln Ser Ile Asn
65                  70                  75                  80
Asn Ile Glu Ala Tyr Pro Val Thr Gly Tyr Thr Val Phe Phe Asn Gly
                85                  90                  95
Glu Gln Val Asp Ile Pro Tyr Pro Tyr Lys Ala Asp Ile Pro Lys Val
            100                 105                 110
Glu Lys Leu Lys Asp Leu Val Lys Asp Gly Asn Asp Lys Val Leu Glu
        115                 120                 125
Asp Ser Thr Ile His Ile Lys Asp Tyr Glu Asp Asp Glu Arg Glu Arg
    130                 135                 140
Gly Val Ala Phe Val His Gly Arg Phe Leu Asn Asn Leu Arg Asn Ile
145                 150                 155                 160
Thr Ala Gln Glu Pro Asn Val Thr Arg Val Gln Gly Asn Cys Ile Glu
                165                 170                 175
Ile Leu Lys Asp Glu Lys Asn Glu Val Val Gly Ala Lys Val Asp Ile
            180                 185                 190
Asp Gly Arg Gly Lys Val Glu Phe Lys Ala His Leu Thr Phe Ile Cys
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        195                 200                 205
Asp Gly Ile Phe Ser Arg Phe Arg Lys Glu Leu His Pro Asp His Val
    210                 215                 220
Pro Thr Val Gly Ser Ser Phe Val Gly Met Ser Leu Phe Asn Ala Lys
225                 230                 235                 240
Asn Pro Ala Pro Met His Gly His Val Ile Leu Gly Ser Asp His Met
                245                 250                 255
Pro Ile Leu Val Tyr Gln Ile Ser Pro Glu Glu Thr Arg Ile Leu Cys
            260                 265                 270
Ala Tyr Asn Ser Pro Lys Val Pro Ala Asp Ile Lys Ser Trp Met Ile
        275                 280                 285
Lys Asp Val Gln Pro Phe Ile Pro Lys Ser Leu Arg Pro Ser Phe Asp
    290                 295                 300
Glu Ala Val Ser Gln Gly Lys Phe Arg Ala Met Pro Asn Ser Tyr Leu
305                 310                 315                 320
Pro Ala Arg Gln Asn Asp Val Thr Gly Met Cys Val Ile Gly Asp Ala
                325                 330                 335
Leu Asn Met Arg His Pro Leu Thr Gly Gly Gly Met Thr Val Gly Leu
            340                 345                 350
His Asp Val Val Leu Leu Ile Lys Lys Ile Gly Asp Leu Asp Phe Ser
        355                 360                 365
Asp Arg Glu Lys Val Leu Asp Glu Leu Leu Asp Tyr His Phe Glu Arg
    370                 375                 380
Lys Ser Tyr Asp Ser Val Ile Asn Val Leu Ser Val Ala Leu Tyr Ser
385                 390                 395                 400
Leu Phe Ala Ala Asp Ser Asp Asn Leu Lys Ala Leu Gln Lys Gly Cys
                405                 410                 415
Phe Lys Tyr Phe Gln Arg Gly Gly Asp Cys Val Asn Lys Pro Val Glu
            420                 425                 430
Phe Leu Ser Gly Val Leu Pro Lys Pro Leu Gln Leu Thr Arg Val Phe
        435                 440                 445
Phe Ala Val Ala Phe Tyr Thr Ile Tyr Leu Asn Met Glu Glu Arg Gly
    450                 455                 460
Phe Leu Gly Leu Pro Met Ala Leu Leu Glu Gly Ile Met Ile Leu Ile
465                 470                 475                 480
Thr Ala Ile Arg Val Phe Thr Pro Phe Leu Phe Gly Glu Leu Ile Gly
                485                 490                 495
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<210> 51
<211> 525
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Gynostemma pentaphyllum
Squalene epoxidase

<400> 51

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Met Val Asp Gln Phe Ser Leu Ala Phe Ile Phe Ala Ser Val Leu Gly
 1               5                  10                  15
Ala Val Ala Phe Tyr Tyr Leu Phe Leu Arg Asn Arg Ile Phe Arg Val
            20                  25                  30
Ser Arg Glu Pro Arg Arg Glu Ser Leu Lys Asn Ile Ala Thr Thr Asn
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        35                  40                  45
Gly Glu Cys Lys Ser Ser Tyr Ser Asp Gly Asp Ile Ile Ile Val Gly
    50                  55                  60
Ala Gly Val Ala Gly Ser Ala Leu Ala Tyr Thr Leu Gly Lys Asp Gly
65                  70                  75                  80
Arg Arg Val His Val Ile Glu Arg Asp Leu Thr Glu Pro Asp Arg Thr
                85                  90                  95
Val Gly Glu Leu Leu Gln Pro Gly Gly Tyr Leu Lys Leu Thr Glu Leu
            100                 105                 110
Gly Leu Glu Asp Cys Val Asn Glu Ile Asp Ala Gln Arg Val Tyr Gly
        115                 120                 125
Tyr Ala Leu Phe Lys Asp Gly Lys Asp Thr Lys Leu Ser Tyr Pro Leu
    130                 135                 140
Glu Lys Phe His Ser Asp Val Ser Gly Arg Ser Phe His Asn Gly Arg
145                 150                 155                 160
Phe Ile Gln Arg Met Arg Glu Lys Ala Ala Thr Leu Pro Asn Val Arg
                165                 170                 175
Leu Glu Gln Gly Thr Val Thr Ser Leu Leu Glu Glu Asn Gly Ile Ile
            180                 185                 190
Lys Gly Val Gln Tyr Lys Ser Lys Thr Gly Gln Glu Met Thr Ala Tyr
        195                 200                 205
Ala Pro Leu Thr Ile Val Cys Asp Gly Cys Phe Ser Asn Leu Arg Arg
    210                 215                 220
Ser Leu Cys Asn Pro Lys Val Asp Val Pro Ser Cys Phe Val Ala Leu
225                 230                 235                 240
Val Leu Glu Asn Cys Glu Leu Pro His Ala Asn Tyr Gly His Val Ile
                245                 250                 255
Leu Ala Asp Pro Ser Pro Ile Leu Phe Tyr Pro Ile Ser Ser Thr Glu
            260                 265                 270
Val Arg Cys Leu Val Asp Val Pro Gly Gln Lys Val Pro Ser Ile Ser
        275                 280                 285
Asn Gly Glu Met Ala Asn Tyr Leu Lys Ser Val Val Ala Pro Gln Ile
    290                 295                 300
Pro Pro Gln Ile Tyr Asp Ala Leu Arg Ser Cys Tyr Asp Lys Gly Asn
305                 310                 315                 320
Ile Arg Thr Met Pro Asn Arg Ser Met Pro Ala Asp Pro Tyr Pro Thr
                325                 330                 335
Pro Gly Ala Leu Leu Met Gly Asp Ala Phe Asn Met Arg His Pro Leu
            340                 345                 350
Thr Gly Gly Gly Met Thr Val Ala Leu Ser Asp Ile Val Val Leu Arg
        355                 360                 365
Asp Leu Leu Lys Pro Leu Arg Asp Leu His Asp Ala Pro Ile Leu Ser
    370                 375                 380
Asn Tyr Leu Glu Ala Phe Tyr Thr Leu Arg Lys Pro Val Ala Ser Thr
385                 390                 395                 400
Ile Asn Thr Leu Ala Gly Ala Leu Tyr Lys Val Phe Cys Ala Ser Pro
                405                 410                 415
Asp Gln Ala Arg Arg Glu Met Arg Gln Ala Cys Phe Asp Tyr Leu Ser
            420                 425                 430
Leu Gly Gly Val Phe Ser Asn Gly Pro Val Ser Leu Leu Ser Gly Leu
        435                 440                 445
Asn Pro Arg Pro Leu Ser Leu Val Leu His Phe Phe Ala Val Ala Ile
    450                 455                 460
Tyr Gly Val Gly Arg Leu Leu Ile Pro Phe Pro Ser Pro Arg Arg Val
```

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465                 470                 475                 480
Trp Ile Gly Ala Arg Leu Ile Ser Gly Ala Ser Gly Ile Ile Phe Pro
                485                 490                 495
Ile Ile Lys Ala Glu Gly Val Arg Gln Ile Phe Phe Pro Ala Thr Leu
            500                 505                 510
Pro Ala Tyr Tyr Arg Ala Pro Pro Leu Val Arg Gly Arg
        515                 520                 525


<210> 52
<211> 531
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Arabidopsis thaliana
      Squaiene epoxidase 1

<400> 52
Met Glu Ser Gln Leu Trp Asn Trp Ile Leu Pro Leu Leu Ile Ser Ser
 1               5                  10                  15
Leu Leu Ile Ser Phe Val Ala Phe Tyr Gly Phe Phe Val Lys Pro Lys
            20                  25                  30
Arg Asn Gly Leu Arg His Asp Arg Lys Thr Val Ser Thr Val Thr Ser
        35                  40                  45
Asp Val Gly Ser Val Asn Ile Thr Gly Asp Thr Val Ala Asp Val Ile
    50                  55                  60
Val Val Gly Ala Gly Val Ala Gly Ser Ala Leu Ala Tyr Thr Leu Gly
65                  70                  75                  80
Lys Asp Lys Arg Arg Val His Val Ile Glu Arg Asp Leu Ser Glu Pro
                85                  90                  95
Asp Arg Ile Val Gly Glu Leu Leu Gln Pro Gly Gly Tyr Leu Lys Leu
            100                 105                 110
Leu Glu Leu Gly Ile Glu Asp Cys Val Glu Glu Ile Asp Ala Gln Arg
        115                 120                 125
Val Tyr Gly Tyr Ala Leu Phe Lys Asn Gly Lys Arg Ile Arg Leu Ala
    130                 135                 140
Tyr Pro Leu Glu Lys Phe His Glu Asp Val Ser Gly Arg Ser Phe His
145                 150                 155                 160
Asn Gly Arg Phe Ile Gln Arg Met Arg Glu Lys Ala Ala Ser Leu Pro
                165                 170                 175
Asn Val Gln Leu Glu Gln Gly Thr Val Leu Ser Leu Leu Glu Glu Asn
            180                 185                 190
Gly Thr Ile Lys Gly Val Arg Tyr Lys Asn Lys Ala Gly Glu Glu Gln
        195                 200                 205
Thr Ala Phe Ala Ala Leu Thr Ile Val Cys Asp Gly Cys Phe Ser Asn
    210                 215                 220
Leu Arg Arg Ser Leu Cys Asn Pro Gln Val Glu Val Pro Ser Cys Phe
225                 230                 235                 240
Val Gly Leu Val Leu Glu Asn Cys Asn Leu Pro Tyr Ala Asn His Gly
                245                 250                 255
His Val Val Leu Ala Asp Pro Ser Pro Ile Leu Met Tyr Pro Ile Ser
            260                 265                 270
Ser Thr Glu Val Arg Cys Leu Val Asp Val Pro Gly Gln Lys Val Pro
```

```
        275                 280                 285
Ser Ile Ala Asn Gly Glu Met Lys Asn Tyr Leu Lys Thr Val Val Ala
    290                 295                 300
Pro Gln Met Pro His Glu Val Tyr Asp Ser Phe Ile Ala Ala Val Asp
305                 310                 315                 320
Lys Gly Asn Ile Lys Ser Met Pro Asn Arg Ser Met Pro Ala Ser Pro
                325                 330                 335
Tyr Pro Thr Pro Gly Ala Leu Leu Met Gly Asp Ala Phe Asn Met Arg
            340                 345                 350
His Pro Leu Thr Gly Gly Gly Met Thr Val Ala Leu Ala Asp Ile Val
        355                 360                 365
Val Leu Arg Asn Leu Leu Arg Pro Leu Arg Asp Leu Ser Asp Gly Ala
    370                 375                 380
Ser Leu Cys Lys Tyr Leu Glu Ser Phe Tyr Thr Leu Arg Lys Pro Val
385                 390                 395                 400
Ala Ala Thr Ile Asn Thr Leu Ala Asn Ala Leu Tyr Gln Val Phe Cys
                405                 410                 415
Ser Ser Glu Asn Glu Ala Arg Asn Glu Met Arg Glu Ala Cys Phe Asp
            420                 425                 430
Tyr Leu Gly Leu Gly Gly Met Cys Thr Ser Gly Pro Val Ser Leu Leu
        435                 440                 445
Ser Gly Leu Asn Pro Arg Pro Leu Thr Leu Val Cys His Phe Phe Ala
    450                 455                 460
Val Ala Val Tyr Gly Val Ile Arg Leu Leu Ile Pro Phe Pro Ser Pro
465                 470                 475                 480
Lys Arg Ile Trp Leu Gly Ala Lys Leu Ile Ser Gly Ala Ser Gly Ile
                485                 490                 495
Ile Phe Pro Ile Ile Lys Ala Glu Gly Val Arg Gln Met Phe Phe Pro
            500                 505                 510
Ala Thr Val Pro Ala Tyr Tyr Tyr Lys Ala Pro Thr Val Gly Glu Thr
        515                 520                 525
Lys Cys Ser
    530
```

<210> 53
<211> 516
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Arabidopsis thaliana
Squalene epoxidase 4

<400> 53

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

```
65                  70                  75                  80
Arg Phe Met Gly Glu Leu Met Gln Ala Gly Gly Arg Phe Met Leu Ala
                85                  90                  95
Gln Leu Gly Leu Glu Asp Cys Leu Glu Asp Ile Asp Ala Gln Glu Ala
            100                 105                 110
Lys Ser Leu Ala Ile Tyr Lys Asp Gly Lys His Ala Thr Leu Pro Phe
        115                 120                 125
Pro Asp Asp Lys Ser Phe Pro His Glu Pro Val Gly Arg Leu Leu Arg
    130                 135                 140
Asn Gly Arg Leu Val Gln Arg Leu Arg Gln Lys Ala Ala Ser Leu Ser
145                 150                 155                 160
Asn Val Gln Leu Glu Glu Gly Thr Val Lys Ser Leu Ile Glu Glu Glu
                165                 170                 175
Gly Val Val Lys Gly Val Thr Tyr Lys Asn Ser Ala Gly Glu Glu Ile
            180                 185                 190
Thr Ala Phe Ala Pro Leu Thr Val Val Cys Asp Gly Cys Tyr Ser Asn
        195                 200                 205
Leu Arg Arg Ser Leu Val Asp Asn Thr Glu Glu Val Leu Ser Tyr Met
    210                 215                 220
Val Gly Tyr Val Thr Lys Asn Ser Arg Leu Glu Asp Pro His Ser Leu
225                 230                 235                 240
His Leu Ile Phe Ser Lys Pro Leu Val Cys Val Ile Tyr Gln Ile Thr
                245                 250                 255
Ser Asp Glu Val Arg Cys Val Ala Glu Val Pro Ala Asp Ser Ile Pro
            260                 265                 270
Ser Ile Ser Asn Gly Glu Met Ser Thr Phe Leu Lys Lys Ser Met Ala
        275                 280                 285
Pro Gln Ile Pro Glu Thr Gly Asn Leu Arg Glu Ile Phe Leu Lys Gly
    290                 295                 300
Ile Glu Glu Gly Leu Pro Glu Ile Lys Ser Thr Ala Thr Lys Ser Met
305                 310                 315                 320
Ser Ser Arg Leu Cys Asp Lys Arg Gly Val Ile Val Leu Gly Asp Ala
                325                 330                 335
Phe Asn Met Arg His Pro Ile Ile Ala Ser Gly Met Met Val Ala Leu
            340                 345                 350
Ser Asp Ile Cys Ile Leu Arg Asn Leu Leu Lys Pro Leu Pro Asn Leu
        355                 360                 365
Ser Asn Thr Lys Lys Val Ser Asp Leu Val Lys Ser Phe Tyr Ile Ile
    370                 375                 380
Arg Lys Pro Met Ser Ala Thr Val Asn Thr Leu Ala Ser Ile Phe Ser
385                 390                 395                 400
Gln Val Leu Val Ala Thr Thr Asp Glu Ala Arg Glu Gly Met Arg Gln
                405                 410                 415
Gly Cys Phe Asn Tyr Leu Ala Arg Gly Asp Phe Lys Thr Arg Gly Leu
            420                 425                 430
Met Thr Ile Leu Gly Gly Met Asn Pro His Pro Leu Thr Leu Val Leu
        435                 440                 445
His Leu Val Ala Ile Thr Leu Thr Ser Met Gly His Leu Leu Ser Pro
    450                 455                 460
Phe Pro Ser Pro Arg Arg Phe Trp His Ser Leu Arg Ile Leu Ala Trp
465                 470                 475                 480
Ala Leu Gln Met Leu Gly Ala His Leu Val Asp Glu Gly Phe Lys Glu
                485                 490                 495
Met Leu Ile Pro Thr Asn Ala Ala Ala Tyr Arg Arg Asn Tyr Ile Ala
```

```
            500                 505                 510
Thr Thr Thr Val
        515


<210> 54
<211> 517
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Arabidopsis thaliana
      Squalene epoxidase 6

<400> 54
Met Ala Phe Thr His Val Cys Leu Trp Thr Leu Val Ala Phe Val Leu
 1               5                  10                  15
Thr Trp Thr Val Phe Tyr Leu Thr Asn Met Lys Lys Lys Ala Thr Asp
            20                  25                  30
Leu Ala Asp Thr Val Ala Glu Asp Gln Lys Asp Gly Ala Ala Asp Val
        35                  40                  45
Ile Ile Val Gly Ala Gly Val Gly Gly Ser Ala Leu Ala Tyr Ala Leu
    50                  55                  60
Ala Lys Asp Gly Arg Arg Val His Val Ile Glu Arg Asp Met Arg Glu
65                  70                  75                  80
Pro Glu Arg Met Met Gly Glu Phe Met Gln Pro Gly Gly Arg Leu Met
                85                  90                  95
Leu Ser Lys Leu Gly Leu Gln Asp Cys Leu Glu Asp Ile Asp Ala Gln
            100                 105                 110
Lys Ala Thr Gly Leu Ala Val Tyr Lys Asp Gly Lys Glu Ala Asp Ala
        115                 120                 125
Pro Phe Pro Val Asp Asn Asn Asn Phe Ser Tyr Glu Pro Ser Ala Arg
    130                 135                 140
Ser Phe His Asn Gly Arg Phe Val Gln Gln Leu Arg Arg Lys Ala Phe
145                 150                 155                 160
Ser Leu Ser Asn Val Arg Leu Glu Glu Gly Thr Val Lys Ser Leu Leu
                165                 170                 175
Glu Glu Lys Gly Val Val Lys Gly Val Thr Tyr Lys Asn Lys Glu Gly
            180                 185                 190
Glu Glu Thr Thr Ala Leu Ala Pro Leu Thr Val Val Cys Asp Gly Cys
        195                 200                 205
Tyr Ser Asn Leu Arg Arg Ser Leu Asn Asp Asp Asn Asn Ala Glu Ile
    210                 215                 220
Met Ser Tyr Ile Val Gly Tyr Ile Ser Lys Asn Cys Arg Leu Glu Glu
225                 230                 235                 240
Pro Glu Lys Leu His Leu Ile Leu Ser Lys Pro Ser Phe Thr Met Val
                245                 250                 255
Tyr Gln Ile Ser Ser Thr Asp Val Arg Cys Gly Phe Glu Val Leu Pro
            260                 265                 270
Glu Asn Phe Pro Ser Ile Ala Asn Gly Glu Met Ser Thr Phe Met Lys
        275                 280                 285
Asn Thr Ile Val Pro Gln Val Pro Pro Lys Leu Arg Lys Ile Phe Leu
    290                 295                 300
Lys Gly Ile Asp Glu Gly Ala His Ile Lys Val Val Pro Ala Lys Arg
```

305 310 315 320
Met Thr Ser Thr Leu Ser Lys Lys Lys Gly Val Ile Val Leu Gly Asp
325 330 335
Ala Phe Asn Met Arg His Pro Val Val Ala Ser Gly Met Met Val Leu
340 345 350
Leu Ser Asp Ile Leu Ile Leu Arg Arg Leu Leu Gln Pro Leu Ser Asn
355 360 365
Leu Gly Asp Ala Asn Lys Val Ser Glu Val Ile Asn Ser Phe Tyr Asp
370 375 380
Ile Arg Lys Pro Met Ser Ala Thr Val Asn Thr Leu Gly Asn Ala Phe
385 390 395 400
Ser Gln Val Leu Ile Gly Ser Thr Asp Glu Ala Lys Glu Ala Met Arg
405 410 415
Gln Gly Val Tyr Asp Tyr Leu Cys Ser Gly Gly Phe Arg Thr Ser Gly
420 425 430
Met Met Ala Leu Leu Gly Gly Met Asn Pro Arg Pro Leu Ser Leu Val
435 440 445
Tyr His Leu Cys Ala Ile Thr Leu Ser Ser Ile Gly Gln Leu Leu Ser
450 455 460
Pro Phe Pro Ser Pro Leu Arg Ile Trp His Ser Leu Lys Leu Phe Gly
465 470 475 480
Leu Ala Met Lys Met Leu Val Pro Asn Leu Lys Ala Glu Gly Val Ser
485 490 495
Gln Met Leu Phe Pro Ala Asn Ala Ala Ala Tyr His Lys Ser Tyr Met
500 505 510
Ala Ala Thr Thr Leu
515

<210> 55
<211> 516
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Arabidopsis thaliana
Squalene epoxidase 5

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

```
        115                 120                 125
Ser Phe Pro Val Asp Asn Asn Asn Phe Pro Phe Asp Pro Ser Ala Arg
    130                 135                 140
Ser Phe His Asn Gly Arg Phe Val Gln Arg Leu Arg Gln Lys Ala Ser
145                 150                 155                 160
Ser Leu Pro Asn Val Arg Leu Glu Glu Gly Thr Val Lys Ser Leu Ile
                165                 170                 175
Glu Glu Lys Gly Val Ile Lys Gly Val Thr Tyr Lys Asn Ser Ala Gly
            180                 185                 190
Glu Glu Thr Thr Ala Leu Ala Pro Leu Thr Val Val Cys Asp Gly Cys
        195                 200                 205
Tyr Ser Asn Leu Arg Arg Ser Leu Asn Asp Asn Asn Ala Glu Val Leu
    210                 215                 220
Ser Tyr Gln Val Gly Phe Ile Ser Lys Asn Cys Gln Leu Glu Glu Pro
225                 230                 235                 240
Glu Lys Leu Lys Leu Ile Met Ser Lys Pro Ser Phe Thr Met Leu Tyr
                245                 250                 255
Gln Ile Ser Ser Thr Asp Val Arg Cys Val Phe Glu Val Leu Pro Asn
            260                 265                 270
Asn Ile Pro Ser Ile Ser Asn Gly Glu Met Ala Thr Phe Val Lys Asn
        275                 280                 285
Thr Ile Ala Pro Gln Val Pro Leu Lys Leu Arg Lys Ile Phe Leu Lys
    290                 295                 300
Gly Ile Asp Glu Gly Glu His Ile Lys Ala Met Pro Thr Lys Lys Met
305                 310                 315                 320
Thr Ala Thr Leu Ser Glu Lys Lys Gly Val Ile Leu Leu Gly Asp Ala
                325                 330                 335
Phe Asn Met Arg His Pro Ala Ile Ala Ser Gly Met Met Val Leu Leu
            340                 345                 350
Ser Asp Ile Leu Ile Leu Arg Arg Leu Leu Gln Pro Leu Ser Asn Leu
        355                 360                 365
Gly Asn Ala Gln Lys Ile Ser Gln Val Ile Lys Ser Phe Tyr Asp Ile
    370                 375                 380
Arg Lys Pro Met Ser Ala Thr Val Asn Thr Leu Gly Asn Ala Phe Ser
385                 390                 395                 400
Gln Val Leu Val Ala Ser Thr Asp Glu Ala Lys Glu Ala Met Arg Gln
                405                 410                 415
Gly Cys Tyr Asp Tyr Leu Ser Ser Gly Gly Phe Arg Thr Ser Gly Met
            420                 425                 430
Met Ala Leu Leu Gly Gly Met Asn Pro Arg Pro Ile Ser Leu Ile Tyr
        435                 440                 445
His Leu Cys Ala Ile Thr Leu Ser Ser Ile Gly His Leu Leu Ser Pro
    450                 455                 460
Phe Pro Ser Pro Leu Arg Ile Trp His Ser Leu Arg Leu Phe Gly Leu
465                 470                 475                 480
Ala Met Lys Met Leu Val Pro His Leu Lys Ala Glu Gly Val Ser Gln
                485                 490                 495
Met Leu Phe Pro Val Asn Ala Ala Ala Tyr Ser Lys Ser Tyr Met Ala
            500                 505                 510
Ala Thr Ala Leu
        515
```

<210> 56

<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Arabidopsis thaliana
Squalene epoxidase 2

<400> 56
Met Lys Pro Phe Val Ile Arg Asn Leu Pro Arg Phe Gln Ser Thr Leu
1 5 10 15
Arg Ser Ser Leu Leu Tyr Thr Asn His Arg Pro Ser Ser Arg Phe Ser
20 25 30
Leu Ser Thr Arg Arg Phe Thr Thr Gly Ala Thr Tyr Ile Arg Arg Trp
35 40 45
Lys Ala Thr Ala Ala Gln Thr Leu Lys Leu Ser Ala Val Asn Ser Thr
50 55 60
Val Met Met Lys Pro Ala Lys Ile Ala Leu Asp Gln Phe Ile Ala Ser
65 70 75 80
Leu Phe Thr Phe Leu Leu Leu Tyr Ile Leu Arg Arg Ser Ser Asn Lys
85 90 95
Asn Lys Lys Asn Arg Gly Leu Val Val Ser Gln Asn Asp Thr Val Ser
100 105 110
Lys Asn Leu Glu Thr Glu Val Asp Ser Gly Thr Asp Val Ile Ile Val
115 120 125
Gly Ala Gly Val Ala Gly Ser Ala Leu Ala His Thr Leu Gly Lys Glu
130 135 140
Gly Arg Arg Val His Val Ile Glu Arg Asp Phe Ser Glu Gln Asp Arg
145 150 155 160
Ile Val Gly Glu Leu Leu Gln Pro Gly Gly Tyr Leu Lys Leu Ile Glu
165 170 175
Leu Gly Leu Glu Asp Cys Val Lys Lys Ile Asp Ala Gln Arg Val Leu
180 185 190
Gly Tyr Val Leu Phe Lys Asp Gly Lys His Thr Lys Leu Ala Tyr Pro
195 200 205
Leu Glu Thr Phe Asp Ser Asp Val Ala Gly Arg Ser Phe His Asn Gly
210 215 220
Arg Phe Val Gln Arg Met Arg Glu Lys Ala Leu Thr Leu Ser Asn Val
225 230 235 240
Arg Leu Glu Gln Gly Thr Val Thr Ser Leu Leu Glu Glu His Gly Thr
245 250 255
Ile Lys Gly Val Arg Tyr Arg Thr Lys Glu Gly Asn Glu Phe Arg Ser
260 265 270
Phe Ala Pro Leu Thr Ile Val Cys Asp Gly Cys Phe Ser Asn Leu Arg
275 280 285
Arg Ser Leu Cys Lys Pro Lys Val Asp Val Pro Ser Thr Phe Val Gly
290 295 300
Leu Val Leu Glu Asn Cys Glu Leu Pro Phe Ala Asn His Gly His Val
305 310 315 320
Val Leu Gly Asp Pro Ser Pro Ile Leu Met Tyr Pro Ile Ser Ser Ser
325 330 335
Glu Val Arg Cys Leu Val Asp Val Pro Gly Gln Lys Leu Pro Pro Ile
340 345 350
Ala Asn Gly Glu Met Ala Lys Tyr Leu Lys Thr Arg Val Ala Pro Gln

```
        355                 360                 365
Val Pro Thr Lys Val Arg Glu Ala Phe Ile Thr Ala Val Glu Lys Gly
    370                 375                 380
Asn Ile Arg Thr Met Pro Asn Arg Ser Met Pro Ala Asp Pro Ile Pro
385                 390                 395                 400
Thr Pro Gly Ala Leu Leu Leu Gly Asp Ala Phe Asn Met Arg His Pro
                405                 410                 415
Leu Thr Gly Gly Gly Met Thr Val Ala Leu Ala Asp Ile Val Val Leu
            420                 425                 430
Arg Asp Leu Leu Arg Pro Ile Arg Asn Leu Asn Asp Lys Glu Ala Leu
        435                 440                 445
Ser Lys Tyr Ile Glu Ser Phe Tyr Thr Leu Arg Lys Pro Val Ala Ser
    450                 455                 460
Thr Ile Asn Thr Leu Ala Asp Ala Leu Tyr Lys Val Phe Leu Ala Ser
465                 470                 475                 480
Ser Asp Glu Ala Arg Thr Glu Met Arg Glu Ala Cys Phe Asp Tyr Leu
                485                 490                 495
Ser Leu Gly Gly Val Phe Ser Ser Gly Pro Val Ala Leu Leu Ser Gly
            500                 505                 510
Leu Asn Pro Arg Pro Leu Ser Leu Val Leu His Phe Phe Ala Val Ala
        515                 520                 525
Ile Tyr Ala Val Cys Arg Leu Met Leu Pro Phe Pro Ser Ile Glu Ser
    530                 535                 540
Phe Trp Leu Gly Ala Arg Ile Ile Ser Ser Ala Ser Ser Ile Ile Phe
545                 550                 555                 560
Pro Ile Ile Lys Ala Glu Gly Val Arg Gln Met Phe Phe Pro Arg Thr
                565                 570                 575
Ile Pro Ala Ile Tyr Arg Ala Pro Pro
            580                 585
```

<210> 57
<211> 525
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Arabidopsis thaliana
Squalene epoxidase 3

<400> 57

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

```
            100                 105                 110
Asp Cys Val Lys Asp Ile Asp Ala Gln Arg Val Leu Gly Tyr Ala Leu
        115                 120                 125
Phe Lys Asp Gly Lys His Thr Lys Leu Ser Tyr Pro Leu Asp Gln Phe
    130                 135                 140
Asp Ser Asp Val Ala Gly Arg Ser Phe His Asn Gly Arg Phe Val Gln
145                 150                 155                 160
Arg Met Arg Glu Lys Ala Ser Leu Leu Pro Asn Val Arg Met Glu Gln
                165                 170                 175
Gly Thr Val Thr Ser Leu Val Glu Glu Asn Gly Ile Ile Lys Gly Val
            180                 185                 190
Gln Tyr Lys Thr Lys Asp Gly Gln Glu Leu Lys Ser Phe Ala Pro Leu
        195                 200                 205
Thr Ile Val Cys Asp Gly Cys Phe Ser Asn Leu Arg Arg Ser Leu Cys
    210                 215                 220
Lys Pro Lys Val Glu Val Pro Ser Asn Phe Val Gly Leu Val Leu Glu
225                 230                 235                 240
Asn Cys Glu Leu Pro Phe Pro Asn His Gly His Val Val Leu Gly Asp
                245                 250                 255
Pro Ser Pro Ile Leu Phe Tyr Pro Ile Ser Ser Ser Glu Val Arg Cys
            260                 265                 270
Leu Val Asp Val Pro Gly Ser Lys Leu Pro Ser Val Ala Ser Gly Glu
        275                 280                 285
Met Ala His His Leu Lys Thr Met Val Ala Pro Gln Val Pro Pro Gln
    290                 295                 300
Ile Arg Asp Ala Phe Ile Ser Ala Val Glu Lys Gly Asn Ile Arg Thr
305                 310                 315                 320
Met Pro Asn Arg Ser Met Pro Ala Asp Pro Ile His Thr Pro Gly Ala
                325                 330                 335
Leu Leu Leu Gly Asp Ala Phe Asn Met Arg His Pro Leu Thr Gly Gly
            340                 345                 350
Gly Met Thr Val Ala Leu Ser Asp Ile Val Ile Leu Arg Asp Leu Leu
        355                 360                 365
Asn Pro Leu Val Asp Leu Thr Asn Lys Glu Ser Leu Ser Lys Tyr Ile
    370                 375                 380
Glu Ser Phe Tyr Thr Leu Arg Lys Pro Val Ala Ser Thr Ile Asn Thr
385                 390                 395                 400
Leu Ala Gly Ala Leu Tyr Lys Val Phe Leu Ala Ser Pro Asp Asp Ala
                405                 410                 415
Arg Ser Glu Met Arg Arg Ala Cys Phe Asp Tyr Leu Ser Leu Gly Gly
            420                 425                 430
Val Cys Ser Ser Gly Pro Val Ala Leu Leu Ser Gly Leu Asn Pro Arg
        435                 440                 445
Pro Met Ser Leu Val Leu His Phe Phe Ala Val Ala Ile Phe Gly Val
    450                 455                 460
Gly Arg Leu Leu Val Pro Leu Pro Ser Val Lys Arg Leu Trp Leu Gly
465                 470                 475                 480
Ala Arg Leu Ile Ser Ser Ala Ser Gly Ile Ile Phe Pro Ile Ile Lys
                485                 490                 495
Ala Glu Gly Val Arg Gln Met Phe Phe Pro Arg Thr Ile Pro Ala Ile
            500                 505                 510
Tyr Arg Ala Pro Pro Thr Pro Ser Ser Ser Ser Pro Gln
        515                 520                 525
```

<210> 58
<211> 506
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Brassica napus Squaiene
monooxygenase 1,1

<400> 58
Met Asp Leu Ala Phe Pro His Val Cys Leu Trp Thr Leu Leu Ala Phe
1 5 10 15
Val Leu Thr Trp Thr Val Phe Tyr Val Asn Asn Arg Arg Lys Lys Val
20 25 30
Ala Lys Leu Pro Asp Ala Ala Thr Glu Val Arg Arg Asp Gly Asp Ala
35 40 45
Asp Val Ile Ile Val Gly Ala Gly Val Gly Gly Ser Ala Leu Ala Tyr
50 55 60
Ala Leu Ala Lys Asp Gly Arg Arg Val His Val Ile Glu Arg Asp Met
65 70 75 80
Arg Glu Pro Val Arg Met Met Gly Glu Phe Met Gln Pro Gly Gly Arg
85 90 95
Leu Leu Leu Ser Lys Leu Gly Leu Glu Asp Cys Leu Glu Gly Ile Asp
100 105 110
Glu Gln Ile Ala Thr Gly Leu Ala Val Tyr Lys Asp Gly Gln Lys Ala
115 120 125
Leu Val Ser Phe Pro Glu Asp Asn Asp Phe Pro Tyr Glu Pro Thr Gly
130 135 140
Arg Ala Phe Tyr Asn Gly Arg Phe Val Gln Arg Leu Arg Gln Lys Ala
145 150 155 160
Ser Ser Leu Pro Thr Val Gln Leu Glu Glu Gly Thr Val Lys Ser Leu
165 170 175
Ile Glu Glu Lys Gly Val Ile Lys Gly Val Thr Tyr Lys Asn Ser Ala
180 185 190
Gly Glu Glu Thr Thr Ala Phe Ala Pro Leu Thr Val Val Cys Asp Gly
195 200 205
Cys Tyr Ser Asn Leu Arg Arg Ser Val Asn Asp Asn Asn Ala Glu Val
210 215 220
Ile Ser Tyr Gln Val Gly Tyr Val Ser Lys Asn Cys Gln Leu Glu Asp
225 230 235 240
Pro Glu Lys Leu Lys Leu Ile Met Ser Lys Pro Ser Phe Thr Met Leu
245 250 255
Tyr Gln Ile Ser Ser Thr Asp Val Arg Cys Val Met Glu Ile Phe Pro
260 265 270
Gly Asn Ile Pro Ser Ile Ser Asn Gly Glu Met Ala Val Tyr Leu Lys
275 280 285
Asn Thr Met Ala Pro Gln Val Pro Pro Glu Leu Arg Lys Ile Phe Leu
290 295 300
Lys Gly Ile Asp Glu Gly Ala Gln Ile Lys Ala Met Pro Thr Lys Arg
305 310 315 320
Met Glu Ala Thr Leu Ser Glu Lys Gln Gly Val Ile Val Leu Gly Asp
325 330 335
Ala Phe Asn Met Arg His Pro Ala Ile Ala Ser Gly Met Met Val Val

```
            340                 345                 350
Leu Ser Asp Ile Leu Ile Leu Arg Arg Leu Leu Gln Pro Leu Arg Asn
        355                 360                 365
Leu Ser Asp Ala Asn Lys Val Ser Glu Val Ile Lys Ser Phe Tyr Val
    370                 375                 380
Ile Arg Lys Pro Met Ser Ala Thr Val Asn Thr Leu Gly Asn Ala Phe
385                 390                 395                 400
Ser Gln Val Leu Ile Ala Ser Thr Asp Glu Ala Lys Glu Ala Met Arg
                405                 410                 415
Gln Gly Cys Phe Asp Tyr Leu Ser Ser Gly Gly Phe Arg Thr Ser Gly
            420                 425                 430
Met Met Ala Leu Leu Gly Gly Met Asn Pro Arg Pro Leu Ser Leu Ile
        435                 440                 445
Phe His Leu Cys Gly Ile Thr Leu Ser Ser Ile Gly Gln Leu Leu Ser
    450                 455                 460
Pro Phe Pro Ser Pro Leu Gly Ile Trp His Ser Leu Arg Leu Phe Gly
465                 470                 475                 480
Ala Glu Gly Val Ser Gln Met Leu Ser Pro Ala Tyr Ala Ala Ala Tyr
                485                 490                 495
Arg Lys Ser Tyr Met Thr Ala Thr Ala Leu
            500                 505
```

<210> 59
<211> 518
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Brassica napus Squalene monooxygenase 1,2

<400> 59

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

```
                165                 170                 175
Leu Ile Glu Glu Lys Gly Val Val Lys Gly Val Thr Tyr Lys Asn Ser
            180                 185                 190
Ser Gly Glu Glu Thr Thr Ser Phe Ala Pro Leu Thr Val Val Cys Asp
        195                 200                 205
Gly Cys His Ser Asn Leu Arg Arg Ser Leu Asn Asp Asn Asn Ala Glu
    210                 215                 220
Val Thr Ala Tyr Glu Ile Gly Tyr Ile Ser Arg Asn Cys Arg Leu Glu
225                 230                 235                 240
Gln Pro Asp Lys Leu His Leu Ile Met Ala Lys Pro Ser Phe Ala Met
                245                 250                 255
Leu Tyr Gln Val Ser Ser Thr Asp Val Arg Cys Asn Phe Glu Leu Leu
            260                 265                 270
Ser Lys Asn Leu Pro Ser Val Ser Asn Gly Glu Met Thr Ser Phe Val
        275                 280                 285
Arg Asn Ser Ile Ala Pro Gln Val Pro Leu Lys Leu Arg Lys Thr Phe
    290                 295                 300
Leu Lys Gly Leu Asp Glu Gly Ser His Ile Lys Ile Thr Gln Ala Lys
305                 310                 315                 320
Arg Ile Pro Ala Thr Leu Ser Arg Lys Lys Gly Val Ile Val Leu Gly
                325                 330                 335
Asp Ala Phe Asn Met Arg His Pro Val Ile Ala Ser Gly Met Met Val
            340                 345                 350
Leu Leu Ser Asp Ile Leu Ile Leu Ser Arg Leu Leu Lys Pro Leu Gly
        355                 360                 365
Asn Leu Gly Asp Glu Asn Lys Val Ser Glu Val Met Lys Ser Phe Tyr
    370                 375                 380
Ala Leu Arg Lys Pro Met Ser Ala Thr Val Asn Thr Leu Gly Asn Ser
385                 390                 395                 400
Phe Trp Gln Val Leu Ile Ala Ser Thr Asp Glu Ala Lys Glu Ala Met
                405                 410                 415
Arg Gln Gly Cys Phe Asp Tyr Leu Ser Ser Gly Gly Phe Arg Thr Ser
            420                 425                 430
Gly Leu Met Ala Leu Ile Gly Gly Met Asn Pro Arg Pro Leu Ser Leu
        435                 440                 445
Phe Tyr His Leu Phe Val Ile Ser Leu Ser Ser Ile Gly Gln Leu Leu
    450                 455                 460
Ser Pro Phe Pro Thr Pro Leu Arg Val Trp His Ser Leu Arg Leu Leu
465                 470                 475                 480
Asp Leu Ser Leu Lys Met Leu Val Pro His Leu Lys Ala Glu Gly Ile
                485                 490                 495
Gly Gln Met Leu Ser Pro Thr Asn Ala Ala Ala Tyr Arg Lys Ser Tyr
            500                 505                 510
Met Ala Ala Thr Val Val
        515
```

<210> 60
<211> 531
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Euphorbia tirucalli

Squalene epoxidase

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

```
                405                 410                 415
Asp Glu Ala Arg Lys Glu Met Arg Gln Ala Cys Phe Asp Tyr Leu Ser
            420                 425                 430
Leu Gly Gly Glu Cys Ala Met Gly Pro Val Ser Leu Leu Ser Gly Leu
        435                 440                 445
Asn Pro Ser Pro Leu Thr Leu Val Leu His Phe Phe Gly Val Ala Ile
    450                 455                 460
Tyr Gly Val Gly Arg Leu Leu Ile Pro Phe Pro Thr Pro Lys Gly Met
465                 470                 475                 480
Trp Ile Gly Ala Arg Ile Ile Ser Ser Ala Ser Gly Ile Ile Phe Pro
                485                 490                 495
Ile Ile Lys Ala Glu Gly Val Arg Gln Val Phe Phe Pro Ala Thr Val
            500                 505                 510
Pro Ala Ile Tyr Arg Asn Pro Pro Val Asn Gly Lys Ser Val Glu Val
        515                 520                 525
Pro Lys Ser
    530


<210> 61
<211> 519
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Medicago truncatula
      Squaiene epoxidase

<400> 61
Met Ile Asp Pro Tyr Gly Phe Gly Trp Ile Thr Cys Thr Leu Ile Thr
 1               5                  10                  15
Leu Ala Ala Leu Tyr Asn Phe Leu Phe Ser Arg Lys Asn His Ser Asp
            20                  25                  30
Ser Thr Thr Thr Glu Asn Ile Thr Thr Ala Thr Gly Glu Cys Arg Ser
        35                  40                  45
Phe Asn Pro Asn Gly Asp Val Asp Ile Ile Ile Val Gly Ala Gly Val
    50                  55                  60
Ala Gly Ser Ala Leu Ala Tyr Thr Leu Gly Lys Asp Gly Arg Arg Val
65                  70                  75                  80
Leu Ile Ile Glu Arg Asp Leu Asn Glu Pro Asp Arg Ile Val Gly Glu
                85                  90                  95
Leu Leu Gln Pro Gly Gly Tyr Leu Lys Leu Ile Glu Leu Gly Leu Asp
            100                 105                 110
Asp Cys Val Glu Lys Ile Asp Ala Gln Lys Val Phe Gly Tyr Ala Leu
        115                 120                 125
Phe Lys Asp Gly Lys His Thr Arg Leu Ser Tyr Pro Leu Glu Lys Phe
    130                 135                 140
His Ser Asp Ile Ala Gly Arg Ser Phe His Asn Gly Arg Phe Ile Leu
145                 150                 155                 160
Arg Met Arg Glu Lys Ala Ala Ser Leu Pro Asn Val Arg Leu Glu Gln
                165                 170                 175
Gly Thr Val Thr Ser Leu Leu Glu Glu Asn Gly Thr Ile Lys Gly Val
            180                 185                 190
Gln Tyr Lys Thr Lys Asp Ala Gln Glu Phe Ser Ala Cys Ala Pro Leu
```

```
        195                 200                 205
Thr Ile Val Cys Asp Gly Cys Phe Ser Asn Leu Arg Arg Ser Leu Cys
    210                 215                 220
Asn Pro Lys Val Glu Val Pro Ser Cys Phe Val Gly Leu Val Leu Glu
225                 230                 235                 240
Asn Cys Glu Leu Pro Cys Ala Asp His Gly His Val Ile Leu Gly Asp
                245                 250                 255
Pro Ser Pro Val Leu Phe Tyr Pro Ile Ser Ser Thr Glu Ile Arg Cys
            260                 265                 270
Leu Val Asp Val Pro Gly Gln Lys Val Pro Ser Ile Ser Asn Gly Glu
        275                 280                 285
Met Ala Lys Tyr Leu Lys Thr Val Val Ala Pro Gln Val Pro Pro Glu
    290                 295                 300
Leu His Ala Ala Phe Ile Ala Ala Val Asp Lys Gly His Ile Arg Thr
305                 310                 315                 320
Met Pro Asn Arg Ser Met Pro Ala Asp Pro Tyr Pro Thr Pro Gly Ala
                325                 330                 335
Leu Leu Met Gly Asp Ala Phe Asn Met Arg His Pro Leu Thr Gly Gly
            340                 345                 350
Gly Met Thr Val Ala Leu Ser Asp Ile Val Val Leu Arg Asn Leu Leu
        355                 360                 365
Lys Pro Leu Arg Asp Leu Asn Asp Ala Ser Ser Leu Cys Lys Tyr Leu
    370                 375                 380
Glu Ser Phe Tyr Thr Leu Arg Lys Pro Val Ala Ser Thr Ile Asn Thr
385                 390                 395                 400
Leu Ala Gly Ala Leu Tyr Lys Val Phe Cys Ala Ser Pro Asp Pro Ala
                405                 410                 415
Arg Lys Glu Met Arg Gln Ala Cys Phe Asp Tyr Leu Ser Leu Gly Gly
            420                 425                 430
Leu Phe Ser Glu Gly Pro Val Ser Leu Leu Ser Gly Leu Asn Pro Cys
        435                 440                 445
Pro Leu Ser Leu Val Leu His Phe Phe Ala Val Ala Ile Tyr Gly Val
    450                 455                 460
Gly Arg Leu Leu Leu Pro Phe Pro Ser Pro Lys Arg Leu Trp Ile Gly
465                 470                 475                 480
Ile Arg Leu Ile Ala Ser Ala Ser Gly Ile Ile Leu Pro Ile Ile Lys
                485                 490                 495
Ala Glu Gly Ile Arg Gln Met Phe Phe Pro Ala Thr Val Pro Ala Tyr
            500                 505                 510
Tyr Arg Ala Pro Pro Asp Ala
        515
```

<210> 62
<211> 526
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Medicago truncatula
Squaiene monooxygenase

<400> 62
```
Met Asp Leu Tyr Asn Ile Gly Trp Ile Leu Ser Ser Val Leu Ser Leu
```

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

```
        435                 440                 445
Gly Leu Asn Pro Arg Pro Leu Ser Leu Val Leu His Phe Phe Ala Val
    450                 455                 460
Ala Val Phe Gly Val Gly Arg Leu Leu Leu Pro Phe Pro Ser Pro Lys
465                 470                 475                 480
Arg Val Trp Ile Gly Ala Arg Leu Leu Ser Gly Ala Ser Gly Ile Ile
                485                 490                 495
Leu Pro Ile Ile Lys Ala Glu Gly Ile Arg Gln Met Phe Phe Pro Ala
            500                 505                 510
Thr Val Pro Ala Tyr Tyr Arg Ala Pro Pro Val Asn Ala Phe
        515                 520                 525


<210> 63
<211> 534
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Ricinus communis Squaiene
      monooxygenase

<400> 63
Met Ala Asp Asn Tyr Leu Leu Gly Trp Ile Leu Cys Ser Ile Ile Gly
 1               5                  10                  15
Leu Phe Gly Leu Tyr Tyr Met Val Tyr Leu Val Val Lys Arg Glu Glu
            20                  25                  30
Glu Asp Asn Asn Arg Lys Ala Leu Leu Gln Ala Arg Ser Asp Ser Ala
        35                  40                  45
Lys Thr Met Ser Ala Val Ser Gln Asn Gly Glu Cys Arg Ser Asp Asn
    50                  55                  60
Pro Ala Asp Ala Asp Ile Ile Ile Val Gly Ala Gly Val Ala Gly Ser
65                  70                  75                  80
Ala Leu Ala His Thr Leu Gly Lys Asp Gly Arg Arg Val His Val Ile
                85                  90                  95
Glu Arg Asp Leu Thr Glu Pro Asp Arg Ile Val Gly Glu Leu Leu Gln
            100                 105                 110
Pro Gly Gly Tyr Leu Lys Leu Ile Glu Leu Gly Leu Glu Asp Cys Val
        115                 120                 125
Glu Glu Ile Asp Ala Gln Arg Val Phe Gly Tyr Ala Leu Phe Met Asp
    130                 135                 140
Gly Lys His Thr Gln Leu Ser Tyr Pro Leu Glu Lys Phe His Ser Asp
145                 150                 155                 160
Val Ala Gly Arg Ser Phe His Asn Gly Arg Phe Ile Gln Arg Met Arg
                165                 170                 175
Glu Lys Ala Ser Ser Ile Pro Asn Val Arg Leu Glu Gln Gly Thr Val
            180                 185                 190
Thr Ser Leu Ile Glu Glu Lys Gly Ile Ile Arg Gly Val Val Tyr Lys
        195                 200                 205
Thr Lys Thr Gly Glu Glu Leu Thr Ala Phe Ala Pro Leu Thr Ile Val
    210                 215                 220
Cys Asp Gly Cys Phe Ser Asn Leu Arg Arg Ser Leu Cys Asn Pro Lys
225                 230                 235                 240
Val Asp Val Pro Ser Cys Phe Val Gly Leu Val Leu Glu Asp Cys Lys
```

```
                245                 250                 255
Leu Pro Tyr Gln Tyr His Gly His Val Val Leu Ala Asp Pro Ser Pro
            260                 265                 270
Ile Leu Phe Tyr Gln Ile Ser Ser Thr Glu Val Arg Cys Leu Val Asp
        275                 280                 285
Val Pro Gly Gln Lys Val Pro Ser Ile Ser Asn Gly Glu Met Ala Lys
    290                 295                 300
Tyr Leu Lys Asn Val Val Ala Pro Gln Val Pro Pro Glu Ile Tyr Asp
305                 310                 315                 320
Ser Phe Val Ala Ala Val Asp Lys Gly Asn Ile Arg Thr Met Pro Asn
                325                 330                 335
Arg Ser Met Pro Ala Ser Pro Tyr Pro Thr Pro Gly Ala Leu Leu Met
            340                 345                 350
Gly Asp Ala Phe Asn Met Arg His Pro Leu Thr Gly Gly Gly Met Thr
        355                 360                 365
Val Ala Leu Ser Asp Ile Val Val Leu Arg Glu Leu Leu Lys Pro Leu
    370                 375                 380
Arg Asp Leu His Asp Ala Pro Thr Leu Cys Arg Tyr Leu Glu Ser Phe
385                 390                 395                 400
Tyr Thr Leu Arg Lys Pro Val Ala Ser Thr Ile Asn Thr Leu Ala Gly
                405                 410                 415
Ala Leu Tyr Lys Val Phe Cys Ala Ser Ser Asp Glu Ala Arg Asn Glu
            420                 425                 430
Met Arg Gln Ala Cys Phe Asp Tyr Leu Ser Leu Gly Gly Val Phe Ser
        435                 440                 445
Thr Gly Pro Ile Ser Leu Leu Ser Gly Leu Asn Pro Arg Pro Leu Ser
    450                 455                 460
Leu Val Val His Phe Phe Ala Val Ala Ile Tyr Gly Val Gly Arg Leu
465                 470                 475                 480
Leu Leu Pro Phe Pro Ser Pro Lys Arg Val Trp Val Gly Ala Arg Leu
                485                 490                 495
Ile Ser Gly Ala Ser Gly Ile Ile Phe Pro Ile Ile Lys Ala Glu Gly
            500                 505                 510
Val Arg Gln Met Phe Phe Pro Ala Thr Val Pro Ala Tyr Tyr Arg Ala
        515                 520                 525
Pro Pro Val Glu Cys Asn
    530
```

<210> 64
<211> 521
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Ricinus communis Squaiene monooxygenase

<400> 64

```
Met Glu Tyr Lys Leu Ala Val Ala Gly Ile Ile Ala Ser Leu Trp Ala
 1               5                  10                  15
Leu Phe Met Leu Cys Ser Leu Lys Arg Lys Lys Asn Ile Thr Arg Ala
            20                  25                  30
Ser Phe Asn Asn Tyr Thr Asp Glu Thr Leu Lys Ser Ser Ser Lys Glu
```

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

```
465                 470                 475                 480
Trp Asp Gly Val Lys Leu Ile Ser Gly Ala Ser Ser Val Ile Phe Pro
                485                 490                 495
Ile Met Lys Ala Glu Gly Ile Gly Gln Ile Phe Phe Pro Ile Thr Lys
            500                 505                 510
Pro Pro Asn His Lys Ser Gln Thr Trp
        515                 520


<210> 65
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Ricinus communis Squaiene
      monooxygenase

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

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


<210> 66
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Ricinus communis Squaiene
      monooxygenase

<400> 66
Met Glu Tyr Gln Tyr Phe Val Gly Gly Ile Ile Ala Ser Ala Leu Leu
 1               5                  10                  15
Phe Val Leu Val Cys Arg Leu Ala Gly Lys Arg Gln Arg Arg Ala Leu
            20                  25                  30
Arg Asp Thr Val Asp Arg Asp Glu Ile Ser Gln Asn Ser Glu Asn Gly
        35                  40                  45
Ile Ser Gln Ser Glu Lys Asn Met Asn Thr Asp Ile Ile Ile Val Gly
    50                  55                  60
Ala Gly Val Ala Gly Ser Thr Leu Ala Tyr Thr Leu Gly Lys Asp Gly
65                  70                  75                  80
Arg Arg Val Arg Val Ile Glu Arg Asp Leu Ser Leu Gln Asp Arg Ile
                85                  90                  95
Val Gly Glu Leu Leu Gln Pro Gly Gly Tyr Leu Lys Leu Ile Glu Leu
            100                 105                 110
Gly Leu Glu Asp Cys Val Glu Glu Ile Asp Ala Leu Gln Val Phe Gly
        115                 120                 125
Tyr Ala Leu Tyr Lys Asn Gly Arg Ser Thr Lys Leu Ser Tyr Pro Leu
    130                 135                 140
Asp Ser Phe Asp Ser Asp Val Ser Gly Arg Ser Phe His Asn Gly Arg
```

```
145                 150                 155                 160
Phe Ile Gln Arg Met Arg Glu Lys Ala Ala Ser Leu Pro Asn Val Arg
                165                 170                 175
Met Glu Gly Gly Thr Val Thr Ser Leu Leu Glu Val Lys Gly Thr Ile
            180                 185                 190
Lys Gly Val Gln Tyr Lys Asn Lys Asn Gly Glu Glu Leu Ile Ala Cys
        195                 200                 205
Ala Pro Leu Thr Ile Val Cys Asp Gly Cys Phe Ser Asn Leu Arg Arg
    210                 215                 220
Ser Leu Cys Asn Ser Lys Val Asp Ile Pro Phe Cys Phe Val Ala Leu
225                 230                 235                 240
Ile Leu Glu Asn Cys Glu Leu Pro Tyr Pro Asn His Gly His Val Ile
                245                 250                 255
Leu Ala Asp Pro Ser Pro Ile Leu Phe Tyr Arg Ile Ser Ile Ser Glu
            260                 265                 270
Ile Arg Cys Leu Val Asp Ile Pro Ala Gly Gln Lys Leu Pro Ser Ile
        275                 280                 285
Ser Asn Gly Glu Met Ala Asn Tyr Leu Lys Ser Val Val Ala Pro Gln
    290                 295                 300
Ile Pro Pro Glu Leu Ser Asn Ala Phe Leu Ser Ala Ile Glu Lys Gly
305                 310                 315                 320
Lys Ile Arg Thr Met Pro Lys Arg Ser Met Pro Ala Ala Pro His Pro
                325                 330                 335
Thr Pro Gly Ala Leu Leu Leu Gly Asp Ala Phe Asn Met Arg His Pro
            340                 345                 350
Leu Thr Gly Gly Val Met Thr Val Ala Leu Ser Asp Ile Val Val Leu
        355                 360                 365
Arg Ser Leu Leu Arg Pro Leu His Asp Leu Thr Asp Ala Ser Ala Leu
    370                 375                 380
Cys Glu Tyr Leu Lys Ser Phe Tyr Ser Leu Arg Lys Pro Met Val Ser
385                 390                 395                 400
Thr Ile Asn Thr Leu Ala Gly Ala Leu Tyr Arg Val Phe Ser Ala Ser
                405                 410                 415
Gln Asp Pro Ala Arg Asp Glu Met Arg Gln Ala Cys Phe Asp Tyr Leu
            420                 425                 430
Ser Leu Gly Gly Val Phe Ser Asn Gly Pro Ile Ala Leu Leu Ser Gly
        435                 440                 445
Leu Asn Pro Arg Pro Leu Ser Leu Ile Val His Phe Phe Ala Val Ala
    450                 455                 460
Val Tyr Gly Val Gly Arg Leu Ile Phe Pro Leu Pro Ser Ala Lys Arg
465                 470                 475                 480
Met Trp Met Gln Glu
                485
```

<210> 67
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Ricinus communis Squaiene monooxygenase

<400> 67
Met Glu Tyr Gln Tyr Leu Met Gly Gly Gly Ile Met Thr Leu Leu Phe
 1               5                  10                  15
Val Leu Ser Tyr Arg Leu Lys Arg Glu Thr Arg Ala Ser Val Glu Asn
            20                  25                  30
Ala Arg Asp Glu Val Leu Gln Asn Ser Glu Asn Gly Ile Ser Gln Ser
        35                  40                  45
Glu Lys Ala Met Asn Thr Asp Ile Lys Leu Leu Leu Glu Gln Ile Val
    50                  55                  60
Gln Lys Ile Ala Met Leu Asn Ser Ile Arg Leu Glu Glu Gly Thr Val
65                  70                  75                  80
Thr Ser Leu Leu Glu Val Lys Arg Asp Ile Lys Gly Val Gln Tyr Lys
                85                  90                  95
Thr Lys Asn Gly Glu Glu Leu Thr Ala Cys Ala Pro Leu Thr Ile Val
            100                 105                 110
Ser His Gly Cys Phe Ser Asn Leu Arg Leu His Val Thr Pro Ser Thr
        115                 120                 125
Ser Lys Phe Lys Ser Phe Ile Gly Leu Glu Val Asp Ile Pro Ser Ser
    130                 135                 140
Phe Ala Ala Leu Ile Leu Gly Asn Cys Glu Leu Pro Phe Pro Asn His
145                 150                 155                 160
Gly His Val Ile Leu Ala Asp Pro Ser Ser Ile Leu Phe Tyr Arg Ile
                165                 170                 175
Ser Ser Ser Glu Ile Cys Cys Leu Val Asp Val Pro Ala Gly Gln Lys
            180                 185                 190
Leu Pro Ser Ile Ser Asn Gly Glu Met Ala Asn Tyr Leu Lys Ser Val
        195                 200                 205
Val Ala His Gln Ala Phe Lys Val Gly Leu Ala Tyr
    210                 215                 220


<210> 68
<211> 642
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Ricinus communis Squaiene
      monooxygenase

<400> 68
Met Ser Pro Ile Ser Ile Gln Leu Pro Pro Arg Pro Gln Leu Tyr Arg
 1               5                  10                  15
Ser Leu Ile Ser Ser Leu Ser Leu Ser Thr Tyr Lys Gln Pro Pro Ser
            20                  25                  30
Pro Pro Ser Phe Ser Leu Thr Ile Ala Asn Ser Pro Pro Gln Pro Gln
        35                  40                  45
Pro Gln Ala Thr Val Ser Ser Lys Thr Arg Thr Ile Thr Arg Leu Ser
    50                  55                  60
Asn Ser Ser Asn Arg Val Asn Leu Leu Gln Ala Glu Gln His Pro Gln
65                  70                  75                  80
Glu Pro Ser Ser Asp Leu Ser Tyr Ser Ser Ser Pro Pro His Cys Val
                85                  90                  95
Ser Gly Gly Tyr Asn Ile Lys Leu Met Glu Val Gly Thr Asp Asn Tyr

```
            100                 105                 110
Ala Val Ile Ile Ile Leu Gly Thr Phe Phe Ala Ser Leu Phe Ala Phe
        115                 120                 125
Val Phe Leu Ser Ile Leu Arg Tyr Asn Phe Lys Asn Lys Asn Lys Ala
    130                 135                 140
Lys Ile His Asp Glu Thr Thr Leu Lys Thr Gln Asn Asp Asn Val Arg
145                 150                 155                 160
Leu Pro Asp Asn Gly Ser Gly Asn Asp Val Ile Ile Val Gly Ala Gly
                165                 170                 175
Val Ala Gly Ala Ala Leu Ala Tyr Thr Leu Gly Lys Asp Gly Arg Arg
            180                 185                 190
Val His Val Ile Glu Arg Asp Leu Thr Glu Pro Asp Arg Ile Val Gly
        195                 200                 205
Glu Leu Leu Gln Pro Gly Gly Tyr Leu Lys Leu Ile Glu Leu Gly Leu
    210                 215                 220
Glu Asp Cys Val Gln Glu Ile Asp Ala Gln Arg Val Leu Gly Tyr Ala
225                 230                 235                 240
Leu Phe Lys Asp Gly Lys Asn Thr Arg Leu Ser Tyr Pro Leu Glu Lys
                245                 250                 255
Phe His Ala Asp Val Ala Gly Arg Ser Phe His Asn Gly Arg Phe Ile
            260                 265                 270
Gln Arg Met Arg Glu Lys Ala Ala Ser Leu Pro Asn Val Lys Leu Glu
        275                 280                 285
Gln Gly Thr Val Thr Ser Leu Leu Glu Glu Asn Gly Thr Ile Lys Gly
    290                 295                 300
Val Gln Tyr Lys Thr Lys Asp Gly Gln Glu Ile Arg Ala Tyr Ala Pro
305                 310                 315                 320
Leu Thr Ile Val Cys Asp Gly Cys Phe Ser Asn Leu Arg Arg Ser Leu
                325                 330                 335
Cys Asn Pro Lys Val Asp Val Pro Ser Cys Phe Val Gly Leu Val Leu
            340                 345                 350
Glu Asn Cys Gln Leu Pro Phe Ala Asn His Gly His Val Val Leu Ala
        355                 360                 365
Asp Pro Ser Pro Ile Leu Phe Tyr Pro Ile Ser Ser Thr Glu Val Arg
    370                 375                 380
Cys Leu Val Asp Val Pro Gly Gln Lys Val Pro Ser Ile Ala Asn Gly
385                 390                 395                 400
Glu Met Ala Lys Tyr Leu Lys Asn Val Val Ala Pro Gln Ile Pro Pro
                405                 410                 415
Val Leu His Asp Ala Phe Ile Ser Ala Ile Asp Lys Gly Asn Ile Arg
            420                 425                 430
Thr Met Pro Asn Arg Ser Met Pro Ala Asp Pro His Pro Thr Pro Gly
        435                 440                 445
Ala Leu Leu Met Gly Asp Ala Phe Asn Met Arg His Pro Leu Thr Gly
    450                 455                 460
Gly Gly Met Thr Val Ala Leu Ser Asp Ile Val Val Leu Arg Asp Leu
465                 470                 475                 480
Leu Lys Pro Leu Arg Asp Leu Asn Asp Ala Thr Ser Leu Thr Lys Tyr
                485                 490                 495
Leu Glu Ser Phe Tyr Thr Leu Arg Lys Pro Val Ala Ser Thr Ile Asn
            500                 505                 510
Thr Leu Ala Gly Ala Leu Tyr Lys Val Phe Ser Ala Ser Pro Asp Gln
        515                 520                 525
Ala Arg Lys Glu Met Arg Gln Ala Cys Phe Asp Tyr Leu Ser Leu Gly
```

```
    530                 535                 540
Gly Ile Phe Ser Ser Gly Pro Val Ala Leu Leu Ser Gly Leu Asn Pro
545                 550                 555                 560
Arg Pro Leu Ser Leu Val Met His Phe Phe Ala Val Ala Ile Tyr Gly
                565                 570                 575
Val Gly Arg Leu Leu Leu Pro Phe Pro Ser Pro Lys Ser Val Trp Ile
            580                 585                 590
Gly Ala Arg Leu Ile Ser Ser Ala Ser Gly Ile Ile Phe Pro Ile Ile
        595                 600                 605
Lys Ala Glu Gly Val Arg Gln Met Phe Phe Pro Ala Thr Ile Pro Ala
    610                 615                 620
Ile Tyr Arg Pro Pro Pro Val Lys Asp Thr Ser Asp Asp Glu Gln Lys
625                 630                 635                 640
Ser Arg
```

<210> 69
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of S. cerevisiae ERG9

<400> 69

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

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

<210> 70
<211> 759
<212> PRT
<213> Artificial Sequence

<220>
<223> Siraitia grosvenorii protein sequence or amino
acid sequence of S. grosvenorli cucurbitadienol
synthase

<400> 70

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

```
            100                 105                 110
Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro Met Phe
        115                 120                 125
Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val Thr Gly Val Leu Asn
    130                 135                 140
Ser Val Leu Ser Lys His His Arg Gln Glu Met Cys Arg Tyr Val Tyr
145                 150                 155                 160
Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly Pro
                165                 170                 175
Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu Leu
            180                 185                 190
Gly Glu Asp Ala Asn Ala Gly Ala Met Pro Lys Ala Arg Ala Trp Ile
        195                 200                 205
Leu Asp His Gly Gly Ala Thr Gly Ile Thr Ser Trp Gly Lys Leu Trp
    210                 215                 220
Leu Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn Pro Leu Pro
225                 230                 235                 240
Pro Glu Phe Trp Leu Phe Pro Tyr Phe Leu Pro Phe His Pro Gly Arg
                245                 250                 255
Met Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr
            260                 265                 270
Gly Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu Ser Leu Arg
        275                 280                 285
Lys Glu Leu Tyr Ala Val Pro Tyr His Glu Ile Asp Trp Asn Lys Ser
    290                 295                 300
Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met
305                 310                 315                 320
Gln Asp Ile Leu Trp Gly Ser Leu His His Val Tyr Glu Pro Leu Phe
                325                 330                 335
Thr Arg Trp Pro Ala Lys Arg Leu Arg Glu Lys Ala Leu Gln Thr Ala
            340                 345                 350
Met Gln His Ile His Tyr Glu Asp Glu Asn Thr Arg Tyr Ile Cys Leu
        355                 360                 365
Gly Pro Val Asn Lys Val Leu Asn Leu Leu Cys Cys Trp Val Glu Asp
    370                 375                 380
Pro Tyr Ser Asp Ala Phe Lys Leu His Leu Gln Arg Val His Asp Tyr
385                 390                 395                 400
Leu Trp Val Ala Glu Asp Gly Met Lys Met Gln Gly Tyr Asn Gly Ser
                405                 410                 415
Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Val Ser Thr Lys
            420                 425                 430
Leu Val Asp Asn Tyr Gly Pro Thr Leu Arg Lys Ala His Asp Phe Val
        435                 440                 445
Lys Ser Ser Gln Ile Gln Gln Asp Cys Pro Gly Asp Pro Asn Val Trp
    450                 455                 460
Tyr Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His
465                 470                 475                 480
Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ala Leu
                485                 490                 495
Met Leu Ser Lys Leu Pro Ser Glu Thr Val Gly Glu Ser Leu Glu Arg
            500                 505                 510
Asn Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Asp
        515                 520                 525
Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu
```

```
    530                 535                 540
Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr
545                 550                 555                 560
Pro Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Thr Leu Phe
                565                 570                 575
Lys Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Thr Ala Ile
            580                 585                 590
Val Arg Ala Ala Asn Phe Leu Glu Asn Met Gln Arg Thr Asp Gly Ser
        595                 600                 605
Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly
    610                 615                 620
Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Leu Ala
625                 630                 635                 640
Ile Arg Lys Ala Cys Asp Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly
                645                 650                 655
Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn
            660                 665                 670
Leu Glu Gly Asn Arg Pro His Leu Val Asn Thr Ala Trp Val Leu Met
        675                 680                 685
Ala Leu Ile Glu Ala Gly Gln Ala Glu Arg Asp Pro Thr Pro Leu His
    690                 695                 700
Arg Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Asn Gly Asp Phe
705                 710                 715                 720
Pro Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr
                725                 730                 735
Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr
            740                 745                 750
Cys His Arg Val Leu Thr Glu
        755
```

<210> 71
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Cucurbitadienol synthase UniProtKB-Q6BE24

<400> 71

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

```
Ala Val Gln Thr Arg Asp Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro
        115                 120                 125
Leu Phe Leu Leu Pro Gly Leu Val Ile Ala Leu His Val Thr Gly Val
    130                 135                 140
Leu Asn Ser Val Leu Ser Lys His His Arg Val Glu Met Cys Arg Tyr
145                 150                 155                 160
Leu Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile Glu
                165                 170                 175
Gly Thr Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg
            180                 185                 190
Leu Leu Gly Glu Asp Ala Asp Gly Gly Asp Gly Gly Ala Met Thr Lys
        195                 200                 205
Ala Arg Ala Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser
    210                 215                 220
Trp Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp Ser Gly
225                 230                 235                 240
Asn Asn Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro
                245                 250                 255
Phe His Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr Leu Pro
            260                 265                 270
Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr Pro Lys
        275                 280                 285
Val Leu Ser Leu Arg Gln Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile
    290                 295                 300
Asp Trp Asn Lys Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr
305                 310                 315                 320
Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His Val
                325                 330                 335
Tyr Glu Pro Leu Phe Thr Arg Trp Pro Gly Lys Arg Leu Arg Glu Lys
            340                 345                 350
Ala Leu Gln Ala Ala Met Lys His Ile His Tyr Glu Asp Glu Asn Ser
        355                 360                 365
Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu Cys
    370                 375                 380
Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Leu His Leu Gln
385                 390                 395                 400
Arg Val His Asp Tyr Leu Trp Val Ala Glu Asp Gly Met Arg Met Gln
                405                 410                 415
Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala
            420                 425                 430
Ile Val Ala Thr Lys Leu Val Asp Ser Tyr Ala Pro Thr Leu Arg Lys
        435                 440                 445
Ala His Asp Phe Val Lys Asp Ser Gln Ile Gln Glu Asp Cys Pro Gly
    450                 455                 460
Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp Pro Leu
465                 470                 475                 480
Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly
                485                 490                 495
Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Thr Met Val Gly
            500                 505                 510
Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val Leu Leu
        515                 520                 525
Ser Leu Gln Asn Asp Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg
    530                 535                 540
```

```
Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp
545                 550                 555                 560
Ile Val Ile Asp Tyr Pro Tyr Val Glu Cys Thr Ala Ala Thr Met Glu
                565                 570                 575
Ala Leu Thr Leu Phe Lys Lys Leu His Pro Gly His Arg Thr Lys Glu
            580                 585                 590
Ile Asp Thr Ala Ile Gly Lys Ala Ala Asn Phe Leu Glu Lys Met Gln
        595                 600                 605
Arg Ala Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr
    610                 615                 620
Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr
625                 630                 635                 640
Asn Ser Cys Leu Ala Ile Arg Lys Ala Cys Glu Phe Leu Leu Ser Lys
                645                 650                 655
Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn
            660                 665                 670
Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val Asn Thr
        675                 680                 685
Ala Trp Val Leu Met Ala Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp
    690                 695                 700
Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu Met Asn Ser Gln Leu
705                 710                 715                 720
Glu Asn Gly Asp Phe Val Gln Gln Glu Ile Met Gly Val Phe Asn Lys
                725                 730                 735
Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp
            740                 745                 750
Ala Leu Gly Glu Tyr Cys His Arg Val Leu Thr Glu
        755                 760
```

<210> 72
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of C. pepo cucurbitadienol synthase

<400> 72

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

```
Ala Val Gln Thr Arg Asp Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro
        115                 120                 125
Leu Phe Leu Leu Pro Gly Leu Val Ile Ala Leu His Val Thr Gly Val
    130                 135                 140
Leu Asn Ser Val Leu Ser Lys His His Arg Val Glu Met Cys Arg Tyr
145                 150                 155                 160
Leu Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile Glu
                165                 170                 175
Gly Thr Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg
            180                 185                 190
Leu Leu Gly Glu Asp Ala Asp Gly Gly Asp Gly Gly Ala Met Thr Lys
        195                 200                 205
Ala Arg Ala Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser
    210                 215                 220
Trp Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp Ser Gly
225                 230                 235                 240
Asn Asn Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro
                245                 250                 255
Phe His Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr Leu Pro
            260                 265                 270
Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr Pro Lys
        275                 280                 285
Val Leu Ser Leu Arg Gln Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile
    290                 295                 300
Asp Trp Asn Lys Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr
305                 310                 315                 320
Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His Val
                325                 330                 335
Tyr Glu Pro Leu Phe Thr Arg Trp Pro Gly Lys Arg Leu Arg Glu Lys
            340                 345                 350
Ala Leu Gln Ala Ala Met Lys His Ile His Tyr Glu Asp Glu Asn Ser
        355                 360                 365
Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu Cys
    370                 375                 380
Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Leu His Leu Gln
385                 390                 395                 400
Arg Val His Asp Tyr Leu Trp Val Ala Glu Asp Gly Met Arg Met Gln
                405                 410                 415
Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala
            420                 425                 430
Ile Val Ala Thr Lys Leu Val Asp Ser Tyr Ala Pro Thr Leu Arg Lys
        435                 440                 445
Ala His Asp Phe Val Lys Asp Ser Gln Ile Gln Glu Asp Cys Pro Gly
    450                 455                 460
Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp Pro Leu
465                 470                 475                 480
Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly
                485                 490                 495
Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Thr Met Val Gly
            500                 505                 510
Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val Leu Leu
        515                 520                 525
Ser Leu Gln Asn Asp Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg
    530                 535                 540
```

```
Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp
545                 550                 555                 560
Ile Val Ile Asp Tyr Pro Tyr Val Glu Cys Thr Ala Ala Thr Met Glu
                565                 570                 575
Ala Leu Thr Leu Phe Lys Lys Leu His Pro Gly His Arg Thr Lys Glu
            580                 585                 590
Ile Asp Thr Ala Ile Gly Lys Ala Ala Asn Phe Leu Glu Lys Met Gln
        595                 600                 605
Arg Ala Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr
    610                 615                 620
Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr
625                 630                 635                 640
Asn Ser Cys Leu Ala Ile Arg Lys Ala Cys Glu Phe Leu Leu Ser Lys
                645                 650                 655
Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn
            660                 665                 670
Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val Asn Thr
        675                 680                 685
Ala Trp Val Leu Met Ala Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp
    690                 695                 700
Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu Met Asn Ser Gln Leu
705                 710                 715                 720
Glu Asn Gly Asp Phe Val Gln Gln Glu Ile Met Gly Val Phe Asn Lys
                725                 730                 735
Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp
            740                 745                 750
Ala Leu Gly Glu Tyr Cys His Arg Val Leu Thr Glu
        755                 760
```

<210> 73
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> C terminal portion of S. Grosvenorrii
cucurbitadienol synthase

<400> 73

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

```
Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn
        115                 120                 125
Cys Leu Ala Ile Arg Lys Ala Cys Asp Phe Leu Leu Ser Lys Glu Leu
    130                 135                 140
Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val
145                 150                 155                 160
Tyr Thr Asn Leu Glu Gly Asn Arg Pro His Leu Val Asn Thr Ala Trp
                165                 170                 175
Val Leu Met Ala Leu Ile Glu Ala Gly Gln Ala Glu Arg Asp Pro Thr
            180                 185                 190
Pro Leu His Arg Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Asn
        195                 200                 205
Gly Asp Phe Pro Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys
    210                 215                 220
Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu
225                 230                 235                 240
Gly Glu Tyr Cys His Arg Val Leu Thr Glu
                245                 250
```

<210> 74
<211> 2280
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon optimized cucurbitadienol synthase from
Siraitia grosvenorii

<400> 74

```
atgtggagat tgaaagtagg tgctgaatcc gtaggtgaaa acgacgaaaa gtggttgaaa 60
agtataagta atcatttggg tagacaagtc tgggaatttt gtccagatgc aggtacacaa 120
caacaattgt tgcaagtaca taaggctaga aaggcatttc atgatgacag attccacaga 180
aagcaatctt cagatttgtt catcaccatc caatacggca aggaagtaga aaacggtggc 240
aagactgctg gtgttaaatt gaaggaaggt gaagaagtta gaaaagaagc agttgaatcc 300
agtttggaaa gagccttgtc tttctactct tcaatccaaa cctctgatgg taattgggca 360
tcagacttgg gtggtccaat gttcttgtta cctggtttgg tcattgcctt gtacgtaact 420
ggtgttttga actctgtatt gtcaaagcat cacagacaag aaatgtgtag atacgtttac 480
aaccatcaaa acgaagatgg tggttggggt ttgcacattg aaggtccatc cactatgttt 540
ggtagtgcat tgaattatgt cgccttaaga ttgttaggtg aagatgcaaa cgccggtgct 600
atgcctaagg caagagcctg gatattagac catggtggtg ctactggtat cacatcctgg 660
ggtaaattgt ggttaagtgt cttaggtgta tatgaatggt ctggtaataa cccattgcca 720
cctgaatttt ggttgttccc ttacttttta ccattccatc ctggtagaat gtggtgtcac 780
tgcagaatgg tttacttgcc aatgtcttac ttgtacggca agagattcgt tggtccaata 840
acacctatcg tcttgtcatt gagaaaggaa ttgtacgcag ttccttacca tgaaatcgat 900
tggaacaagt ccagaaacac ctgtgctaag gaagatttgt attacccaca ccctaaaatg 960
caagacattt tgtggggtag tttacatcac gtttacgaac cattatttac tagatggcct 1020
gctaaaagat tgagagaaaa ggcattacaa acagccatgc aacatatcca ctacgaagat 1080
gaaaacacca gatacatctg cttgggtcca gttaacaagg tcttgaactt gttgtgttgc 1140
tgggttgaag atccttattc tgacgctttc aagttgcatt tgcaaagagt acacgattac 1200
ttgtgggttg cagaagacgg tatgaaaatg caaggttaca atggttcaca attgtgggat 1260
acagcttttt ccattcaagc aatagtcagt actaagttgg tagataacta cggtccaaca 1320
ttaagaaaag ctcatgactt cgtaaagtcc agtcaaatac aacaagattg tccaggtgac 1380
cctaatgttt ggtatagaca tatccacaaa ggtgcatggc cattttctac cagagatcat 1440
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ggttggttga tttcagactg tactgctgaa ggtttgaagg ctgcattgat gttgtctaag 1500
ttgccatcag aaactgttgg tgaatccttg gaaagaaata gattatgcga tgccgttaac 1560
gtcttgttga gtttgcaaaa cgacaacggt ggtttcgctt cttacgaatt gactagatca 1620
tacccatggt tggaattaat taatcctgct gaaacattcg gtgatatcgt cattgactat 1680
ccatacgtag aatgtacctc cgctactatg gaagcattga ccttgttcaa gaagttgcat 1740
cctggtcaca gaacaaagga aatcgatacc gcaattgtta gagccgctaa tttcttggaa 1800
aacatgcaaa gaacagacgg ttcttggtat ggttgttggg gtgtttgctt tacctacgct 1860
ggttggttcg gtattaaagg tttagtcgca gccggtagaa catacaataa ctgtttggcc 1920
ataagaaaag cttgcgattt cttgttatct aaggaattac caggtggtgg ttggggtgaa 1980
tcctacttga gttgtcaaaa caaggtttac actaatttgg aaggcaacag acctcattta 2040
gttaacacag cctgggtctt gatggcttta atcgaagccg gtcaagctga aagagatcca 2100
actcctttgc atagagctgc aagattgttg atcaactcac aattggaaaa cggtgatttt 2160
ccacaacaag aaatcatggg tgttttcaac aagaactgca tgataacata tgccgcttac 2220
agaaacattt ttcctatatg ggctttgggt gaatactgcc acagagtctt gaccgaataa 2280

<210> 75
<211> 757
<212> PRT
<213> Artificial Sequence

<220>
<223> cycloartenol synthase

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

```
225                 230                 235                 240
Trp Leu Leu Pro Tyr Ala Leu Pro Phe His Pro Gly Arg Met Trp Cys
                245                 250                 255
His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly Lys Arg
            260                 265                 270
Phe Val Gly Pro Ile Thr Pro Thr Ile Leu Ser Leu Arg Lys Glu Leu
        275                 280                 285
Phe Thr Ile Pro Tyr His Asp Ile Asp Trp Asn Gln Ala Arg Asn Leu
    290                 295                 300
Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Leu Val Gln Asp Ile
305                 310                 315                 320
Leu Trp Ala Ser Leu His Lys Val Val Glu Pro Val Leu Met Gln Trp
                325                 330                 335
Pro Gly Lys Lys Leu Arg Glu Lys Ala Ile Asn Ser Val Met Glu His
            340                 345                 350
Ile His Tyr Glu Asp Glu Asn Thr Arg Tyr Ile Cys Ile Gly Pro Val
        355                 360                 365
Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro Asn Ser
    370                 375                 380
Glu Ala Phe Lys Leu His Leu Pro Arg Ile Tyr Asp Tyr Leu Trp Ile
385                 390                 395                 400
Ala Glu Asp Gly Met Lys Met Gln Gly Tyr Asn Gly Ser Gln Leu Trp
                405                 410                 415
Asp Thr Ala Phe Ala Ala Gln Ala Ile Ile Ser Thr Asn Leu Ile Glu
            420                 425                 430
Glu Tyr Gly Pro Thr Leu Arg Lys Ala His Thr Phe Ile Lys Asn Ser
        435                 440                 445
Gln Val Leu Glu Asp Cys Pro Gly Asp Leu Asn Lys Trp Tyr Arg His
    450                 455                 460
Ile Ser Lys Gly Ala Trp Pro Phe Ser Thr Ala Asp His Gly Trp Pro
465                 470                 475                 480
Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ile Leu Ser Leu Ser
                485                 490                 495
Lys Ile Ala Pro Asp Ile Val Gly Glu Pro Leu Asp Ala Lys Arg Leu
            500                 505                 510
Tyr Asp Ala Val Asn Val Ile Leu Ser Leu Gln Asn Glu Asp Gly Gly
        515                 520                 525
Leu Ala Thr Tyr Glu Leu Thr Arg Ser Tyr Ser Trp Leu Glu Leu Ile
    530                 535                 540
Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr Pro Tyr Val
545                 550                 555                 560
Glu Cys Thr Ser Ala Ala Ile Gln Ala Leu Thr Ser Phe Arg Lys Leu
                565                 570                 575
Tyr Pro Gly His Arg Arg Glu Glu Ile Gln His Ser Ile Glu Lys Ala
            580                 585                 590
Ala Ala Phe Ile Glu Lys Ile Gln Ser Ser Asp Gly Ser Trp Tyr Gly
        595                 600                 605
Ser Trp Gly Val Cys Phe Thr Tyr Gly Thr Trp Phe Gly Val Lys Gly
    610                 615                 620
Leu Ile Ala Ala Gly Lys Ser Phe Ser Asn Cys Ser Ser Ile Arg Lys
625                 630                 635                 640
Ala Cys Glu Phe Leu Leu Ser Lys Gln Leu Pro Ser Gly Gly Trp Gly
                645                 650                 655
Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Ser Asn Leu Glu Gly
```

```
            660                 665                 670
Asn Arg Pro His Ala Val Asn Thr Gly Trp Ala Met Leu Ala Leu Ile
        675                 680                 685
Glu Ala Glu Gln Ala Lys Arg Asp Pro Thr Pro Leu His Arg Ala Ala
    690                 695                 700
Leu Tyr Leu Ile Asn Ser Gln Met Glu Asn Gly Asp Phe Pro Gln Gln
705                 710                 715                 720
Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr Ala Ala
                725                 730                 735
Tyr Arg Ser Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Arg Cys Arg
            740                 745                 750
Val Leu Gln Ala Arg
        755


<210> 76
<211> 763
<212> PRT
<213> Artificial Sequence

<220>
<223> hypothetical protein

<400> 76
Met Trp Lys Leu Thr Ile Gly Ala Glu Ser Val His Asp Asn Gly Gln
 1               5                  10                  15
Ser Ser Ser Trp Leu Lys Ser Val Asn Asn His Leu Gly Arg Gln Val
            20                  25                  30
Trp Glu Phe Cys Pro Gln Leu Gly Ser Pro Asp Glu Leu Leu Gln Leu
        35                  40                  45
Gln Asn Val Arg Leu Ser Phe Gln Ala Gln Arg Phe Asp Lys Lys His
    50                  55                  60
Ser Ala Asp Leu Leu Met Arg Phe Gln Phe Glu Lys Glu Asn Pro Cys
65                  70                  75                  80
Val Asn Leu Pro Gln Ile Lys Val Lys Asp Asp Glu Asp Val Thr Glu
                85                  90                  95
Glu Ala Val Thr Thr Thr Leu Arg Arg Ala Val Asn Phe Tyr Arg Lys
            100                 105                 110
Ile Gln Ala His Asp Gly His Trp Pro Gly Asp Tyr Gly Gly Pro Met
        115                 120                 125
Phe Leu Leu Pro Gly Leu Ile Ile Thr Leu Ser Ile Thr Gly Ala Leu
    130                 135                 140
Asn Ala Val Leu Ser Lys Glu His Gln Arg Glu Met Cys Arg Tyr Leu
145                 150                 155                 160
Tyr Asn His Gln Asn Arg Asp Gly Gly Trp Gly Leu His Ile Glu Gly
                165                 170                 175
Pro Ser Thr Met Phe Gly Thr Cys Leu Asn Tyr Val Thr Leu Arg Leu
            180                 185                 190
Leu Gly Glu Gly Ala Glu Gly Gly Asp Gly Glu Met Glu Lys Gly Arg
        195                 200                 205
Lys Trp Ile Leu Asp His Gly Gly Ala Thr Glu Ile Thr Ser Trp Gly
    210                 215                 220
Lys Met Trp Leu Ser Val Leu Gly Val His Glu Trp Ser Gly Asn Asn
225                 230                 235                 240
```

```
Pro Leu Pro Pro Glu Val Trp Leu Cys Pro Tyr Leu Leu Pro Met His
                245                 250                 255
Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser
            260                 265                 270
Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr Pro Thr Ile Gln
        275                 280                 285
Ser Leu Arg Lys Glu Ile Tyr Thr Val Pro Tyr His Glu Val Asp Trp
    290                 295                 300
Asn Thr Ala Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His
305                 310                 315                 320
Pro Leu Val Gln Asp Ile Leu Trp Ala Ser Leu His Tyr Ala Tyr Glu
                325                 330                 335
Pro Ile Leu Thr Arg Trp Pro Leu Asn Arg Leu Arg Glu Lys Ala Leu
            340                 345                 350
His Lys Val Met Gln His Ile His Tyr Glu Asp Glu Asn Thr Gln Tyr
        355                 360                 365
Ile Cys Ile Gly Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp
    370                 375                 380
Val Glu Asp Pro His Ser Glu Ala Phe Lys Leu His Leu Pro Arg Val
385                 390                 395                 400
Phe Asp Tyr Leu Trp Ile Ala Glu Asp Gly Met Lys Met Gln Gly Tyr
                405                 410                 415
Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ala Val Gln Ala Ile Val
            420                 425                 430
Ser Thr Asn Leu Ala Glu Glu Tyr Ser Gly Thr Leu Arg Lys Ala His
        435                 440                 445
Lys Tyr Leu Lys Asp Ser Gln Val Leu Glu Asp Cys Pro Gly Asp Leu
    450                 455                 460
Asn Phe Trp Tyr Arg His Ile Ser Lys Gly Ala Trp Pro Phe Ser Thr
465                 470                 475                 480
Ala Asp His Gly Trp Pro Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys
                485                 490                 495
Ala Val Leu Leu Leu Ser Lys Leu Pro Thr Glu Met Val Gly Asp Pro
            500                 505                 510
Leu Gly Val Glu Arg Leu Arg Asp Ala Val Asn Val Ile Leu Ser Leu
        515                 520                 525
Gln Asn Ala Asp Gly Gly Phe Ala Thr Tyr Glu Leu Thr Arg Ser Tyr
    530                 535                 540
Gln Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val
545                 550                 555                 560
Ile Asp Tyr Pro Tyr Val Glu Cys Thr Ser Ala Ala Ile Gln Ala Leu
                565                 570                 575
Ala Ser Phe Lys Lys Leu Tyr Pro Gly His Arg Arg Glu Glu Ile Asp
            580                 585                 590
Asn Cys Ile Ala Glu Ala Ala Asn Phe Ile Glu Lys Ile Gln Ala Thr
        595                 600                 605
Asp Gly Ser Trp Tyr Gly Ser Trp Gly Val Cys Phe Thr Tyr Ala Gly
    610                 615                 620
Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Met Thr Tyr Asn Ser
625                 630                 635                 640
Ser Ser Ser Ile Arg Lys Ala Cys Asp Tyr Met Leu Ser Lys Glu Leu
                645                 650                 655
Ala Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val
            660                 665                 670
```

```
Tyr Thr Asn Leu Lys Asp Asp Arg Pro His Ile Val Asn Thr Gly Trp
        675                 680                 685
Ala Met Leu Ala Leu Ile Glu Ala Gly Gln Ala Glu Arg Asp Pro Ile
    690                 695                 700
Pro Leu His Arg Ala Ala Arg Val Leu Ile Asn Ser Gln Met Glu Asn
705                 710                 715                 720
Gly Asp Phe Pro Gln Glu Glu Ile Met Gly Val Phe Asn Lys Asn Cys
                725                 730                 735
Met Ile Ser Tyr Ser Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu
            740                 745                 750
Gly Glu Tyr Arg Cys Gln Val Leu Gln Ala Leu
        755                 760


<210> 77
<211> 757
<212> PRT
<213> Artificial Sequence

<220>
<223> putative 2,3 oxidosqualene cyclase

<400> 77
Met Trp Lys Leu Lys Ile Ala Glu Gly Glu Asp Pro Trp Leu Arg Ser
 1               5                  10                  15
Val Asn Asn His Val Gly Arg Gln Val Trp Glu Phe Asp Arg Asn Leu
            20                  25                  30
Gly Thr Pro Glu Glu Leu Ile Glu Val Glu Lys Ala Arg Glu Asp Phe
        35                  40                  45
Ser Asn His Lys Phe Glu Lys Lys His Ser Ser Asp Leu Leu Met Arg
    50                  55                  60
Leu Gln Leu Ala Lys Glu Asn Pro Cys Ser Ile Asp Leu Pro Arg Val
65                  70                  75                  80
Gln Val Lys Asp Thr Glu Glu Val Thr Glu Glu Ala Val Thr Thr Thr
                85                  90                  95
Leu Arg Arg Gly Leu Ser Phe Tyr Ser Thr Ile Gln Gly His Asp Gly
            100                 105                 110
His Trp Pro Gly Asp Tyr Gly Gly Pro Leu Phe Leu Met Pro Gly Leu
        115                 120                 125
Val Ile Ala Leu Ser Val Thr Gly Ala Leu Asn Ala Val Leu Ser Ser
    130                 135                 140
Glu His Gln Arg Glu Thr Arg Arg Tyr Ile Tyr Asn His Gln Asn Glu
145                 150                 155                 160
Asp Gly Gly Trp Gly Leu His Ile Glu Gly Ser Ser Thr Met Phe Ile
                165                 170                 175
Thr Thr Leu Asn Tyr Val Thr Leu Arg Leu Leu Gly Glu Gly Ala Asp
            180                 185                 190
Asp Gly Glu Gly Ala Met Glu Lys Ala Arg Lys Trp Ile Leu Asn His
        195                 200                 205
Gly Ser Ala Thr Ala Thr Thr Ser Trp Gly Lys Met Trp Leu Ser Val
    210                 215                 220
Leu Gly Val Phe Glu Trp Ser Gly Asn Asn Pro Leu Pro Pro Glu Met
225                 230                 235                 240
Trp Leu Leu Pro Tyr Cys Leu Pro Phe His Pro Gly Arg Met Trp Cys
```

```
                245                 250                 255
His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly Lys Arg
            260                 265                 270
Phe Val Gly Pro Ile Thr Pro Thr Ile Glu Ser Leu Arg Lys Glu Leu
        275                 280                 285
Tyr Ser Val Pro Tyr His Glu Ile Asp Trp Asn Gln Ala Arg Asn Leu
    290                 295                 300
Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Leu Val Gln Asp Ile
305                 310                 315                 320
Leu Trp Thr Ser Leu His Tyr Gly Val Glu Pro Ile Leu Thr Arg Trp
                325                 330                 335
Pro Ala Asn Lys Leu Arg Glu Lys Ser Leu Leu Thr Thr Met Gln His
            340                 345                 350
Ile His Tyr Glu Asp Glu Asn Thr Arg Tyr Ile Cys Ile Gly Pro Val
        355                 360                 365
Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro Asn Ser
    370                 375                 380
Glu Ala Phe Lys Leu His Ile Pro Arg Ile Tyr Asp Tyr Leu Trp Val
385                 390                 395                 400
Ala Glu Asp Gly Met Lys Met Gln Gly Tyr Asn Gly Ser Gln Leu Trp
                405                 410                 415
Asp Thr Ala Phe Ala Val Gln Ala Ile Ile Ser Thr Asn Leu Phe Glu
            420                 425                 430
Asp Tyr Ala Pro Thr Leu Arg Lys Ala His Lys Tyr Ile Lys Asp Ser
        435                 440                 445
Gln Val Leu Asp Asp Cys Pro Gly Asp Leu Asn Phe Trp Tyr Arg His
    450                 455                 460
Ile Ser Lys Gly Ala Trp Pro Phe Ser Thr Ala Asp His Gly Trp Pro
465                 470                 475                 480
Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ala Leu Leu Leu Ser
                485                 490                 495
Lys Ile Pro Ser Lys Ser Val Gly Asp Pro Ile Asn Ala Lys Gln Leu
            500                 505                 510
Tyr Asp Ala Val Asn Val Ile Leu Ser Leu Gln Asn Gly Asp Gly Gly
        515                 520                 525
Phe Ala Thr Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu Glu Leu Ile
    530                 535                 540
Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr Pro Tyr Val
545                 550                 555                 560
Glu Cys Thr Ala Ala Ala Ile Gln Ala Leu Thr Ser Phe Lys Lys Leu
                565                 570                 575
Tyr Pro Gly His Arg Arg Glu Asp Ile Glu Asn Cys Val Glu Lys Ala
            580                 585                 590
Val Lys Phe Leu Lys Glu Ile Gln Ala Pro Asp Gly Ser Trp Tyr Gly
        595                 600                 605
Ser Trp Gly Val Cys Phe Thr Tyr Gly Ile Trp Phe Gly Ile Lys Gly
    610                 615                 620
Leu Val Ala Ala Gly Glu Thr Phe Thr Asn Ser Ser Ser Ile Arg Lys
625                 630                 635                 640
Ala Cys Asp Phe Leu Leu Ser Lys Glu Leu Asp Ser Gly Gly Trp Gly
                645                 650                 655
Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu Lys Gly
            660                 665                 670
Asn Arg Pro His Leu Val Asn Thr Gly Trp Ala Met Ser Ala Leu Ile
```

```
        675                 680                 685
Asp Ala Gly Gln Ala Glu Arg Asp Pro Lys Pro Leu His Arg Ala Ala
    690                 695                 700
Arg Val Leu Ile Asn Ser Gln Met Asp Asn Gly Asp Phe Pro Gln Glu
705                 710                 715                 720
Glu Ile Met Gly Val Phe Asn Arg Asn Cys Met Ile Ser Tyr Ser Ala
                725                 730                 735
Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Arg Cys Arg
            740                 745                 750
Val Leu Lys Ala Pro
        755
```

<210> 78
<211> 714
<212> PRT
<213> Artificial Sequence

<220>
<223> Produced by native host Bacillus macerans,
AAA22298.1

<400> 78

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

```
                245                 250                 255
Ala Val Lys Gln Tyr Pro Phe Gly Trp Gln Lys Ser Phe Val Ser Ser
            260                 265                 270
Ile Tyr Gly Gly Asp His Pro Val Phe Thr Phe Gly Glu Trp Tyr Leu
        275                 280                 285
Gly Ala Asp Gln Thr Asp Gly Asp Asn Ile Lys Phe Ala Asn Glu Ser
    290                 295                 300
Gly Met Asn Leu Leu Asp Phe Glu Tyr Ala Gln Glu Val Arg Glu Val
305                 310                 315                 320
Phe Arg Asp Lys Thr Glu Thr Met Lys Asp Leu Tyr Glu Val Leu Ala
                325                 330                 335
Ser Thr Glu Ser Gln Tyr Asp Tyr Ile Asn Asn Met Val Thr Phe Ile
            340                 345                 350
Asp Asn His Asp Met Asp Arg Phe Gln Val Ala Gly Ser Gly Thr Arg
        355                 360                 365
Ala Thr Glu Gln Ala Leu Ala Leu Thr Leu Thr Ser Arg Gly Val Pro
    370                 375                 380
Ala Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asp Gly Asp Pro
385                 390                 395                 400
Asn Asn Arg Ala Met Met Thr Ser Phe Asn Thr Gly Thr Thr Ala Tyr
                405                 410                 415
Lys Val Ile Gln Ala Leu Ala Pro Leu Arg Lys Ser Asn Pro Ala Ile
            420                 425                 430
Ala Tyr Gly Thr Thr Thr Glu Arg Trp Val Asn Asn Asp Val Leu Ile
        435                 440                 445
Ile Glu Arg Lys Phe Gly Ser Ser Ala Ala Leu Val Ala Ile Asn Arg
    450                 455                 460
Asn Ser Ser Ala Ala Tyr Pro Ile Ser Gly Leu Leu Ser Ser Leu Pro
465                 470                 475                 480
Ala Gly Thr Tyr Ser Asp Val Leu Asn Gly Leu Leu Asn Gly Asn Ser
                485                 490                 495
Ile Thr Val Gly Ser Gly Gly Ala Val Thr Asn Phe Thr Leu Ala Ala
            500                 505                 510
Gly Gly Thr Ala Val Trp Gln Tyr Thr Ala Pro Glu Thr Ser Pro Ala
        515                 520                 525
Ile Gly Asn Val Gly Pro Thr Met Gly Gln Pro Gly Asn Ile Val Thr
    530                 535                 540
Ile Asp Gly Arg Gly Phe Gly Gly Thr Ala Gly Thr Val Tyr Phe Gly
545                 550                 555                 560
Thr Thr Ala Val Thr Gly Ser Gly Ile Val Ser Trp Glu Asp Thr Gln
                565                 570                 575
Ile Lys Ala Val Ile Pro Lys Val Ala Ala Gly Lys Thr Gly Val Ser
            580                 585                 590
Val Lys Thr Ser Ser Gly Thr Ala Ser Asn Thr Phe Lys Ser Phe Asn
        595                 600                 605
Val Leu Thr Gly Asp Gln Val Thr Val Arg Phe Leu Val Asn Gln Ala
    610                 615                 620
Asn Thr Asn Tyr Gly Thr Asn Val Tyr Leu Val Gly Asn Ala Ala Glu
625                 630                 635                 640
Leu Gly Thr Trp Asp Pro Asn Lys Ala Ile Gly Pro Met Tyr Asn Gln
                645                 650                 655
Val Ile Ala Lys Tyr Pro Ser Trp Tyr Tyr Asp Val Ser Val Pro Ala
            660                 665                 670
Gly Thr Lys Leu Asp Phe Lys Phe Ile Lys Lys Gly Gly Gly Thr Val
```

675 680 685
Thr Trp Glu Gly Gly Gly Asn His Thr Tyr Thr Thr Pro Ala Ser Gly
690 695 700
Val Gly Thr Val Thr Val Asp Trp Gln Asn
705 710

<210> 79
<211> 726
<212> PRT
<213> Artificial Sequence

<220>
<223> Produced by native host Bacillus macerans, 3WMS_A

<400> 79
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15
Ala Gln Pro Ala Met Ala Met Asp Ile Gly Ile Asn Ser Asp Pro Ser
20 25 30
Pro Asp Thr Ser Val Asp Asn Lys Val Asn Phe Ser Thr Asp Val Ile
35 40 45
Tyr Gln Ile Val Thr Asp Arg Phe Ala Asp Gly Asp Arg Thr Asn Asn
50 55 60
Pro Ala Gly Asp Ala Phe Ser Gly Asp Arg Ser Asn Leu Lys Leu Tyr
65 70 75 80
Phe Gly Gly Asp Trp Gln Gly Ile Ile Asp Lys Ile Asn Asp Gly Tyr
85 90 95
Leu Thr Gly Met Gly Val Thr Ala Leu Trp Ile Ser Gln Pro Val Glu
100 105 110
Asn Ile Thr Ser Val Ile Lys Tyr Ser Gly Val Asn Asn Thr Ser Tyr
115 120 125
His Gly Tyr Trp Ala Arg Asp Phe Lys Gln Thr Asn Asp Ala Phe Gly
130 135 140
Asp Phe Ala Asp Phe Gln Asn Leu Ile Asp Thr Ala His Ala His Asn
145 150 155 160
Ile Lys Val Val Ile Asp Phe Ala Pro Asn His Thr Ser Pro Ala Asp
165 170 175
Arg Asp Asn Pro Gly Phe Ala Glu Asn Gly Ala Leu Tyr Asp Asn Gly
180 185 190
Ser Leu Leu Gly Ala Tyr Ser Asn Asp Thr Ala Gly Leu Phe His His
195 200 205
Asn Gly Gly Thr Asp Phe Ser Thr Ile Glu Asp Gly Ile Tyr Lys Asn
210 215 220
Leu Ile Asp Leu Ala Asp Ile Asn His Asn Asn Asn Ala Met Asp Ala
225 230 235 240
Tyr Phe Lys Ser Ala Ile Asp Leu Trp Leu Gly Met Gly Val Asp Gly
245 250 255
Ile Arg Phe Asp Ala Val Lys His Met Pro Phe Gly Trp Gln Lys Ser
260 265 270
Phe Val Ser Ser Ile Tyr Gly Gly Asp His Pro Val Phe Thr Phe Gly
275 280 285
Glu Trp Tyr Leu Gly Ala Asp Gln Thr Asp Gly Asp Asn Ile Lys Phe
290 295 300

```
Ala Asn Glu Ser Gly Met Asn Leu Leu Asp Phe Glu Tyr Ala Gln Glu
305                 310                 315                 320
Val Arg Glu Val Phe Arg Asp Lys Thr Glu Thr Met Lys Asp Leu Tyr
                325                 330                 335
Glu Val Leu Ala Ser Thr Glu Ser Gln Tyr Asp Tyr Ile Asn Asn Met
            340                 345                 350
Val Thr Phe Ile Asp Asn His Asp Met Asp Arg Phe Gln Val Ala Gly
        355                 360                 365
Ser Gly Thr Arg Ala Thr Glu Gln Ala Leu Ala Leu Thr Leu Thr Ser
    370                 375                 380
Arg Gly Val Pro Ala Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly
385                 390                 395                 400
Asp Gly Asp Pro Asn Asn Arg Ala Met Met Thr Ser Phe Asn Thr Gly
                405                 410                 415
Thr Thr Ala Tyr Lys Val Ile Gln Ala Leu Ala Pro Leu Arg Lys Ser
            420                 425                 430
Asn Pro Ala Ile Ala Tyr Gly Thr Thr Thr Glu Arg Trp Val Asn Asn
        435                 440                 445
Asp Val Leu Ile Ile Glu Arg Lys Phe Gly Ser Ser Ala Ala Leu Val
    450                 455                 460
Ala Ile Asn Arg Asn Ser Ser Ala Ala Tyr Pro Ile Ser Gly Leu Leu
465                 470                 475                 480
Ser Ser Leu Pro Ala Gly Thr Tyr Ser Asp Val Leu Asn Gly Leu Leu
                485                 490                 495
Asn Gly Asn Ser Ile Thr Val Gly Ser Gly Gly Ala Val Thr Asn Phe
            500                 505                 510
Thr Leu Ala Ala Gly Gly Thr Ala Val Trp Gln Tyr Thr Ala Pro Glu
        515                 520                 525
Thr Ser Pro Ala Ile Gly Asn Val Gly Pro Thr Met Gly Gln Pro Gly
    530                 535                 540
Asn Ile Val Thr Ile Asp Gly Arg Gly Phe Gly Gly Thr Ala Gly Thr
545                 550                 555                 560
Val Tyr Phe Gly Thr Thr Ala Val Thr Gly Ser Gly Ile Val Ser Trp
                565                 570                 575
Glu Asp Thr Gln Ile Lys Ala Val Ile Pro Lys Val Ala Ala Gly Lys
            580                 585                 590
Thr Gly Val Ser Val Lys Thr Ser Ser Gly Thr Ala Ser Asn Thr Phe
        595                 600                 605
Lys Ser Phe Asn Val Leu Thr Gly Asp Gln Val Thr Met Arg Phe Leu
    610                 615                 620
Val Asn Gln Ala Asn Thr Asn Tyr Gly Thr Asn Val Tyr Leu Val Gly
625                 630                 635                 640
Asn Ala Ala Glu Leu Gly Ser Trp Asp Pro Asn Lys Ala Ile Gly Pro
                645                 650                 655
Met Tyr Asn Gln Val Ile Ala Lys Tyr Pro Ser Trp Tyr Tyr Asp Val
            660                 665                 670
Ser Val Pro Ala Gly Thr Lys Leu Asp Phe Lys Phe Ile Lys Lys Gly
        675                 680                 685
Gly Gly Thr Val Thr Trp Glu Gly Gly Gly Asn His Thr Tyr Thr Thr
    690                 695                 700
Pro Ala Ser Ser Val Gly Thr Val Thr Val Asp Trp Gln Asn Leu Glu
705                 710                 715                 720
His His His His His His
                725
```

<210> 80
<211> 687
<212> PRT
<213> Artificial Sequence

<220>
<223> Produced by native host Bacillus macerans, 4JCL_A

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

```
            340                 345                 350
Ser Arg Gly Val Pro Ala Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr
        355                 360                 365
Gly Asp Gly Asp Pro Asn Asn Arg Ala Met Met Thr Ser Phe Asn Thr
    370                 375                 380
Gly Thr Thr Ala Tyr Lys Val Ile Gln Ala Leu Ala Pro Leu Arg Lys
385                 390                 395                 400
Ser Asn Pro Ala Ile Ala Tyr Gly Thr Thr Thr Glu Arg Trp Val Asn
                405                 410                 415
Asn Asp Val Leu Ile Ile Glu Arg Lys Phe Gly Ser Ser Ala Ala Leu
            420                 425                 430
Val Ala Ile Asn Arg Asn Ser Ser Ala Ala Tyr Pro Ile Ser Gly Leu
        435                 440                 445
Leu Ser Ser Leu Pro Ala Gly Thr Tyr Ser Asp Val Leu Asn Gly Leu
    450                 455                 460
Leu Asn Gly Asn Ser Ile Thr Val Gly Ser Gly Gly Ala Val Thr Asn
465                 470                 475                 480
Phe Thr Leu Ala Ala Gly Gly Thr Ala Val Trp Gln Tyr Thr Ala Pro
                485                 490                 495
Glu Thr Ser Pro Ala Ile Gly Asn Val Gly Pro Thr Met Gly Gln Pro
            500                 505                 510
Gly Asn Ile Val Thr Ile Asp Gly Arg Gly Phe Gly Gly Thr Ala Gly
        515                 520                 525
Thr Val Tyr Phe Gly Thr Thr Ala Val Thr Gly Ser Gly Ile Val Ser
    530                 535                 540
Trp Glu Asp Thr Gln Ile Lys Ala Val Ile Pro Lys Val Ala Ala Gly
545                 550                 555                 560
Lys Thr Gly Val Ser Val Lys Thr Ser Ser Gly Thr Ala Ser Asn Thr
                565                 570                 575
Phe Lys Ser Phe Asn Val Leu Thr Gly Asp Gln Val Thr Val Arg Phe
            580                 585                 590
Leu Val Asn Gln Ala Asn Thr Asn Tyr Gly Thr Asn Val Tyr Leu Val
        595                 600                 605
Gly Asn Ala Ala Glu Leu Gly Ser Trp Asp Pro Asn Lys Ala Ile Gly
    610                 615                 620
Pro Met Tyr Asn Gln Val Ile Ala Lys Tyr Pro Ser Trp Tyr Tyr Asp
625                 630                 635                 640
Val Ser Val Pro Ala Gly Thr Lys Leu Asp Phe Lys Phe Ile Lys Lys
                645                 650                 655
Gly Gly Gly Thr Val Thr Trp Glu Gly Gly Gly Asn His Thr Tyr Thr
            660                 665                 670
Thr Pro Ala Ser Gly Val Gly Thr Val Thr Val Asp Trp Gln Asn
        675                 680                 685


<210> 81
<211> 714
<212> PRT
<213> Artificial Sequence

<220>
<223> WP_036618292.1

<400> 81
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```
Met Lys Ser Arg Tyr Lys Arg Leu Thr Ser Leu Ala Leu Ser Leu Ser
 1               5                  10                  15
Met Ala Leu Gly Ile Ser Leu Pro Ala Trp Ala Ser Pro Asp Thr Ser
            20                  25                  30
Val Asp Asn Lys Val Asn Phe Ser Thr Asp Val Ile Tyr Gln Ile Val
        35                  40                  45
Thr Asp Arg Phe Ala Asp Gly Asp Arg Thr Asn Asn Pro Ala Gly Asp
    50                  55                  60
Ala Phe Ser Gly Asp Arg Ser Asn Leu Lys Leu Tyr Phe Gly Gly Asp
65                  70                  75                  80
Trp Gln Gly Ile Ile Asp Lys Ile Asn Asp Gly Tyr Leu Thr Gly Met
                85                  90                  95
Gly Val Thr Ala Leu Trp Ile Ser Gln Pro Val Glu Asn Ile Thr Ser
            100                 105                 110
Val Ile Lys Tyr Ser Gly Val Asn Asn Thr Ser Tyr His Gly Tyr Trp
        115                 120                 125
Ala Arg Asp Phe Lys Gln Thr Asn Asp Ala Phe Gly Asp Phe Ala Asp
    130                 135                 140
Phe Gln Asn Leu Ile Asp Thr Ala His Ala His Asn Ile Lys Val Val
145                 150                 155                 160
Ile Asp Phe Ala Pro Asn His Thr Ser Pro Ala Asp Arg Asp Asn Pro
                165                 170                 175
Gly Phe Ala Glu Asn Gly Ala Leu Tyr Asp Asn Gly Ser Leu Leu Gly
            180                 185                 190
Ala Tyr Ser Asn Asp Thr Ala Gly Leu Phe His His Asn Gly Gly Thr
        195                 200                 205
Asp Phe Ser Thr Ile Glu Asp Gly Ile Tyr Lys Asn Leu Tyr Asp Leu
    210                 215                 220
Ala Asp Ile Asn His Asn Asn Asn Ala Met Asp Ala Tyr Phe Lys Ser
225                 230                 235                 240
Ala Ile Asp Leu Trp Leu Gly Met Gly Val Asp Gly Ile Arg Phe Asp
                245                 250                 255
Ala Val Lys His Met Pro Phe Gly Trp Gln Lys Ser Phe Val Ser Ser
            260                 265                 270
Ile Tyr Gly Gly Asp His Pro Val Phe Thr Phe Gly Glu Trp Tyr Leu
        275                 280                 285
Gly Ala Asp Gln Thr Asp Gly Asp Asn Ile Lys Phe Ala Asn Glu Ser
    290                 295                 300
Gly Met Asn Leu Leu Asp Phe Glu Tyr Ala Gln Glu Val Arg Glu Val
305                 310                 315                 320
Phe Arg Asp Lys Thr Glu Thr Met Lys Asp Leu Tyr Glu Val Leu Ala
                325                 330                 335
Ser Thr Glu Ser Gln Tyr Asp Tyr Ile Asn Asn Met Val Thr Phe Ile
            340                 345                 350
Asp Asn His Asp Met Asp Arg Phe Gln Val Ala Gly Ser Gly Thr Arg
        355                 360                 365
Ala Thr Glu Gln Ala Leu Ala Leu Thr Leu Thr Ser Arg Gly Val Pro
    370                 375                 380
Ala Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asp Gly Asp Pro
385                 390                 395                 400
Asn Asn Arg Ala Met Met Thr Ser Phe Asn Thr Gly Thr Thr Ala Tyr
                405                 410                 415
Lys Val Ile Gln Ala Leu Ala Pro Leu Arg Lys Ser Asn Pro Ala Ile
            420                 425                 430
```

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


<210> 82
<211> 714
<212> PRT
<213> Artificial Sequence

<220>
<223> P04830.2

<400> 82
Met Lys Ser Arg Tyr Lys Arg Leu Thr Ser Leu Ala Leu Ser Leu Ser
 1               5                  10                  15
Met Ala Leu Gly Ile Ser Leu Pro Ala Trp Ala Ser Pro Asp Thr Ser
            20                  25                  30
Val Asp Asn Lys Val Asn Phe Ser Thr Asp Val Ile Tyr Gln Ile Val
        35                  40                  45
Thr Asp Arg Phe Ala Asp Gly Asp Arg Thr Asn Asn Pro Ala Gly Asp
```

```
    50                  55                  60
Ala Phe Ser Gly Asp Arg Ser Asn Leu Lys Leu Tyr Phe Gly Gly Asp
65                  70                  75                  80
Trp Gln Gly Ile Ile Asp Lys Ile Asn Asp Gly Tyr Leu Thr Gly Met
                85                  90                  95
Gly Val Thr Ala Leu Trp Ile Ser Gln Pro Val Glu Asn Ile Thr Ser
            100                 105                 110
Val Ile Lys Tyr Ser Gly Val Asn Asn Thr Ser Tyr His Gly Tyr Trp
        115                 120                 125
Ala Arg Asp Phe Lys Gln Thr Asn Asp Ala Phe Gly Asp Phe Ala Asp
    130                 135                 140
Phe Gln Asn Leu Ile Asp Thr Ala His Ala His Asn Ile Lys Val Val
145                 150                 155                 160
Ile Asp Phe Ala Pro Asn His Thr Ser Pro Ala Asp Arg Asp Asn Pro
                165                 170                 175
Gly Phe Ala Glu Asn Gly Gly Met Tyr Asp Asn Gly Ser Leu Leu Gly
            180                 185                 190
Ala Tyr Ser Asn Asp Thr Ala Gly Leu Phe His His Asn Gly Gly Thr
        195                 200                 205
Asp Phe Ser Thr Ile Glu Asp Gly Ile Tyr Lys Asn Leu Tyr Asp Leu
    210                 215                 220
Ala Asp Ile Asn His Asn Asn Asn Ala Met Asp Ala Tyr Phe Lys Ser
225                 230                 235                 240
Ala Ile Asp Leu Trp Leu Gly Met Gly Val Asp Gly Ile Arg Phe Asp
                245                 250                 255
Ala Val Lys His Met Pro Phe Gly Trp Gln Lys Ser Phe Val Ser Ser
            260                 265                 270
Ile Tyr Gly Gly Asp His Pro Val Phe Thr Phe Gly Glu Trp Tyr Leu
        275                 280                 285
Gly Ala Asp Gln Thr Asp Gly Asp Asn Ile Lys Phe Ala Asn Glu Ser
    290                 295                 300
Gly Met Asn Leu Leu Asp Phe Glu Tyr Ala Gln Glu Val Arg Glu Val
305                 310                 315                 320
Phe Arg Asp Lys Thr Glu Thr Met Lys Asp Leu Tyr Glu Val Leu Ala
                325                 330                 335
Ser Thr Glu Ser Gln Tyr Asp Tyr Ile Asn Asn Met Val Thr Phe Ile
            340                 345                 350
Asp Asn His Asp Met Asp Arg Phe Gln Val Ala Gly Ser Gly Thr Arg
        355                 360                 365
Ala Thr Glu Gln Ala Leu Ala Leu Thr Leu Thr Ser Arg Gly Val Pro
    370                 375                 380
Ala Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asp Gly Asp Pro
385                 390                 395                 400
Asn Asn Arg Ala Met Met Thr Ser Phe Asn Thr Gly Thr Thr Ala Tyr
                405                 410                 415
Lys Val Ile Gln Ala Leu Ala Pro Leu Arg Lys Ser Asn Pro Ala Ile
            420                 425                 430
Ala Tyr Gly Thr Thr Thr Glu Arg Trp Val Asn Asn Asp Val Leu Ile
        435                 440                 445
Ile Glu Arg Lys Phe Gly Ser Ser Ala Ala Leu Val Ala Ile Asn Arg
    450                 455                 460
Asn Ser Ser Ala Ala Tyr Pro Ile Ser Gly Leu Leu Ser Ser Leu Pro
465                 470                 475                 480
Ala Gly Thr Tyr Ser Asp Val Leu Asn Gly Leu Leu Asn Gly Asn Ser
```

```
                485                 490                 495
Ile Thr Val Gly Ser Gly Gly Ala Val Thr Asn Phe Thr Leu Ala Ala
            500                 505                 510
Gly Gly Thr Ala Val Trp Gln Tyr Thr Ala Pro Glu Thr Ser Pro Ala
        515                 520                 525
Ile Gly Asn Val Gly Pro Thr Met Gly Gln Pro Gly Asn Ile Val Thr
    530                 535                 540
Ile Asp Gly Arg Gly Phe Gly Gly Thr Ala Gly Thr Val Tyr Phe Gly
545                 550                 555                 560
Thr Thr Ala Val Thr Gly Ser Gly Ile Val Ser Trp Glu Asp Thr Gln
                565                 570                 575
Ile Lys Ala Val Ile Pro Lys Val Ala Ala Gly Lys Thr Gly Val Ser
            580                 585                 590
Val Lys Thr Ser Ser Gly Thr Ala Ser Asn Thr Phe Lys Ser Phe Asn
        595                 600                 605
Val Leu Thr Gly Asp Gln Val Thr Val Arg Phe Leu Val Asn Gln Ala
    610                 615                 620
Asn Thr Asn Tyr Gly Thr Asn Val Tyr Leu Val Gly Asn Ala Ala Glu
625                 630                 635                 640
Leu Gly Ser Trp Asp Pro Asn Lys Ala Ile Gly Pro Met Tyr Asn Gln
                645                 650                 655
Val Ile Ala Lys Tyr Pro Ser Trp Tyr Tyr Asp Val Ser Val Pro Ala
            660                 665                 670
Gly Thr Lys Leu Asp Phe Lys Phe Ile Lys Lys Gly Gly Gly Thr Val
        675                 680                 685
Thr Trp Glu Gly Gly Gly Asn His Thr Tyr Thr Thr Pro Ala Ser Gly
    690                 695                 700
Val Gly Thr Val Thr Val Asp Trp Gln Asn
705                 710
```

<210> 83
<211> 714
<212> PRT
<213> Artificial Sequence

<220>
<223> AAC04359.1

<400> 83

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

```
Val Ile Lys Tyr Ser Gly Val Asn Asn Thr Ser Tyr His Gly Tyr Trp
        115                 120                 125
Ala Arg Asp Phe Lys Gln Thr Asn Asp Ala Phe Gly Asp Phe Ala Asp
    130                 135                 140
Phe Gln Asn Leu Ile Asp Thr Ala His Ala His Asn Ile Lys Val Val
145                 150                 155                 160
Ile Asp Phe Ala Pro Asn His Thr Ser Pro Ala Asp Arg Asp Asn Pro
                165                 170                 175
Gly Phe Ala Glu Asn Gly Ala Leu Tyr Asp Asn Gly Ser Leu Leu Gly
            180                 185                 190
Ala Tyr Ser Asn Asp Thr Ala Gly Leu Phe His His Asn Gly Gly Thr
        195                 200                 205
Asp Phe Ser Thr Ile Glu Asp Gly Ile Tyr Lys Asn Leu Tyr Asp Leu
    210                 215                 220
Ala Asp Ile Asn His Asn Asn Asn Ala Met Asp Ala Tyr Phe Lys Ser
225                 230                 235                 240
Ala Ile Asp Leu Trp Leu Gly Met Gly Val Asp Gly Ile Arg Phe Asp
                245                 250                 255
Ala Val Lys His Met Pro Phe Gly Trp Gln Lys Ser Phe Val Ser Ser
            260                 265                 270
Ile Tyr Gly Gly Asp His Pro Val Phe Thr Phe Gly Glu Trp Tyr Leu
        275                 280                 285
Gly Ala Asp Gln Thr Asp Gly Asp Asn Ile Lys Phe Ala Asn Glu Ser
    290                 295                 300
Gly Met Asn Leu Leu Asp Phe Glu Tyr Ala Gln Glu Val Arg Glu Val
305                 310                 315                 320
Phe Arg Asp Lys Thr Glu Thr Met Lys Asp Leu Tyr Glu Val Leu Ala
                325                 330                 335
Ser Thr Glu Ser Gln Tyr Asp Tyr Ile Asn Asn Met Val Thr Phe Ile
            340                 345                 350
Asp Asn His Asp Met Asp Arg Phe Gln Val Ala Gly Ser Gly Thr Arg
        355                 360                 365
Ala Thr Glu Gln Ala Leu Ala Leu Thr Leu Thr Ser Arg Gly Val Pro
    370                 375                 380
Ala Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asp Gly Asp Pro
385                 390                 395                 400
Asn Asn Arg Ala Met Met Thr Ser Phe Asn Thr Gly Thr Thr Ala Tyr
                405                 410                 415
Lys Val Ile Gln Ala Leu Ala Pro Leu Arg Lys Ser Asn Pro Ala Ile
            420                 425                 430
Ala Tyr Gly Thr Thr Thr Glu Arg Trp Val Asn Asn Asp Val Leu Ile
        435                 440                 445
Ile Glu Arg Lys Phe Gly Ser Ser Ala Ala Leu Val Ala Ile Asn Arg
    450                 455                 460
Asn Ser Ser Ala Ala Tyr Pro Ile Ser Gly Leu Leu Ser Ser Leu Pro
465                 470                 475                 480
Ala Gly Thr Tyr Ser Asp Val Leu Asn Gly Leu Leu Asn Gly Asn Ser
                485                 490                 495
Ile Thr Val Gly Ser Gly Gly Ala Val Thr Asn Phe Thr Leu Ala Ala
            500                 505                 510
Gly Gly Thr Ala Val Trp Gln Tyr Thr Ala Pro Glu Thr Ser Pro Ala
        515                 520                 525
Ile Gly Asn Val Gly Pro Thr Met Gly Gln Pro Gly Asn Ile Val Thr
    530                 535                 540
```

```
Ile Asp Gly Arg Gly Phe Gly Gly Thr Ala Gly Thr Val Tyr Phe Gly
545                 550                 555                 560
Thr Thr Ala Val Thr Gly Ser Gly Ile Val Ser Trp Glu Asp Thr Gln
                565                 570                 575
Ile Lys Ala Val Ile Pro Lys Val Ala Ala Gly Lys Thr Gly Val Ser
            580                 585                 590
Val Lys Thr Ser Ser Gly Thr Ala Ser Asn Thr Phe Lys Ser Phe Asn
        595                 600                 605
Val Leu Thr Gly Asp Gln Val Thr Val Arg Phe Leu Val Asn Gln Ala
    610                 615                 620
Asn Thr Asn Tyr Gly Thr Asn Val Tyr Leu Val Gly Asn Ala Ala Glu
625                 630                 635                 640
Leu Gly Ser Trp Asp Pro Asn Lys Ala Ile Gly Pro Met Tyr Asn Gln
                645                 650                 655
Val Ile Ala Lys Tyr Pro Ser Trp Tyr Tyr Asp Val Ser Val Pro Ala
            660                 665                 670
Gly Thr Lys Leu Asp Phe Lys Phe Ile Lys Lys Gly Gly Gly Thr Val
        675                 680                 685
Thr Trp Glu Gly Gly Gly Asn His Thr Tyr Thr Thr Pro Ala Ser Gly
    690                 695                 700
Val Gly Thr Val Thr Val Asp Trp Gln Asn
705                 710
```

<210> 84
<211> 714
<212> PRT
<213> Artificial Sequence

<220>
<223> CAA41773.1

<400> 84

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

```
                165                 170                 175
Gly Phe Ala Glu Asn Gly Gly Met Tyr Asp Asn Gly Ser Leu Leu Gly
            180                 185                 190
Ala Tyr Ser Asn Asp Thr Ala Gly Leu Phe His His Asn Gly Gly Thr
        195                 200                 205
Asp Phe Ser Thr Ile Glu Asp Gly Ile Tyr Lys Asn Leu Tyr Asp Leu
    210                 215                 220
Ala Asp Ile Asn His Asn Asn Asn Ala Met Asp Ala Tyr Phe Lys Ser
225                 230                 235                 240
Ala Ile Asp Leu Trp Leu Gly Met Gly Val Asp Gly Ile Arg Phe Asp
                245                 250                 255
Ala Val Lys His Met Pro Phe Gly Trp Gln Lys Ser Phe Val Ser Ser
            260                 265                 270
Ile Tyr Gly Gly Asp His Pro Val Phe Thr Phe Gly Glu Trp Tyr Leu
        275                 280                 285
Gly Ala Asp Gln Thr Asp Gly Asp Asn Ile Lys Phe Ala Asn Glu Ser
    290                 295                 300
Gly Met Asn Leu Leu Asp Phe Glu Tyr Ala Gln Glu Val Arg Glu Val
305                 310                 315                 320
Phe Arg Asp Lys Thr Glu Thr Met Lys Asp Leu Tyr Glu Val Leu Ala
                325                 330                 335
Ser Thr Glu Ser Gln Tyr Asp Tyr Ile Asn Asn Met Val Thr Phe Ile
            340                 345                 350
Asp Asn His Asp Met Asp Arg Phe Gln Val Ala Gly Ser Gly Thr Arg
        355                 360                 365
Ala Thr Glu Gln Ala Leu Ala Leu Thr Leu Thr Ser Arg Gly Val Pro
    370                 375                 380
Ala Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asp Gly Asp Pro
385                 390                 395                 400
Asn Asn Arg Ala Met Met Thr Ser Phe Asn Thr Gly Thr Thr Ala Tyr
                405                 410                 415
Lys Val Ile Gln Ala Leu Ala Pro Leu Arg Lys Ser Asn Pro Ala Ile
            420                 425                 430
Ala Tyr Gly Thr Thr Thr Glu Arg Trp Val Asn Asn Asp Val Leu Ile
        435                 440                 445
Ile Glu Arg Lys Phe Gly Ser Ser Ala Ala Leu Val Ala Ile Asn Arg
    450                 455                 460
Asn Ser Ser Ala Ala Tyr Pro Ile Ser Gly Leu Leu Ser Ser Leu Pro
465                 470                 475                 480
Ala Gly Thr Tyr Ser Asp Val Leu Asn Gly Leu Leu Asn Gly Asn Ser
                485                 490                 495
Ile Thr Val Gly Ser Gly Gly Ala Val Thr Asn Phe Thr Leu Ala Ala
            500                 505                 510
Gly Gly Thr Ala Val Trp Gln Tyr Thr Ala Pro Glu Thr Ser Pro Ala
        515                 520                 525
Ile Gly Asn Val Gly Pro Thr Met Gly Gln Pro Gly Asn Ile Val Thr
    530                 535                 540
Ile Asp Gly Arg Gly Phe Gly Gly Thr Ala Gly Thr Val Tyr Phe Gly
545                 550                 555                 560
Thr Thr Ala Val Thr Gly Ser Gly Ile Val Ser Trp Glu Asp Thr Gln
                565                 570                 575
Ile Lys Ala Val Ile Pro Lys Val Ala Ala Gly Lys Thr Gly Val Ser
            580                 585                 590
Val Lys Thr Ser Ser Gly Thr Ala Ser Asn Thr Phe Lys Ser Phe Asn
```

```
        595                 600                 605
Val Leu Thr Gly Asp Gln Val Thr Val Arg Phe Leu Val Asn Gln Ala
    610                 615                 620
Asn Thr Asn Tyr Gly Thr Asn Val Tyr Leu Val Gly Asn Ala Ala Glu
625                 630                 635                 640
Leu Gly Ser Trp Asp Pro Asn Lys Ala Ile Gly Pro Met Tyr Asn Gln
                645                 650                 655
Val Ile Ala Lys Tyr Pro Ser Trp Tyr Tyr Asp Val Ser Val Pro Ala
            660                 665                 670
Gly Thr Lys Leu Asp Phe Lys Phe Ile Lys Lys Gly Gly Gly Thr Val
        675                 680                 685
Thr Trp Glu Gly Gly Gly Asn His Thr Tyr Thr Thr Pro Ala Ser Gly
    690                 695                 700
Val Gly Thr Val Thr Val Asp Trp Gln Asn
705                 710


<210> 85
<211> 687
<212> PRT
<213> Artificial Sequence

<220>
<223> AGT21379.1

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

```
Gly Ile Arg Phe Asp Ala Val Lys His Met Pro Phe Gly Trp Gln Lys
225                 230                 235                 240
Ser Phe Val Ser Ser Ile Tyr Gly Gly Asp His Pro Val Phe Thr Phe
                245                 250                 255
Gly Glu Trp Tyr Leu Gly Ala Asp Gln Thr Asp Gly Asp Asn Ile Lys
            260                 265                 270
Phe Ala Asn Glu Ser Gly Met Asn Leu Leu Asp Phe Glu Tyr Ala Gln
        275                 280                 285
Glu Val Arg Glu Val Phe Arg Asp Lys Thr Glu Thr Met Lys Asp Leu
    290                 295                 300
Tyr Glu Val Leu Ala Ser Thr Glu Ser Gln Tyr Asp Tyr Ile Asn Asn
305                 310                 315                 320
Met Val Thr Phe Ile Asp Asn His Asp Met Asp Arg Phe Gln Val Ala
                325                 330                 335
Gly Ser Gly Thr Arg Ala Thr Glu Gln Ala Leu Ala Leu Thr Leu Thr
            340                 345                 350
Ser Arg Gly Val Pro Ala Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr
        355                 360                 365
Gly Asp Gly Asp Pro Asn Asn Arg Ala Met Met Thr Ser Phe Asn Thr
    370                 375                 380
Gly Thr Thr Ala Tyr Lys Val Ile Gln Ala Leu Ala Pro Leu Arg Lys
385                 390                 395                 400
Ser Asn Pro Ala Ile Ala Tyr Gly Thr Thr Thr Glu Arg Trp Val Asn
                405                 410                 415
Asn Asp Val Leu Ile Ile Glu Arg Lys Phe Gly Ser Ser Ala Ala Leu
            420                 425                 430
Val Ala Ile Asn Arg Asn Ser Ser Ala Ala Tyr Pro Ile Ser Gly Leu
        435                 440                 445
Leu Ser Ser Leu Pro Ala Gly Thr Tyr Ser Asp Val Leu Asn Gly Leu
    450                 455                 460
Leu Asn Gly Asn Ser Ile Thr Val Gly Ser Gly Gly Ala Val Thr Asn
465                 470                 475                 480
Phe Thr Leu Ala Ala Gly Gly Thr Ala Val Trp Gln Tyr Thr Ala Pro
                485                 490                 495
Glu Thr Ser Pro Ala Ile Gly Asn Val Gly Pro Thr Met Gly Gln Pro
            500                 505                 510
Gly Asn Ile Val Thr Ile Asp Gly Arg Gly Phe Gly Gly Thr Ala Gly
        515                 520                 525
Thr Val Tyr Phe Gly Thr Thr Ala Val Thr Gly Ser Gly Ile Val Ser
    530                 535                 540
Trp Glu Asp Thr Gln Ile Lys Ala Val Ile Pro Lys Val Ala Ala Gly
545                 550                 555                 560
Lys Thr Gly Val Ser Val Lys Thr Ser Ser Gly Thr Ala Ser Asn Thr
                565                 570                 575
Phe Lys Ser Phe Asn Val Leu Thr Gly Asp Gln Val Thr Met Arg Phe
            580                 585                 590
Leu Val Asn Gln Ala Asn Thr Asn Tyr Gly Thr Asn Val Tyr Leu Val
        595                 600                 605
Gly Asn Ala Ala Glu Leu Gly Ser Trp Asp Pro Asn Lys Ala Ile Gly
    610                 615                 620
Pro Met Tyr Asn Gln Val Ile Ala Lys Tyr Pro Ser Trp Tyr Tyr Asp
625                 630                 635                 640
Val Ser Val Pro Ala Gly Thr Lys Leu Asp Phe Lys Phe Ile Lys Lys
                645                 650                 655
```

Gly Gly Gly Thr Val Thr Trp Glu Gly Gly Gly Asn His Thr Tyr Thr
660 665 670
Thr Pro Ala Ser Ser Val Gly Thr Val Thr Val Asp Trp Gln Asn
675 680 685

<210> 86
<211> 687
<212> PRT
<213> Artificial Sequence

<220>
<223> AGT95840.1 CGTase Amano

<220>
<221> VARIANT
<222> 485, 487
<223> Xaa = Any Amino Acid

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

```
Phe Ala Asn Glu Ser Gly Met Asn Leu Leu Asp Phe Glu Tyr Ala Gln
        275                 280                 285
Glu Val Arg Glu Val Phe Arg Asp Lys Thr Glu Thr Met Lys Asp Leu
    290                 295                 300
Tyr Glu Val Leu Ala Ser Thr Glu Ser Gln Tyr Asp Tyr Ile Asn Asn
305                 310                 315                 320
Met Val Thr Phe Ile Asp Asn His Asp Met Asp Arg Phe Gln Val Ala
                325                 330                 335
Gly Ser Gly Thr Arg Ala Thr Glu Gln Ala Leu Ala Leu Thr Leu Thr
            340                 345                 350
Ser Arg Gly Val Pro Ala Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr
        355                 360                 365
Gly Asp Gly Asp Pro Asn Asn Arg Ala Met Met Thr Ser Phe Asn Thr
    370                 375                 380
Gly Thr Thr Ala Tyr Lys Val Ile Gln Ala Leu Ala Pro Leu Arg Lys
385                 390                 395                 400
Ser Asn Pro Ala Ile Ala Tyr Gly Thr Thr Thr Glu Arg Trp Val Asn
                405                 410                 415
Asn Asp Val Leu Ile Ile Glu Arg Lys Phe Gly Ser Ser Ala Ala Leu
            420                 425                 430
Val Ala Ile Asn Arg Asn Ser Ser Ala Ala Tyr Pro Ile Ser Gly Leu
        435                 440                 445
Leu Ser Ser Leu Pro Ala Gly Thr Tyr Ser Asp Val Leu Asn Gly Leu
    450                 455                 460
Leu Asn Gly Asn Ser Ile Thr Val Gly Ser Gly Gly Ala Val Thr Asn
465                 470                 475                 480
Phe Thr Leu Ala Xaa Gly Xaa Thr Ala Val Trp Gln Tyr Thr Ala Pro
                485                 490                 495
Glu Thr Ser Pro Ala Ile Gly Asp Val Gly Pro Thr Met Gly Gln Pro
            500                 505                 510
Gly Asn Ile Val Thr Ile Asp Gly Arg Gly Phe Gly Gly Thr Ala Gly
        515                 520                 525
Thr Val Tyr Phe Gly Thr Thr Ala Val Thr Gly Ser Gly Ile Val Ser
    530                 535                 540
Trp Glu Asp Thr Gln Ile Lys Ala Val Ile Pro Lys Val Ala Ala Gly
545                 550                 555                 560
Lys Thr Gly Val Ser Val Lys Thr Ser Ser Gly Thr Ala Ser Asn Thr
                565                 570                 575
Phe Lys Ser Phe Asn Val Leu Thr Gly Asp Gln Val Thr Val Arg Phe
            580                 585                 590
Leu Val Asn Gln Ala Asn Thr Asn Tyr Gly Thr Asn Val Tyr Leu Val
        595                 600                 605
Gly Asn Ala Ala Glu Leu Asp Ser Trp Asp Pro Asn Lys Ala Ile Gly
    610                 615                 620
Pro Met Tyr Asn Gln Val Ile Ala Lys Tyr Pro Ser Trp Tyr Tyr Asp
625                 630                 635                 640
Val Ser Val Pro Ala Gly Thr Lys Leu Asp Phe Lys Phe Ile Lys Lys
                645                 650                 655
Gly Gly Gly Thr Val Thr Trp Glu Gly Gly Gly Asn His Thr Tyr Thr
            660                 665                 670
Thr Pro Ala Ser Gly Val Gly Thr Val Thr Ala Asp Trp Gln Asn
        675                 680                 685
```

<210> 87
<211> 713
<212> PRT
<213> Artificial Sequence

<220>
<223> P31835.1

<400> 87
Met Lys Lys Gln Val Lys Trp Leu Thr Ser Val Ser Met Ser Val Gly
 1               5                  10                  15
Ile Ala Leu Gly Ala Ala Leu Pro Val Trp Ala Ser Pro Asp Thr Ser
            20                  25                  30
Val Asn Asn Lys Leu Asn Phe Ser Thr Asp Thr Val Tyr Gln Ile Val
        35                  40                  45
Thr Asp Arg Phe Val Asp Gly Asn Ser Ala Asn Asn Pro Thr Gly Ala
    50                  55                  60
Ala Phe Ser Ser Asp His Ser Asn Leu Lys Leu Tyr Phe Gly Gly Asp
65                  70                  75                  80
Trp Gln Gly Ile Thr Asn Lys Ile Asn Asp Gly Tyr Leu Thr Gly Met
                85                  90                  95
Gly Ile Thr Ala Leu Trp Ile Ser Gln Pro Val Glu Asn Ile Thr Ala
            100                 105                 110
Val Ile Asn Tyr Ser Gly Val Asn Asn Thr Ala Tyr His Gly Tyr Trp
        115                 120                 125
Pro Arg Asp Phe Lys Lys Thr Asn Ala Ala Phe Gly Ser Phe Thr Asp
    130                 135                 140
Phe Ser Asn Leu Ile Ala Ala Ala His Ser His Asn Ile Lys Val Val
145                 150                 155                 160
Met Asp Phe Ala Pro Asn His Thr Asn Pro Ala Ser Ser Thr Asp Pro
                165                 170                 175
Ser Phe Ala Glu Asn Gly Ala Leu Tyr Asn Asn Gly Thr Leu Leu Gly
            180                 185                 190
Lys Tyr Ser Asn Asp Thr Ala Gly Leu Phe His His Asn Gly Gly Thr
        195                 200                 205
Asp Phe Ser Thr Thr Glu Ser Gly Ile Tyr Lys Asn Leu Tyr Asp Leu
    210                 215                 220
Ala Asp Ile Asn Gln Asn Asn Asn Thr Ile Asp Ser Tyr Leu Lys Glu
225                 230                 235                 240
Ser Ile Gln Leu Trp Leu Asn Leu Gly Val Asp Gly Ile Arg Phe Asp
                245                 250                 255
Ala Val Lys His Met Pro Gln Gly Trp Gln Lys Ser Tyr Val Ser Ser
            260                 265                 270
Ile Tyr Ser Ser Ala Asn Pro Val Phe Thr Phe Gly Glu Trp Phe Leu
        275                 280                 285
Gly Pro Asp Glu Met Thr Gln Asp Asn Ile Asn Phe Ala Asn Gln Ser
    290                 295                 300
Gly Met His Leu Leu Asp Phe Ala Phe Ala Gln Glu Ile Arg Glu Val
305                 310                 315                 320
Phe Arg Asp Lys Ser Glu Thr Met Thr Asp Leu Asn Ser Val Ile Ser
                325                 330                 335
Ser Thr Gly Ser Ser Tyr Asn Tyr Ile Asn Asn Met Val Thr Phe Ile
            340                 345                 350
Asp Asn His Asp Met Asp Arg Phe Gln Gln Ala Gly Ala Ser Thr Arg

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        355                 360                 365
Pro Thr Glu Gln Ala Leu Ala Val Thr Leu Thr Ser Arg Gly Val Pro
    370                 375                 380
Ala Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asn Gly Asp Pro
385                 390                 395                 400
Asn Asn Arg Gly Met Met Thr Gly Phe Asp Thr Asn Lys Thr Ala Tyr
                405                 410                 415
Lys Val Ile Lys Ala Leu Ala Pro Leu Arg Lys Ser Asn Pro Ala Leu
            420                 425                 430
Ala Tyr Gly Ser Thr Thr Gln Arg Trp Val Asn Ser Asp Val Tyr Val
        435                 440                 445
Tyr Glu Arg Lys Phe Gly Ser Asn Val Ala Leu Val Ala Val Asn Arg
    450                 455                 460
Ser Ser Thr Thr Ala Tyr Pro Ile Ser Gly Ala Leu Thr Ala Leu Pro
465                 470                 475                 480
Asn Gly Thr Tyr Thr Asp Val Leu Gly Gly Leu Leu Asn Gly Asn Ser
                485                 490                 495
Ile Thr Val Asn Gly Gly Thr Val Ser Asn Phe Thr Leu Ala Ala Gly
            500                 505                 510
Gly Thr Ala Val Trp Gln Tyr Thr Thr Thr Glu Ser Ser Pro Ile Ile
        515                 520                 525
Gly Asn Val Gly Pro Thr Met Gly Lys Pro Gly Asn Thr Ile Thr Ile
    530                 535                 540
Asp Gly Arg Gly Phe Gly Thr Thr Lys Asn Lys Val Thr Phe Gly Thr
545                 550                 555                 560
Thr Ala Val Thr Gly Ala Asn Ile Val Ser Trp Glu Asp Thr Glu Ile
                565                 570                 575
Lys Val Lys Val Pro Asn Val Ala Ala Gly Asn Thr Ala Val Thr Val
            580                 585                 590
Thr Asn Ala Ala Gly Thr Thr Ser Ala Ala Phe Asn Asn Phe Asn Val
        595                 600                 605
Leu Thr Ala Asp Gln Val Thr Val Arg Phe Lys Val Asn Asn Ala Thr
    610                 615                 620
Thr Ala Leu Gly Gln Asn Val Tyr Leu Thr Gly Asn Val Ala Glu Leu
625                 630                 635                 640
Gly Asn Trp Thr Ala Ala Asn Ala Ile Gly Pro Met Tyr Asn Gln Val
                645                 650                 655
Glu Ala Ser Tyr Pro Thr Trp Tyr Phe Asp Val Ser Val Pro Ala Asn
            660                 665                 670
Thr Ala Leu Gln Phe Lys Phe Ile Lys Val Asn Gly Ser Thr Val Thr
        675                 680                 685
Trp Glu Gly Gly Asn Asn His Thr Phe Thr Ser Pro Ser Ser Gly Val
    690                 695                 700
Ala Thr Val Thr Val Asp Trp Gln Asn
705                 710
```

<210> 88
<211> 714
<212> PRT
<213> Artificial Sequence

<220>
<223> KFM94552.1

<400> 88
Met Lys Ser Arg Tyr Lys Arg Leu Thr Ser Leu Ala Leu Ser Leu Ser
 1               5                  10                  15
Met Ala Leu Gly Ile Ser Leu Pro Ala Trp Ala Ser Pro Asp Thr Ser
            20                  25                  30
Val Asp Asn Lys Val Asn Phe Ser Thr Asp Val Ile Tyr Gln Ile Val
        35                  40                  45
Thr Asp Arg Phe Ala Asp Gly Asp Arg Thr Asn Asn Pro Ala Gly Asp
    50                  55                  60
Ala Phe Ser Gly Asp Arg Ser Asn Leu Lys Leu Tyr Phe Gly Gly Asp
65                  70                  75                  80
Trp Gln Gly Ile Ile Asp Lys Ile Asn Asp Gly Tyr Leu Thr Gly Met
                85                  90                  95
Gly Val Thr Ala Leu Trp Ile Ser Gln Pro Val Glu Asn Ile Thr Ser
            100                 105                 110
Val Ile Lys Tyr Ser Gly Val Asn Asn Thr Ser Tyr His Gly Tyr Trp
        115                 120                 125
Ala Arg Asp Phe Lys Gln Thr Asn Asp Ala Phe Gly Asp Phe Ala Asp
    130                 135                 140
Phe Gln Asn Leu Ile Asp Thr Ala His Ala His Asn Ile Lys Val Val
145                 150                 155                 160
Ile Asp Phe Ala Pro Asn His Thr Ser Pro Ala Asp Arg Asp Asn Pro
                165                 170                 175
Gly Phe Ala Glu Asn Gly Ala Leu Tyr Asp Asn Gly Ser Leu Leu Gly
            180                 185                 190
Ala Tyr Ser Asn Asp Thr Ala Gly Leu Phe His His Asn Gly Gly Thr
        195                 200                 205
Asp Phe Ser Thr Ile Glu Asp Gly Ile Tyr Lys Asn Leu Tyr Asp Leu
    210                 215                 220
Ala Asp Ile Asn His Asn Asn Asn Ala Met Asp Ala Tyr Phe Lys Ser
225                 230                 235                 240
Ala Ile Asp Leu Trp Leu Gly Met Gly Val Asp Gly Ile Arg Phe Asp
                245                 250                 255
Ala Val Lys His Met Pro Phe Gly Trp Gln Lys Ser Phe Val Ser Ser
            260                 265                 270
Ile Tyr Gly Gly Asp His Pro Val Phe Thr Phe Gly Glu Trp Tyr Leu
        275                 280                 285
Gly Ala Asp Gln Thr Asp Gly Asp Asn Ile Lys Phe Ala Asn Glu Ser
    290                 295                 300
Gly Met Asn Leu Leu Asp Phe Glu Tyr Ala Gln Glu Val Arg Glu Val
305                 310                 315                 320
Phe Arg Asp Lys Thr Glu Thr Met Lys Asp Leu Tyr Glu Val Leu Ala
                325                 330                 335
Ser Thr Glu Ser Gln Tyr Asp Tyr Ile Asn Asn Met Val Thr Phe Ile
            340                 345                 350
Asp Asn His Asp Met Asp Arg Phe Gln Val Ala Gly Ser Gly Thr Arg
        355                 360                 365
Ala Thr Glu Gln Ala Leu Ala Leu Thr Leu Thr Ser Arg Gly Val Pro
    370                 375                 380
Ala Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asp Gly Asp Pro
385                 390                 395                 400
Asn Asn Arg Ala Met Met Thr Ser Phe Asn Thr Gly Thr Thr Ala Tyr
                405                 410                 415

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

<210> 89
<211> 710
<212> PRT
<213> Artificial Sequence

<220>
<223> Toruzyme AJE25826.1

<400> 89

```
Met Lys Lys Thr Leu Lys Leu Leu Ser Ile Leu Leu Ile Thr Ile Ala
 1               5                  10                  15
Leu Leu Phe Ser Thr Ile Pro Ser Val Pro Ala Ala Pro Asp Thr Ser
            20                  25                  30
Val Ser Asn Val Val Asn Tyr Ser Thr Asp Val Ile Tyr Gln Ile Val
```

```
        35                  40                  45
Thr Asp Arg Phe Leu Asp Gly Asn Pro Ser Asn Asn Pro Thr Gly Asp
    50                  55                  60
Leu Tyr Asp Pro Thr His Thr Ser Leu Lys Lys Tyr Phe Gly Gly Asp
65                  70                  75                  80
Trp Gln Gly Ile Ile Asn Lys Ile Asn Asp Gly Tyr Leu Thr Gly Met
                85                  90                  95
Gly Ile Thr Ala Ile Trp Ile Ser Gln Pro Val Glu Asn Ile Tyr Ala
            100                 105                 110
Val Leu Pro Asp Ser Thr Phe Gly Gly Ser Thr Ser Tyr His Gly Tyr
        115                 120                 125
Trp Ala Arg Asp Phe Lys Lys Thr Asn Pro Phe Phe Gly Ser Phe Thr
    130                 135                 140
Asp Phe Gln Asn Leu Ile Ala Thr Ala His Ala His Asn Ile Lys Val
145                 150                 155                 160
Ile Ile Asp Phe Ala Pro Asn His Thr Ser Pro Ala Ser Glu Thr Asp
                165                 170                 175
Pro Thr Tyr Gly Glu Asn Gly Arg Leu Tyr Asp Asn Gly Glu Leu Leu
            180                 185                 190
Gly Gly Tyr Thr Asn Asp Thr Asn Gly Tyr Phe His His Tyr Gly Gly
        195                 200                 205
Thr Asn Phe Ser Ser Tyr Glu Asp Gly Ile Tyr Arg Asn Leu Phe Asp
    210                 215                 220
Leu Ala Asp Leu Asp Gln Gln Asn Asn Thr Ile Asp Ser Tyr Leu Lys
225                 230                 235                 240
Ala Ala Ile Lys Leu Trp Leu Asp Met Gly Ile Asp Gly Ile Arg Met
                245                 250                 255
Asp Ala Val Lys His Met Ala Phe Gly Trp Gln Lys Asn Phe Met Asp
            260                 265                 270
Ser Ile Leu Ser Tyr Arg Pro Val Phe Thr Phe Gly Glu Trp Tyr Leu
        275                 280                 285
Gly Thr Asn Glu Val Asp Pro Asn Asn Thr Tyr Phe Ala Asn Glu Ser
    290                 295                 300
Gly Met Asn Leu Leu Asp Phe Arg Phe Ala Gln Lys Val Arg Gln Val
305                 310                 315                 320
Phe Arg Asp Asn Thr Asp Thr Met Tyr Gly Leu Asp Ser Met Ile Gln
                325                 330                 335
Ser Thr Ala Ala Asp Tyr Asn Phe Ile Asn Asp Met Val Thr Phe Ile
            340                 345                 350
Asp Asn His Asp Met Asp Arg Phe Tyr Thr Gly Gly Ser Thr Arg Pro
        355                 360                 365
Val Glu Gln Ala Leu Ala Phe Thr Leu Thr Ser Arg Gly Val Pro Ala
    370                 375                 380
Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asn Gly Asp Pro Tyr
385                 390                 395                 400
Asn Arg Ala Met Met Thr Ser Phe Asn Thr Asn Thr Thr Ala Tyr Asn
                405                 410                 415
Val Ile Lys Lys Leu Ala Pro Leu Arg Lys Ser Asn Pro Ala Ile Ala
            420                 425                 430
Tyr Gly Thr Gln Lys Gln Arg Trp Val Asn Asn Asp Val Tyr Ile Tyr
        435                 440                 445
Glu Arg Gln Phe Gly Asn Asn Val Ala Leu Ile Ala Ile Asn Arg Asn
    450                 455                 460
Leu Ser Thr Ser Tyr Asn Ile Thr Gly Leu Tyr Thr Ala Leu Pro Ala
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465                 470                 475                 480
Gly Thr Tyr Ser Asp Val Leu Gly Gly Leu Leu Asn Gly Asn Ser Ile
                485                 490                 495
Thr Val Ser Ser Asn Gly Ser Val Thr Ser Phe Thr Leu Ala Pro Gly
            500                 505                 510
Ala Val Ala Val Trp Gln Tyr Val Ser Thr Thr Asn Pro Pro Leu Ile
        515                 520                 525
Gly His Val Gly Pro Thr Met Thr Lys Ala Gly Gln Thr Ile Thr Ile
    530                 535                 540
Asp Gly Arg Gly Phe Gly Thr Thr Ala Gly Gln Val Leu Phe Gly Thr
545                 550                 555                 560
Thr Pro Ala Thr Ile Val Ser Trp Glu Asp Thr Glu Val Lys Val Lys
                565                 570                 575
Val Pro Ala Leu Thr Pro Gly Lys Tyr Asn Ile Thr Leu Lys Thr Ala
            580                 585                 590
Ser Glu Val Thr Ser Asn Ser Tyr Asn Asn Ile Asn Val Leu Thr Gly
        595                 600                 605
Asn Gln Val Cys Val Arg Phe Val Val Asn Asn Ala Thr Thr Val Trp
    610                 615                 620
Gly Glu Asn Val Tyr Leu Thr Gly Asn Val Ala Glu Leu Gly Asn Trp
625                 630                 635                 640
Asp Thr Ser Lys Ala Ile Gly Pro Met Phe Asn Gln Val Val Tyr Gln
                645                 650                 655
Tyr Pro Thr Trp Tyr Tyr Asp Val Ser Val Pro Ala Gly Thr Thr Ile
            660                 665                 670
Glu Phe Lys Phe Ile Lys Lys Asn Gly Ser Thr Val Thr Trp Glu Gly
        675                 680                 685
Gly Tyr Asn His Val Tyr Thr Thr Pro Thr Ser Gly Thr Ala Thr Val
    690                 695                 700
Ile Val Asn Trp Gln Asn
705                 710
```

<210> 90
<211> 526
<212> PRT
<213> Artificial Sequence

<220>
<223> Toruzyme KHO62967.1

<400> 90

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

```
Trp Ile Ser Pro Val Val Asp Asn Ile Asn Lys Pro Ala Ile Tyr Asn
            100                 105                 110
Gly Glu Ile Asn Ala Pro Tyr His Gly Tyr Trp Ala Arg Asp Phe Lys
        115                 120                 125
Arg Val Glu Glu His Phe Gly Ser Trp Glu Asp Phe Asp Asn Phe Val
    130                 135                 140
Lys Thr Ala His Ala Asn Gly Ile Lys Val Ile Leu Asp Phe Ala Pro
145                 150                 155                 160
Asn His Thr Ser Pro Ala Asp Lys Asn Asn Pro Asp Phe Ala Glu Asn
                165                 170                 175
Gly Ala Leu Tyr Asp Asp Gly Asn Leu Leu Gly Thr Tyr Ser Asn Asp
            180                 185                 190
Val Asn Lys Leu Phe His His Asn Gly Gly Ile Thr Asn Trp Asn Asn
        195                 200                 205
Leu Lys Asp Leu Gln Asp Lys Asn Leu Phe Asp Leu Ala Asp Leu Asp
    210                 215                 220
Gln Ser Asn Pro Ile Val Asp Lys Tyr Leu Lys Asp Ser Ile Lys Leu
225                 230                 235                 240
Trp Phe Ser His Gly Ile Asp Gly Val Arg Leu Asp Ala Val Lys His
                245                 250                 255
Met Pro Met Glu Trp Val Lys Ser Phe Ala Asp Thr Ile Tyr Gly Val
            260                 265                 270
Asn Lys Asp Ala Ile Leu Phe Gly Glu Trp Met Leu Asn Gly Pro Thr
        275                 280                 285
Asp Pro Leu Tyr Gly Tyr Asn Ile Gln Phe Ala Asn Thr Ser Gly Phe
    290                 295                 300
Ser Val Leu Asp Phe Met Leu Asn Ser Ala Ile Lys Asp Val Phe Glu
305                 310                 315                 320
Lys Gly Tyr Gly Phe Asp Arg Leu Asn Asp Thr Ile Glu Glu Thr Asn
                325                 330                 335
Lys Asp Tyr Asp Asn Pro Tyr Lys Leu Val Thr Phe Val Asp Asn His
            340                 345                 350
Asp Met Pro Arg Phe Leu Ser Val Asn Asp Asp Lys Asp Lys Leu His
        355                 360                 365
Glu Ala Ile Ala Phe Ile Met Thr Ser Arg Gly Ile Pro Ala Ile Tyr
    370                 375                 380
Tyr Gly Thr Glu Gln Tyr Leu His Asn Asp Thr Asn Gly Gly Asn Asp
385                 390                 395                 400
Pro Tyr Asn Arg Pro Met Met Glu Lys Phe Asp Glu Asn Thr Thr Ala
                405                 410                 415
Tyr Val Leu Ile Arg Glu Leu Ser Asn Leu Arg Lys Ala Thr Gln Ala
            420                 425                 430
Leu Gln Tyr Gly Lys Thr Val Ser Arg Tyr Val Ser Asn Asp Val Tyr
        435                 440                 445
Ile Tyr Glu Arg Gln Tyr Gly Lys Asp Ile Val Val Val Ala Ile Asn
    450                 455                 460
Lys Gly Glu Glu Thr Thr Val Lys Asn Ile Glu Thr Ser Leu Arg Lys
465                 470                 475                 480
Gly Lys Tyr Ser Asp Tyr Leu Lys Gly Leu Leu Lys Gly Gly Asn Leu
                485                 490                 495
Lys Val Glu Arg Gly Asn Ser Glu Asn Asp Ile Leu Ser Ile Thr Leu
            500                 505                 510
Pro Lys Asp Ser Val Ser Ile Trp Thr Asn Val Lys Val Lys
        515                 520                 525
```

<210> 91
<211> 710
<212> PRT
<213> Artificial Sequence

<220>
<223> Toruzyme KHO61869.1

<400> 91
Met Lys Lys Thr Leu Lys Leu Leu Ser Ile Leu Leu Ile Thr Ile Ala
 1               5                  10                  15
Leu Leu Phe Ser Ser Ile Pro Ser Val Pro Ala Ala Pro Asp Thr Ser
            20                  25                  30
Val Ser Asn Val Val Asn Tyr Ser Thr Asp Val Ile Tyr Gln Ile Val
        35                  40                  45
Thr Asp Arg Phe Leu Asp Gly Asn Pro Asn Asn Asn Pro Thr Gly Asp
    50                  55                  60
Leu Tyr Asp Pro Thr His Thr Ser Leu Lys Lys Tyr Phe Gly Gly Asp
65                  70                  75                  80
Trp Gln Gly Ile Ile Asn Lys Ile Asn Asp Gly Tyr Leu Thr Gly Met
                85                  90                  95
Gly Ile Thr Ala Ile Trp Ile Ser Gln Pro Val Glu Asn Ile Tyr Ala
            100                 105                 110
Val Leu Pro Asp Ser Thr Phe Gly Gly Ser Thr Ser Tyr His Gly Tyr
        115                 120                 125
Trp Ala Arg Asp Phe Lys Lys Thr Asn Pro Phe Phe Gly Ser Phe Thr
    130                 135                 140
Asp Phe Gln Asn Leu Ile Ala Thr Ala His Ala His Asn Ile Lys Val
145                 150                 155                 160
Ile Ile Asp Phe Ala Pro Asn His Thr Ser Pro Ala Ser Glu Thr Asp
                165                 170                 175
Pro Thr Tyr Gly Glu Asn Gly Arg Leu Tyr Asp Asn Gly Val Leu Leu
            180                 185                 190
Gly Gly Tyr Thr Asn Asp Thr Asn Gly Tyr Phe His His Tyr Gly Gly
        195                 200                 205
Thr Asn Phe Ser Ser Tyr Glu Asp Gly Ile Tyr Arg Asn Leu Phe Asp
    210                 215                 220
Leu Ala Asp Leu Asp Gln Gln Asn Asn Thr Ile Asp Ser Tyr Leu Lys
225                 230                 235                 240
Ala Ala Ile Lys Leu Trp Leu Asp Met Gly Ile Asp Gly Ile Arg Met
                245                 250                 255
Asp Ala Val Lys His Met Ala Phe Gly Trp Gln Lys Asn Phe Met Asp
            260                 265                 270
Ser Ile Leu Ser Tyr Arg Pro Val Phe Thr Phe Gly Glu Trp Tyr Leu
        275                 280                 285
Gly Thr Asn Glu Val Asp Pro Asn Asn Thr Tyr Phe Ala Asn Glu Ser
    290                 295                 300
Gly Met Ser Leu Leu Asp Phe Arg Phe Ala Gln Lys Val Arg Gln Val
305                 310                 315                 320
Phe Arg Asp Asn Thr Asp Thr Met Tyr Gly Leu Asp Ser Met Leu Gln
                325                 330                 335

```
Ser Thr Ala Ala Asp Tyr Asn Phe Ile Asn Asp Met Val Thr Phe Ile
            340                 345                 350
Asp Asn His Asp Met Asp Arg Phe Tyr Thr Gly Gly Ser Thr Arg Pro
        355                 360                 365
Val Glu Gln Ala Leu Ala Phe Thr Leu Thr Ser Arg Gly Val Pro Ala
    370                 375                 380
Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asn Gly Asp Pro Tyr
385                 390                 395                 400
Asn Arg Ala Met Met Thr Ser Phe Asp Thr Thr Thr Thr Ala Tyr Asn
                405                 410                 415
Val Ile Lys Lys Leu Ala Pro Leu Arg Lys Ser Asn Pro Ala Ile Ala
            420                 425                 430
Tyr Gly Thr Gln Lys Gln Arg Trp Ile Asn Asn Asp Val Tyr Ile Tyr
        435                 440                 445
Glu Arg Gln Phe Gly Asn Asn Val Ala Leu Val Ala Ile Asn Arg Asn
    450                 455                 460
Leu Ser Thr Ser Tyr Tyr Ile Thr Gly Leu Tyr Thr Ala Leu Pro Ala
465                 470                 475                 480
Gly Thr Tyr Ser Asp Val Leu Gly Gly Leu Leu Asn Gly Asn Asn Ile
                485                 490                 495
Ser Val Ala Ser Asp Gly Ser Val Thr Pro Phe Thr Leu Ala Pro Gly
            500                 505                 510
Glu Val Ala Val Trp Gln Tyr Val Ser Thr Thr Asn Pro Pro Leu Ile
        515                 520                 525
Gly His Val Gly Pro Thr Met Thr Lys Ala Gly Gln Thr Ile Thr Ile
    530                 535                 540
Asp Gly Arg Gly Phe Gly Thr Thr Ala Gly Gln Val Leu Phe Gly Thr
545                 550                 555                 560
Thr Pro Ala Thr Ile Val Ser Trp Glu Asp Thr Glu Val Lys Val Lys
                565                 570                 575
Val Pro Ala Leu Thr Pro Gly Lys Tyr Asn Val Thr Leu Lys Thr Ala
            580                 585                 590
Ser Gly Val Thr Ser Asn Ser Tyr Asn Asn Ile Asn Val Leu Thr Gly
        595                 600                 605
Asn Gln Val Cys Val Arg Phe Val Val Asn Asn Ala Ser Thr Val Trp
    610                 615                 620
Gly Glu Asn Val Tyr Leu Thr Gly Asn Val Ala Glu Leu Gly Ser Trp
625                 630                 635                 640
Asp Thr Ser Lys Ala Ile Gly Pro Met Phe Asn Gln Val Val Tyr Gln
                645                 650                 655
Tyr Pro Thr Trp Tyr Tyr Asp Val Ser Val Pro Ala Gly Thr Thr Ile
            660                 665                 670
Glu Phe Lys Phe Ile Lys Lys Asn Gly Ser Thr Val Thr Trp Glu Gly
        675                 680                 685
Gly Tyr Asn His Val Tyr Thr Thr Pro Thr Ser Gly Thr Ala Thr Val
    690                 695                 700
Ile Val Asn Trp Gln Asn
705                 710
```

<210> 92
<211> 710
<212> PRT
<213> Artificial Sequence

<220>
<223> Toruzyme KHO61665.1

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

385 390 395 400
Asn Arg Ala Met Met Thr Ser Phe Asp Thr Thr Thr Thr Ala Tyr Asn
405 410 415
Val Ile Lys Lys Leu Ala Pro Leu Arg Lys Ser Asn Pro Ala Ile Ala
420 425 430
Tyr Gly Thr Gln Lys Gln Arg Trp Ile Asn Asn Asp Val Tyr Ile Tyr
435 440 445
Glu Arg Gln Phe Gly Asn Asn Val Ala Leu Val Ala Ile Asn Arg Asn
450 455 460
Leu Ser Thr Ser Tyr Tyr Ile Thr Gly Leu Tyr Thr Ala Leu Pro Ala
465 470 475 480
Gly Thr Tyr Ser Asp Val Leu Gly Gly Leu Leu Asn Gly Asn Asn Ile
485 490 495
Ser Val Ala Ser Asp Gly Ser Val Thr Pro Phe Thr Leu Ala Pro Gly
500 505 510
Glu Val Ala Val Trp Gln Tyr Val Ser Thr Thr Asn Pro Pro Leu Ile
515 520 525
Gly His Val Gly Pro Thr Met Thr Lys Ala Gly Gln Thr Ile Thr Ile
530 535 540
Asp Gly Arg Gly Phe Gly Thr Thr Ala Gly Gln Val Leu Phe Gly Thr
545 550 555 560
Thr Pro Ala Thr Ile Val Ser Trp Glu Asp Thr Glu Val Lys Val Lys
565 570 575
Val Pro Ala Leu Thr Pro Gly Lys Tyr Asn Val Thr Leu Lys Thr Ala
580 585 590
Ser Gly Val Thr Ser Asn Ser Tyr Asn Asn Ile Asn Val Leu Thr Gly
595 600 605
Asn Gln Val Cys Val Arg Phe Val Val Asn Asn Ala Ser Thr Val Trp
610 615 620
Gly Glu Asn Val Tyr Leu Thr Gly Asn Val Ala Glu Leu Gly Ser Trp
625 630 635 640
Asp Thr Ser Lys Ala Ile Gly Pro Met Phe Asn Gln Val Val Tyr Gln
645 650 655
Tyr Pro Thr Trp Tyr Tyr Asp Val Ser Val Pro Ala Gly Thr Thr Ile
660 665 670
Glu Phe Lys Phe Ile Lys Lys Asn Gly Ser Thr Val Thr Trp Glu Gly
675 680 685
Gly Tyr Asn His Val Tyr Thr Thr Pro Thr Ser Gly Thr Ala Thr Val
690 695 700
Ile Val Asn Trp Gln Asn
705 710

<210> 93
<211> 710
<212> PRT
<213> Artificial Sequence

<220>
<223> Toruzyme WP_042834654.1

<400> 93
Met Lys Lys Thr Leu Lys Leu Leu Ser Ile Leu Leu Ile Thr Ile Ala
1 5 10 15

```
Leu Leu Phe Ser Ser Ile Pro Ser Val Pro Ala Ala Pro Asp Thr Ser
            20                  25                  30
Val Ser Asn Val Val Asn Tyr Ser Thr Asp Val Ile Tyr Gln Ile Val
        35                  40                  45
Thr Asp Arg Phe Leu Asp Gly Asn Pro Asn Asn Asn Pro Thr Gly Asp
    50                  55                  60
Leu Tyr Asp Pro Thr His Thr Ser Leu Lys Lys Tyr Phe Gly Gly Asp
65                  70                  75                  80
Trp Gln Gly Ile Ile Asn Lys Ile Asn Asp Gly Tyr Leu Thr Gly Met
                85                  90                  95
Gly Ile Thr Ala Ile Trp Ile Ser Gln Pro Val Glu Asn Ile Tyr Ala
            100                 105                 110
Val Leu Pro Asp Ser Thr Phe Gly Gly Ser Thr Ser Tyr His Gly Tyr
        115                 120                 125
Trp Ala Arg Asp Phe Lys Lys Thr Asn Pro Phe Phe Gly Ser Phe Thr
    130                 135                 140
Asp Phe Gln Asn Leu Ile Ala Thr Ala His Ala His Asn Ile Lys Val
145                 150                 155                 160
Ile Ile Asp Phe Ala Pro Asn His Thr Ser Pro Ala Ser Glu Thr Asp
                165                 170                 175
Pro Thr Tyr Gly Glu Asn Gly Arg Leu Tyr Asp Asn Gly Val Leu Leu
            180                 185                 190
Gly Gly Tyr Thr Asn Asp Thr Asn Gly Tyr Phe His His Tyr Gly Gly
        195                 200                 205
Thr Asn Phe Ser Ser Tyr Glu Asp Gly Ile Tyr Arg Asn Leu Phe Asp
    210                 215                 220
Leu Ala Asp Leu Asp Gln Gln Asn Asn Thr Ile Asp Ser Tyr Leu Lys
225                 230                 235                 240
Ala Ala Ile Lys Leu Trp Leu Asp Met Gly Ile Asp Gly Ile Arg Met
                245                 250                 255
Asp Ala Val Lys His Met Ala Phe Gly Trp Gln Lys Asn Phe Met Asp
            260                 265                 270
Ser Ile Leu Ser Tyr Arg Pro Val Phe Thr Phe Gly Glu Trp Tyr Leu
        275                 280                 285
Gly Thr Asn Glu Val Asp Pro Asn Asn Thr Tyr Phe Ala Asn Glu Ser
    290                 295                 300
Gly Met Ser Leu Leu Asp Phe Arg Phe Ala Gln Lys Val Arg Gln Val
305                 310                 315                 320
Phe Arg Asp Asn Thr Asp Thr Met Tyr Gly Leu Asp Ser Met Leu Gln
                325                 330                 335
Ser Thr Ala Ala Asp Tyr Asn Phe Ile Asn Asp Met Val Thr Phe Ile
            340                 345                 350
Asp Asn His Asp Met Asp Arg Phe Tyr Thr Gly Gly Ser Thr Arg Pro
        355                 360                 365
Val Glu Gln Ala Leu Ala Phe Thr Leu Thr Ser Arg Gly Val Pro Ala
    370                 375                 380
Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asn Gly Asp Pro Tyr
385                 390                 395                 400
Asn Arg Ala Met Met Thr Ser Phe Asp Thr Thr Thr Thr Ala Tyr Asn
                405                 410                 415
Val Ile Lys Lys Leu Ala Pro Leu Arg Lys Ser Asn Pro Ala Ile Ala
            420                 425                 430
Tyr Gly Thr Gln Lys Gln Arg Trp Ile Asn Asn Asp Val Tyr Ile Tyr
        435                 440                 445
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Glu Arg Gln Phe Gly Asn Asn Val Ala Leu Val Ala Ile Asn Arg Asn
    450                 455                 460
Leu Ser Thr Ser Tyr Tyr Ile Thr Gly Leu Tyr Thr Ala Leu Pro Ala
465                 470                 475                 480
Gly Thr Tyr Ser Asp Val Leu Gly Gly Leu Leu Asn Gly Asn Asn Ile
                485                 490                 495
Ser Val Ala Ser Asp Gly Ser Val Thr Pro Phe Thr Leu Ala Pro Gly
            500                 505                 510
Glu Val Ala Val Trp Gln Tyr Val Ser Thr Thr Asn Pro Pro Leu Ile
        515                 520                 525
Gly His Val Gly Pro Thr Met Thr Lys Ala Gly Gln Thr Ile Thr Ile
    530                 535                 540
Asp Gly Arg Gly Phe Gly Thr Thr Ala Gly Gln Val Leu Phe Gly Thr
545                 550                 555                 560
Thr Pro Ala Thr Ile Val Ser Trp Glu Asp Thr Glu Val Lys Val Lys
                565                 570                 575
Val Pro Ala Leu Thr Pro Gly Lys Tyr Asn Val Thr Leu Lys Thr Ala
            580                 585                 590
Ser Gly Val Thr Ser Asn Ser Tyr Asn Asn Ile Asn Val Leu Thr Gly
        595                 600                 605
Asn Gln Val Cys Val Arg Phe Val Val Asn Asn Ala Ser Thr Val Trp
    610                 615                 620
Gly Glu Asn Val Tyr Leu Thr Gly Asn Val Ala Glu Leu Gly Ser Trp
625                 630                 635                 640
Asp Thr Ser Lys Ala Ile Gly Pro Met Phe Asn Gln Val Val Tyr Gln
                645                 650                 655
Tyr Pro Thr Trp Tyr Tyr Asp Val Ser Val Pro Ala Gly Thr Thr Ile
            660                 665                 670
Glu Phe Lys Phe Ile Lys Lys Asn Gly Ser Thr Val Thr Trp Glu Gly
        675                 680                 685
Gly Tyr Asn His Val Tyr Thr Thr Pro Thr Ser Gly Thr Ala Thr Val
    690                 695                 700
Ile Val Asn Trp Gln Asn
705                 710


<210> 94
<211> 710
<212> PRT
<213> Artificial Sequence

<220>
<223> Toruzyme WP_042834464.1

<400> 94
Met Lys Lys Thr Leu Lys Leu Leu Ser Ile Leu Leu Ile Thr Ile Ala
 1               5                  10                  15
Leu Leu Phe Ser Ser Ile Pro Ser Val Pro Ala Ala Pro Asp Thr Ser
            20                  25                  30
Val Ser Asn Val Val Asn Tyr Ser Thr Asp Val Ile Tyr Gln Ile Val
        35                  40                  45
Thr Asp Arg Phe Leu Asp Gly Asn Pro Ser Asn Asn Pro Thr Gly Asp
    50                  55                  60
Leu Tyr Asp Pro Thr His Thr Ser Leu Lys Lys Tyr Phe Gly Gly Asp
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65                  70                  75                  80
Trp Gln Gly Ile Ile Asn Lys Ile Asn Asp Gly Tyr Leu Thr Gly Met
                85                  90                  95
Gly Ile Thr Ala Ile Trp Ile Ser Gln Pro Val Glu Asn Ile Tyr Ala
            100                 105                 110
Val Leu Pro Asp Ser Thr Phe Gly Gly Ser Thr Ser Tyr His Gly Tyr
        115                 120                 125
Trp Ala Arg Asp Phe Lys Lys Thr Asn Pro Phe Phe Gly Ser Phe Thr
    130                 135                 140
Asp Phe Gln Asn Leu Ile Ala Thr Ala His Ala His Asn Ile Lys Val
145                 150                 155                 160
Ile Ile Asp Phe Ala Pro Asn His Thr Ser Pro Ala Ser Glu Thr Asp
                165                 170                 175
Pro Thr Tyr Gly Glu Asn Gly Arg Leu Tyr Asp Asn Gly Val Leu Leu
            180                 185                 190
Gly Gly Tyr Thr Asn Asp Thr Asn Gly Tyr Phe His His Tyr Gly Gly
        195                 200                 205
Thr Asn Phe Ser Ser Tyr Glu Asp Gly Ile Tyr Arg Asn Leu Phe Asp
    210                 215                 220
Leu Ala Asp Leu Asp Gln Gln Asn Asn Thr Ile Asp Ser Tyr Leu Lys
225                 230                 235                 240
Val Ala Ile Lys Leu Trp Leu Asn Met Gly Ile Asp Gly Ile Arg Met
                245                 250                 255
Asp Ala Val Lys His Met Ala Phe Gly Trp Gln Lys Asn Phe Met Asp
            260                 265                 270
Ser Ile Leu Ser Tyr Arg Pro Val Phe Thr Phe Gly Glu Trp Tyr Leu
        275                 280                 285
Gly Thr Asn Glu Val Asp Pro Asn Asn Thr Tyr Phe Ala Asn Glu Ser
    290                 295                 300
Gly Met Ser Leu Leu Asp Phe Arg Phe Ala Gln Lys Val Arg Gln Val
305                 310                 315                 320
Phe Arg Asp Asn Thr Asp Thr Met Tyr Gly Leu Asp Ser Met Leu Gln
                325                 330                 335
Ser Thr Ala Ala Asp Tyr Asn Phe Ile Asn Asp Met Val Thr Phe Ile
            340                 345                 350
Asp Asn His Asp Met Asp Arg Phe Tyr Thr Gly Gly Ser Thr Arg Pro
        355                 360                 365
Val Glu Gln Ala Leu Ala Phe Thr Leu Thr Ser Arg Gly Val Pro Ala
    370                 375                 380
Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asn Gly Asp Pro Tyr
385                 390                 395                 400
Asn Arg Ala Met Met Thr Ser Phe Asp Thr Thr Thr Thr Ala Tyr Asn
                405                 410                 415
Val Ile Lys Lys Leu Ala Pro Leu Arg Lys Ser Asn Pro Ala Ile Ala
            420                 425                 430
Tyr Gly Thr Gln Lys Gln Arg Trp Ile Asn Asn Asp Val Tyr Ile Tyr
        435                 440                 445
Glu Arg Gln Phe Gly Asn Asn Val Ala Leu Val Ala Ile Asn Arg Asn
    450                 455                 460
Leu Ser Thr Ser Tyr Tyr Ile Thr Gly Leu Tyr Thr Ala Leu Pro Ala
465                 470                 475                 480
Gly Thr Tyr Ser Asp Val Leu Gly Gly Leu Leu Asn Gly Asn Asn Ile
                485                 490                 495
Ser Val Ala Ser Asp Gly Ser Val Thr Pro Phe Thr Leu Ala Pro Gly
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```
            500                 505                 510
Glu Val Ala Val Trp Gln Tyr Val Ser Thr Thr Asn Pro Pro Leu Ile
        515                 520                 525
Gly His Val Gly Pro Thr Met Thr Lys Ala Gly Gln Thr Ile Thr Ile
    530                 535                 540
Asp Gly Arg Gly Phe Gly Thr Thr Ala Gly Gln Val Leu Phe Gly Thr
545                 550                 555                 560
Thr Pro Ala Thr Ile Val Ser Trp Glu Asp Thr Glu Val Lys Val Lys
                565                 570                 575
Val Pro Ala Leu Thr Pro Gly Lys Tyr Asn Val Thr Leu Lys Thr Ala
            580                 585                 590
Ser Gly Val Thr Ser Asn Ser Tyr Asn Asn Ile Asn Val Leu Thr Gly
        595                 600                 605
Asn Gln Val Cys Val Arg Phe Val Val Asn Asn Ala Ser Thr Val Trp
    610                 615                 620
Gly Glu Asn Val Tyr Leu Thr Gly Asn Val Ala Glu Leu Gly Ser Trp
625                 630                 635                 640
Asp Thr Ser Lys Ala Ile Gly Pro Met Phe Asn Gln Val Val Tyr Gln
                645                 650                 655
Tyr Pro Thr Trp Tyr Tyr Asp Val Ser Val Pro Ala Gly Thr Thr Ile
            660                 665                 670
Glu Phe Lys Phe Ile Lys Lys Asn Gly Ser Thr Val Thr Trp Glu Gly
        675                 680                 685
Gly Tyr Asn His Val Tyr Thr Thr Pro Thr Ser Gly Thr Ala Thr Val
    690                 695                 700
Ile Val Asn Trp Gln Asn
705                 710


<210> 95
<211> 711
<212> PRT
<213> Artificial Sequence

<220>
<223> Cyclomaltodextrin glucanotransferase

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

```
Ala Arg Asp Phe Lys Lys Pro Asn Pro Phe Phe Gly Thr Leu Ser Asp
    130                 135                 140
Phe Gln Arg Leu Val Asp Ala Ala His Ala Lys Gly Ile Lys Val Ile
145                 150                 155                 160
Ile Asp Phe Ala Pro Asn His Thr Ser Pro Ala Ser Glu Thr Asn Pro
                165                 170                 175
Ser Tyr Met Glu Asn Gly Arg Leu Tyr Asp Asn Gly Thr Leu Leu Gly
            180                 185                 190
Gly Tyr Thr Asn Asp Ala Asn Met Tyr Phe His His Asn Gly Gly Thr
        195                 200                 205
Thr Phe Ser Ser Leu Glu Asp Gly Ile Tyr Arg Asn Leu Phe Asp Leu
    210                 215                 220
Ala Asp Leu Asn His Gln Asn Pro Val Ile Asp Arg Tyr Leu Lys Asp
225                 230                 235                 240
Ala Val Lys Met Trp Ile Asp Met Gly Ile Asp Gly Ile Arg Met Asp
                245                 250                 255
Ala Val Lys His Met Pro Phe Gly Trp Gln Lys Ser Leu Met Asp Glu
            260                 265                 270
Ile Asp Asn Tyr Arg Pro Val Phe Thr Phe Gly Glu Trp Phe Leu Ser
        275                 280                 285
Glu Asn Glu Val Asp Ala Asn Asn His Tyr Phe Ala Asn Glu Ser Gly
    290                 295                 300
Met Ser Leu Leu Asp Phe Arg Phe Gly Gln Lys Leu Arg Gln Val Leu
305                 310                 315                 320
Arg Asn Asn Ser Asp Asn Trp Tyr Gly Phe Asn Gln Met Ile Gln Asp
                325                 330                 335
Thr Ala Ser Ala Tyr Asp Glu Val Leu Asp Gln Val Thr Phe Ile Asp
            340                 345                 350
Asn His Asp Met Asp Arg Phe Met Ile Asp Gly Gly Asp Pro Arg Lys
        355                 360                 365
Val Asp Met Ala Leu Ala Val Leu Leu Thr Ser Arg Gly Val Pro Asn
    370                 375                 380
Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asn Gly Asp Pro Asn
385                 390                 395                 400
Asn Arg Lys Met Met Ser Ser Phe Asn Lys Asn Thr Arg Ala Tyr Gln
                405                 410                 415
Val Ile Gln Lys Leu Ser Ser Leu Arg Arg Asn Asn Pro Ala Leu Ala
            420                 425                 430
Tyr Gly Asp Thr Glu Gln Arg Trp Ile Asn Gly Asp Val Tyr Val Tyr
        435                 440                 445
Glu Arg Gln Phe Gly Lys Asp Val Val Leu Val Ala Val Asn Arg Ser
    450                 455                 460
Ser Ser Ser Asn Tyr Ser Ile Thr Gly Leu Phe Thr Ala Leu Pro Ala
465                 470                 475                 480
Gly Thr Tyr Thr Asp Gln Leu Gly Gly Leu Leu Asp Gly Asn Thr Ile
                485                 490                 495
Gln Val Gly Ser Asn Gly Ser Val Asn Ala Phe Asp Leu Gly Pro Gly
            500                 505                 510
Glu Val Gly Val Trp Ala Tyr Ser Ala Thr Glu Ser Thr Pro Ile Ile
        515                 520                 525
Gly His Val Gly Pro Met Met Gly Gln Val Gly His Gln Val Thr Ile
    530                 535                 540
Asp Gly Glu Gly Phe Gly Thr Asn Thr Gly Thr Val Lys Phe Gly Thr
545                 550                 555                 560
```

```
Thr Ala Ala Asn Val Val Ser Trp Ser Asn Asn Gln Ile Val Val Ala
                565                 570                 575
Val Pro Asn Val Ser Pro Gly Lys Tyr Asn Ile Thr Val Gln Ser Ser
            580                 585                 590
Ser Gly Gln Thr Ser Ala Ala Tyr Asp Asn Phe Glu Val Leu Thr Asn
        595                 600                 605
Asp Gln Val Ser Val Arg Phe Val Val Asn Asn Ala Thr Thr Asn Leu
    610                 615                 620
Gly Gln Asn Ile Tyr Ile Val Gly Asn Val Tyr Glu Leu Gly Asn Trp
625                 630                 635                 640
Asp Thr Ser Lys Ala Ile Gly Pro Met Phe Asn Gln Val Val Tyr Ser
                645                 650                 655
Tyr Pro Thr Trp Tyr Ile Asp Val Ser Val Pro Glu Gly Lys Thr Ile
            660                 665                 670
Glu Phe Lys Phe Ile Lys Lys Asp Ser Gln Gly Asn Val Thr Trp Glu
        675                 680                 685
Ser Gly Ser Asn His Val Tyr Thr Thr Pro Thr Asn Thr Thr Gly Lys
    690                 695                 700
Ile Ile Val Asp Trp Gln Asn
705                 710
```

<210> 96
<211> 711
<212> PRT
<213> Artificial Sequence

<220>
<223> Cyclomaltodextrin glucanotransferase

<400> 96

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

```
            180                 185                 190
Gly Tyr Thr Asn Asp Ala Asn Met Tyr Phe His His Asn Gly Gly Thr
        195                 200                 205
Thr Phe Ser Ser Leu Glu Asp Gly Ile Tyr Arg Asn Leu Phe Asp Leu
    210                 215                 220
Ala Asp Leu Asn His Gln Asn Pro Val Ile Asp Arg Tyr Leu Lys Asp
225                 230                 235                 240
Ala Val Lys Met Trp Ile Asp Met Gly Ile Asp Gly Ile Arg Met Asp
                245                 250                 255
Ala Val Lys His Met Pro Phe Gly Trp Gln Lys Ser Leu Met Asp Glu
            260                 265                 270
Ile Asp Asn Tyr Arg Pro Val Phe Thr Phe Gly Glu Trp Phe Leu Ser
        275                 280                 285
Glu Asn Glu Val Asp Ala Asn Asn His Tyr Phe Ala Asn Glu Ser Gly
    290                 295                 300
Met Ser Leu Leu Asp Phe Arg Phe Gly Gln Lys Leu Arg Gln Val Leu
305                 310                 315                 320
Arg Asn Asn Ser Asp Asn Trp Tyr Gly Phe Asn Gln Met Ile Gln Asp
                325                 330                 335
Thr Ala Ser Ala Tyr Asp Glu Val Leu Asp Gln Val Thr Phe Ile Asp
            340                 345                 350
Asn His Asp Met Asp Arg Phe Met Ile Asp Gly Gly Asp Pro Arg Lys
        355                 360                 365
Val Asp Met Ala Leu Ala Val Leu Leu Thr Ser Arg Gly Val Pro Asn
    370                 375                 380
Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asn Gly Asp Pro Asn
385                 390                 395                 400
Asn Arg Lys Met Met Ser Ser Phe Asn Lys Asn Thr Arg Ala Tyr Gln
                405                 410                 415
Val Ile Gln Lys Leu Ser Ser Leu Arg Arg Asn Asn Pro Ala Leu Ala
            420                 425                 430
Tyr Gly Asp Thr Glu Gln Arg Trp Ile Asn Gly Asp Val Tyr Val Tyr
        435                 440                 445
Glu Arg Gln Phe Gly Lys Asp Val Val Leu Val Ala Val Asn Arg Ser
    450                 455                 460
Ser Ser Ser Asn Tyr Ser Ile Thr Gly Leu Phe Thr Ala Leu Pro Ala
465                 470                 475                 480
Gly Thr Tyr Thr Asp Gln Leu Gly Gly Leu Leu Asp Gly Asn Thr Ile
                485                 490                 495
Gln Val Gly Ser Asn Gly Ser Val Asn Ala Phe Asp Leu Gly Pro Gly
            500                 505                 510
Glu Val Gly Val Trp Ala Tyr Ser Ala Thr Glu Ser Thr Pro Ile Ile
        515                 520                 525
Gly His Val Gly Pro Met Met Gly Gln Val Gly His Gln Val Thr Ile
    530                 535                 540
Asp Gly Glu Gly Phe Gly Thr Asn Thr Gly Thr Val Lys Phe Gly Thr
545                 550                 555                 560
Thr Ala Ala Asn Val Val Ser Trp Ser Asn Asn Gln Ile Val Val Ala
                565                 570                 575
Val Pro Asn Val Ser Pro Gly Lys Tyr Asn Ile Thr Val Gln Ser Ser
            580                 585                 590
Ser Gly Gln Thr Ser Ala Ala Tyr Asp Asn Phe Glu Val Leu Thr Asn
        595                 600                 605
Asp Gln Val Ser Val Arg Phe Val Val Asn Asn Ala Thr Thr Asn Leu
```

```
    610                 615                 620
Gly Gln Asn Ile Tyr Ile Val Gly Asn Val Tyr Glu Leu Gly Asn Trp
625                 630                 635                 640
Asp Thr Ser Lys Ala Ile Gly Pro Met Phe Asn Gln Val Val Tyr Ser
                645                 650                 655
Tyr Pro Thr Trp Tyr Ile Asp Val Ser Val Pro Glu Gly Lys Thr Ile
            660                 665                 670
Glu Phe Lys Phe Ile Lys Lys Asp Ser Gln Gly Asn Val Thr Trp Glu
        675                 680                 685
Ser Gly Ser Asn His Val Tyr Thr Thr Pro Thr Asn Thr Thr Gly Lys
    690                 695                 700
Ile Ile Val Asp Trp Gln Asn
705                 710


<210> 97
<211> 711
<212> PRT
<213> Artificial Sequence

<220>
<223> Cyclomaltodextrin glucanotransferase

<400> 97
Met Arg Arg Trp Leu Ser Leu Val Leu Ser Met Ser Phe Val Phe Ser
 1               5                  10                  15
Ala Ile Phe Ile Val Ser Asp Thr Gln Lys Val Thr Val Glu Ala Ala
            20                  25                  30
Gly Asn Leu Asn Lys Val Asn Phe Thr Ser Asp Val Val Tyr Gln Ile
        35                  40                  45
Val Val Asp Arg Phe Val Asp Gly Asn Thr Ser Asn Asn Pro Ser Gly
    50                  55                  60
Ala Leu Phe Ser Ser Gly Cys Thr Asn Leu Arg Lys Tyr Cys Gly Gly
65                  70                  75                  80
Asp Trp Gln Gly Ile Ile Asn Lys Ile Asn Asp Gly Tyr Leu Thr Asp
                85                  90                  95
Met Gly Val Thr Ala Ile Trp Ile Ser Gln Pro Val Glu Asn Val Phe
            100                 105                 110
Ser Val Met Asn Asp Ala Ser Gly Ser Ala Ser Tyr His Gly Tyr Trp
        115                 120                 125
Ala Arg Asp Phe Lys Lys Pro Asn Pro Phe Phe Gly Thr Leu Ser Asp
    130                 135                 140
Phe Gln Arg Leu Val Asp Ala Ala His Ala Lys Gly Ile Lys Val Ile
145                 150                 155                 160
Ile Asp Phe Ala Pro Asn His Thr Ser Pro Ala Ser Glu Thr Asn Pro
                165                 170                 175
Ser Tyr Met Glu Asn Gly Arg Leu Tyr Asp Asn Gly Thr Leu Leu Gly
            180                 185                 190
Gly Tyr Thr Asn Asp Ala Asn Met Tyr Phe His His Asn Gly Gly Thr
        195                 200                 205
Thr Phe Ser Ser Leu Glu Asp Gly Ile Tyr Arg Asn Leu Phe Asp Leu
    210                 215                 220
Ala Asp Leu Asn His Gln Asn Pro Val Ile Asp Arg Tyr Leu Lys Asp
225                 230                 235                 240
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```
Ala Val Lys Met Trp Ile Asp Met Gly Ile Asp Gly Ile Arg Met Asp
                245                 250                 255
Ala Val Lys His Met Pro Phe Gly Trp Gln Lys Ser Leu Met Asp Glu
            260                 265                 270
Ile Asp Asn Tyr Arg Pro Val Phe Thr Phe Gly Glu Trp Phe Leu Ser
        275                 280                 285
Glu Asn Glu Val Asp Ala Asn Asn His Tyr Phe Ala Asn Glu Ser Gly
    290                 295                 300
Met Ser Leu Leu Asp Phe Arg Phe Gly Gln Lys Leu Arg Gln Val Leu
305                 310                 315                 320
Arg Asn Asn Ser Asp Asn Trp Tyr Gly Phe Asn Gln Met Ile Gln Asp
                325                 330                 335
Thr Ala Ser Ala Tyr Asp Glu Val Leu Asp Gln Val Thr Phe Ile Asp
            340                 345                 350
Asn His Asp Met Asp Arg Phe Met Ile Asp Gly Gly Asp Pro Arg Lys
        355                 360                 365
Val Asp Met Ala Leu Ala Val Leu Leu Thr Ser Arg Gly Val Pro Asn
    370                 375                 380
Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asn Gly Asp Pro Asn
385                 390                 395                 400
Asn Arg Lys Met Met Ser Ser Phe Asn Lys Asn Thr Arg Ala Tyr Gln
                405                 410                 415
Val Ile Gln Lys Leu Ser Ser Leu Arg Arg Asn Asn Pro Ala Leu Ala
            420                 425                 430
Tyr Gly Asp Thr Glu Gln Arg Trp Ile Asn Gly Asp Val Tyr Val Tyr
        435                 440                 445
Glu Arg Gln Phe Gly Lys Asp Val Val Leu Val Ala Val Asn Arg Ser
    450                 455                 460
Ser Ser Ser Asn Tyr Ser Ile Thr Gly Leu Phe Thr Ala Leu Pro Ala
465                 470                 475                 480
Gly Thr Tyr Thr Asp Gln Leu Gly Gly Leu Leu Asp Gly Asn Thr Ile
                485                 490                 495
Gln Val Gly Ser Asn Gly Ser Val Asn Ala Phe Asp Leu Gly Pro Gly
            500                 505                 510
Glu Val Gly Val Trp Ala Tyr Ser Ala Thr Glu Ser Thr Pro Ile Ile
        515                 520                 525
Gly His Val Gly Pro Met Met Gly Gln Val Gly His Gln Val Thr Ile
    530                 535                 540
Asp Gly Glu Gly Phe Gly Thr Asn Thr Gly Thr Val Lys Phe Gly Thr
545                 550                 555                 560
Thr Ala Ala Asn Val Val Ser Trp Ser Asn Asn Gln Ile Val Val Ala
                565                 570                 575
Val Pro Asn Val Ser Pro Gly Lys Tyr Asn Ile Thr Val Gln Ser Ser
            580                 585                 590
Ser Gly Gln Thr Ser Ala Ala Tyr Asp Asn Phe Glu Val Leu Thr Asn
        595                 600                 605
Asp Gln Val Ser Val Arg Phe Val Val Asn Asn Ala Thr Thr Asn Leu
    610                 615                 620
Gly Gln Asn Ile Tyr Ile Val Gly Asn Val Tyr Glu Leu Gly Asn Trp
625                 630                 635                 640
Asp Thr Ser Lys Ala Ile Gly Pro Met Phe Asn Gln Val Val Tyr Ser
                645                 650                 655
Tyr Pro Thr Trp Tyr Ile Asp Val Ser Val Pro Glu Gly Lys Thr Ile
            660                 665                 670
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Glu Phe Lys Phe Ile Lys Lys Asp Ser Gln Gly Asn Val Thr Trp Glu
        675                 680                 685
Ser Gly Ser Asn His Val Tyr Thr Thr Pro Thr Asn Thr Thr Gly Lys
    690                 695                 700
Ile Ile Val Asp Trp Gln Asn
705                 710


<210> 98
<211> 680
<212> PRT
<213> Artificial Sequence

<220>
<223> Cyclodextrin Glucanotransferase

<400> 98
Ala Gly Asn Leu Asn Lys Val Asn Phe Thr Ser Asp Val Val Tyr Gln
 1               5                  10                  15
Ile Val Val Asp Arg Phe Val Asp Gly Asn Thr Ser Asn Asn Pro Ser
            20                  25                  30
Gly Ala Leu Phe Ser Ser Gly Cys Thr Asn Leu Arg Lys Tyr Cys Gly
        35                  40                  45
Gly Asp Trp Gln Gly Ile Ile Asn Lys Ile Asn Asp Gly Tyr Leu Thr
    50                  55                  60
Asp Met Gly Val Thr Ala Ile Trp Ile Ser Gln Pro Val Glu Asn Val
65                  70                  75                  80
Phe Ser Val Met Asn Asp Ala Ser Gly Ser Ala Ser Tyr His Gly Tyr
                85                  90                  95
Trp Ala Arg Asp Phe Lys Lys Pro Asn Pro Phe Phe Gly Thr Leu Ser
            100                 105                 110
Asp Phe Gln Arg Leu Val Asp Ala Ala His Ala Lys Gly Ile Lys Val
        115                 120                 125
Ile Ile Asp Phe Ala Pro Asn His Thr Ser Pro Ala Ser Glu Thr Asn
    130                 135                 140
Pro Ser Tyr Met Glu Asn Gly Arg Leu Tyr Asp Asn Gly Thr Leu Leu
145                 150                 155                 160
Gly Gly Tyr Thr Asn Asp Ala Asn Met Tyr Phe His His Asn Gly Gly
                165                 170                 175
Thr Thr Phe Ser Ser Leu Glu Asp Gly Ile Tyr Arg Asn Leu Phe Asp
            180                 185                 190
Leu Ala Asp Leu Asn His Gln Asn Pro Val Ile Asp Arg Tyr Leu Lys
        195                 200                 205
Asp Ala Val Lys Met Trp Ile Asp Met Gly Ile Asp Gly Ile Arg Met
    210                 215                 220
Asp Ala Val Lys His Met Pro Phe Gly Trp Gln Lys Ser Leu Met Asp
225                 230                 235                 240
Glu Ile Asp Asn Tyr Arg Pro Val Phe Thr Phe Gly Glu Trp Phe Leu
                245                 250                 255
Ser Glu Asn Glu Val Asp Ala Asn Asn His Tyr Phe Ala Asn Glu Ser
            260                 265                 270
Gly Met Ser Leu Leu Asp Phe Arg Phe Gly Gln Lys Leu Arg Gln Val
        275                 280                 285
Leu Arg Asn Asn Ser Asp Asn Trp Tyr Gly Phe Asn Gln Met Ile Gln
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```
    290                 295                 300
Asp Thr Ala Ser Ala Tyr Asp Glu Val Leu Asp Gln Val Thr Phe Ile
305                 310                 315                 320
Asp Asn His Asp Met Asp Arg Phe Met Ile Asp Gly Gly Asp Pro Arg
                325                 330                 335
Lys Val Asp Met Ala Leu Ala Val Leu Leu Thr Ser Arg Gly Val Pro
            340                 345                 350
Asn Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asn Gly Asp Pro
        355                 360                 365
Asn Asn Arg Lys Met Met Ser Ser Phe Asn Lys Asn Thr Arg Ala Tyr
    370                 375                 380
Gln Val Ile Gln Lys Leu Ser Ser Leu Arg Arg Asn Asn Pro Ala Leu
385                 390                 395                 400
Ala Tyr Gly Asp Thr Glu Gln Arg Trp Ile Asn Gly Asp Val Tyr Val
                405                 410                 415
Tyr Glu Arg Gln Phe Gly Lys Asp Val Val Leu Val Ala Val Asn Arg
            420                 425                 430
Ser Ser Ser Ser Asn Tyr Ser Ile Thr Gly Leu Phe Thr Ala Leu Pro
        435                 440                 445
Ala Gly Thr Tyr Thr Asp Gln Leu Gly Gly Leu Leu Asp Gly Asn Thr
    450                 455                 460
Ile Gln Val Gly Ser Asn Gly Ser Val Asn Ala Phe Asp Leu Gly Pro
465                 470                 475                 480
Gly Glu Val Gly Val Trp Ala Tyr Ser Ala Thr Glu Ser Thr Pro Ile
                485                 490                 495
Ile Gly His Val Gly Pro Met Met Gly Gln Val Gly His Gln Val Thr
            500                 505                 510
Ile Asp Gly Glu Gly Phe Gly Thr Asn Thr Gly Thr Val Lys Phe Gly
        515                 520                 525
Thr Thr Ala Ala Asn Val Val Ser Trp Ser Asn Asn Gln Ile Val Val
    530                 535                 540
Ala Val Pro Asn Val Ser Pro Gly Lys Tyr Asn Ile Thr Val Gln Ser
545                 550                 555                 560
Ser Ser Gly Gln Thr Ser Ala Ala Tyr Asp Asn Phe Glu Val Leu Thr
                565                 570                 575
Asn Asp Gln Val Ser Val Arg Phe Val Val Asn Asn Ala Thr Thr Asn
            580                 585                 590
Leu Gly Gln Asn Ile Tyr Ile Val Gly Asn Val Tyr Glu Leu Gly Asn
        595                 600                 605
Trp Asp Thr Ser Lys Ala Ile Gly Pro Met Phe Asn Gln Val Val Tyr
    610                 615                 620
Ser Tyr Pro Thr Trp Tyr Ile Asp Val Ser Val Pro Glu Gly Lys Thr
625                 630                 635                 640
Ile Glu Phe Lys Phe Ile Lys Lys Asp Ser Gln Gly Asn Val Thr Trp
                645                 650                 655
Glu Ser Gly Ser Asn His Val Tyr Thr Thr Pro Thr Asn Thr Thr Gly
            660                 665                 670
Lys Ile Ile Val Asp Trp Gln Asn
        675                 680
```

<210> 99
<211> 711
<212> PRT

<213> Artificial Sequence

<220>
<223> Cyclodextrin Glucanotransferase

<400> 99
Met Arg Arg Trp Leu Ser Leu Val Leu Ser Met Ser Phe Val Phe Ser
 1               5                  10                  15
Ala Ile Phe Ile Val Ser Asp Thr Gln Lys Val Thr Val Glu Ala Ala
            20                  25                  30
Gly Asn Leu Asn Lys Val Asn Phe Thr Ser Asp Val Val Tyr Gln Ile
        35                  40                  45
Val Val Asp Arg Phe Val Asp Gly Asn Thr Ser Asn Asn Pro Ser Gly
    50                  55                  60
Ala Leu Phe Ser Ser Gly Cys Thr Asn Leu Arg Lys Tyr Cys Gly Gly
65                  70                  75                  80
Asp Trp Gln Gly Ile Ile Asn Lys Ile Asn Asp Gly Tyr Leu Thr Asp
                85                  90                  95
Met Gly Val Thr Ala Ile Trp Ile Ser Gln Pro Val Glu Asn Val Phe
            100                 105                 110
Ser Val Met Asn Asp Ala Ser Gly Ser Ala Ser Tyr His Gly Tyr Trp
        115                 120                 125
Ala Arg Asp Phe Lys Lys Pro Asn Pro Phe Phe Gly Thr Leu Ser Asp
    130                 135                 140
Phe Gln Arg Leu Val Asp Ala Ala His Ala Lys Gly Ile Lys Val Ile
145                 150                 155                 160
Ile Asp Phe Ala Pro Asn His Thr Ser Pro Ala Ser Glu Thr Asn Pro
                165                 170                 175
Ser Tyr Met Glu Asn Gly Arg Leu Tyr Asp Asn Gly Thr Leu Leu Gly
            180                 185                 190
Gly Tyr Thr Asn Asp Ala Asn Met Tyr Phe His His Asn Gly Gly Thr
        195                 200                 205
Thr Phe Ser Ser Leu Glu Asp Gly Ile Tyr Arg Asn Leu Phe Asp Leu
    210                 215                 220
Ala Asp Leu Asn His Gln Asn Pro Val Ile Asp Arg Tyr Leu Lys Asp
225                 230                 235                 240
Ala Val Lys Met Trp Ile Asp Met Gly Ile Asp Gly Ile Arg Met Asp
                245                 250                 255
Ala Val Lys His Met Pro Phe Gly Trp Gln Lys Ser Leu Met Asp Glu
            260                 265                 270
Ile Asp Asn Tyr Arg Pro Val Phe Thr Phe Gly Glu Trp Phe Leu Ser
        275                 280                 285
Glu Asn Glu Val Asp Ala Asn Asn His Tyr Phe Ala Asn Glu Ser Gly
    290                 295                 300
Met Ser Leu Leu Asp Phe Arg Phe Gly Gln Lys Leu Arg Gln Val Leu
305                 310                 315                 320
Arg Asn Asn Ser Asp Asn Trp Tyr Gly Phe Asn Gln Met Ile Gln Asp
                325                 330                 335
Thr Ala Ser Ala Tyr Asp Glu Val Leu Asp Gln Val Thr Phe Ile Asp
            340                 345                 350
Asn His Asp Met Asp Arg Phe Met Ile Asp Gly Gly Asp Pro Arg Lys
        355                 360                 365
Val Asp Met Ala Leu Ala Val Leu Leu Thr Ser Arg Gly Val Pro Asn
    370                 375                 380

```
Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asn Gly Asp Pro Asn
385                 390                 395                 400
Asn Arg Lys Met Met Ser Ser Phe Asn Lys Asn Thr Arg Ala Tyr Gln
                405                 410                 415
Val Ile Gln Lys Leu Ser Ser Leu Arg Arg Asn Asn Pro Ala Leu Ala
            420                 425                 430
Tyr Gly Asp Thr Glu Gln Arg Trp Ile Asn Gly Asp Val Tyr Val Tyr
        435                 440                 445
Glu Arg Gln Phe Gly Lys Asp Val Val Leu Val Ala Val Asn Arg Ser
    450                 455                 460
Ser Ser Ser Asn Tyr Ser Ile Thr Gly Leu Phe Thr Ala Leu Pro Ala
465                 470                 475                 480
Gly Thr Tyr Thr Asp Gln Leu Gly Gly Leu Leu Asp Gly Asn Thr Ile
                485                 490                 495
Gln Val Gly Ser Asn Gly Ser Val Asn Ala Phe Asp Leu Gly Pro Gly
            500                 505                 510
Glu Val Gly Val Trp Ala Tyr Ser Ala Thr Glu Ser Thr Pro Ile Ile
        515                 520                 525
Gly His Val Gly Pro Met Met Gly Gln Val Gly His Gln Val Thr Ile
    530                 535                 540
Asp Gly Glu Gly Phe Gly Thr Asn Thr Gly Thr Val Lys Phe Gly Thr
545                 550                 555                 560
Thr Ala Ala Asn Val Val Ser Trp Ser Asn Asn Gln Ile Val Val Ala
                565                 570                 575
Val Pro Asn Val Ser Pro Gly Lys Tyr Asn Ile Thr Val Gln Ser Ser
            580                 585                 590
Ser Gly Gln Thr Ser Ala Ala Tyr Asp Asn Phe Glu Val Leu Thr Asn
        595                 600                 605
Asp Gln Val Ser Val Arg Phe Val Val Asn Asn Ala Thr Thr Asn Leu
    610                 615                 620
Gly Gln Asn Ile Tyr Ile Val Gly Asn Val Tyr Glu Leu Gly Asn Trp
625                 630                 635                 640
Asp Thr Ser Lys Ala Ile Gly Pro Met Phe Asn Gln Val Val Tyr Ser
                645                 650                 655
Tyr Pro Thr Trp Tyr Ile Asp Val Ser Val Pro Glu Gly Lys Thr Ile
            660                 665                 670
Glu Phe Lys Phe Ile Lys Lys Asp Ser Gln Gly Asn Val Thr Trp Glu
        675                 680                 685
Ser Gly Ser Asn His Val Tyr Thr Thr Pro Thr Asn Thr Thr Gly Lys
    690                 695                 700
Ile Ile Val Asp Trp Gln Asn
705                 710


<210> 100
<211> 364
<212> PRT
<213> Artificial Sequence

<220>
<223> Hypothetical protein

<400> 100
Met Ser Arg Asn Gly Ala Val Thr Pro Asp Trp Gln Phe Thr Val Glu
```

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

<210> 101
<211> 364
<212> PRT
<213> Artificial Sequence

<220>
<223> Maltodextrin glucosidase

<400> 101
Met Ser Arg Asn Gly Ala Val Thr Pro Asp Trp Gln Phe Thr Val Glu
 1               5                  10                  15
Val Gln Glu Gly Glu Thr Ile Thr Tyr Lys Tyr Val Lys Gly Gly Ser
            20                  25                  30
Trp Asp Gln Glu Gly Leu Ala Asp His Thr Arg Glu Asp Asp Asn Asp
        35                  40                  45
Asp Asp Val Ser Tyr Tyr Gly Tyr Gly Ala Ile Gly Thr Asp Leu Lys
    50                  55                  60
Val Thr Val His Asn Glu Gly Asn Asn Thr Met Ile Val Gln Asp Arg
65                  70                  75                  80
Ile Leu Arg Trp Ile Asp Met Pro Val Val Ile Glu Glu Val Gln Lys
                85                  90                  95
Gln Gly Ser Gln Val Thr Ile Lys Gly Asn Ala Ile Lys Asn Gly Val
            100                 105                 110
Leu Thr Ile Asn Gly Glu Arg Val Pro Ile Asp Gly Arg Met Ala Phe
        115                 120                 125
Ser Tyr Thr Phe Thr Pro Ala Ser His Gln Lys Glu Val Ser Ile His
    130                 135                 140
Ile Glu Pro Ser Ala Glu Ser Lys Thr Ala Ile Phe Asn Asn Asp Gly
145                 150                 155                 160
Gly Ala Ile Ala Lys Asn Thr Lys Asp Tyr Val Leu Asn Leu Glu Thr
                165                 170                 175
Lys Gln Leu Arg Glu Gly Lys Leu Thr Thr Pro Pro Ser Asn Gly Asp
            180                 185                 190
Ser Pro Glu Ser Asp Trp Pro Gly Ser Glu Thr Pro Ser His Asp Gly
        195                 200                 205
Gly Ala Thr Pro Gly Asn Gly Thr Ser Pro Gly Ser Gly Gly Pro Ser
    210                 215                 220
Asp Gly Thr Ser Pro Gly Gly Ser Val Pro Pro Gly Gly Thr Ala Pro
225                 230                 235                 240
Pro Gly Asn Gly Ala Pro Pro Ser Ala Pro Pro Gln Lys Pro Ser Pro
                245                 250                 255
Ser Lys Pro Lys Glu Lys Pro Arg Lys Pro Thr Thr Pro Pro Ser Gln
            260                 265                 270
Val Lys Lys Val Tyr Trp Asp Gly Val Glu Leu Lys Lys Gly Gln Ile
        275                 280                 285
Gly Arg Leu Thr Val Gln Lys Pro Ile Asn Leu Trp Lys Arg Ala Lys
    290                 295                 300
Asp Gly Arg Leu Val Phe Val Arg Ile Leu Gln Pro Gly Glu Val Tyr
305                 310                 315                 320
Arg Val Tyr Gly Tyr Asp Ala Arg Phe Gly Gly Gln Tyr Ala Val Gly
                325                 330                 335
Gly Gly Tyr Tyr Val Thr Asp Ile Asp Thr His Ile Arg Tyr Glu Thr
            340                 345                 350
Pro Ser Lys Glu Lys Leu Lys Leu Val Asn Gly Glu
        355                 360


<210> 102
<211> 542
<212> PRT
<213> Artificial Sequence

<220>
<223> Beta-glucosidase

<400> 102
Met Ala Met Gln Leu Arg Ser Leu Leu Leu Cys Val Leu Leu Leu Leu
 1               5                  10                  15
Leu Gly Phe Ala Leu Ala Asp Thr Asn Ala Ala Ala Arg Ile His Pro
            20                  25                  30
Pro Val Val Cys Ala Asn Leu Ser Arg Ala Asn Phe Asp Thr Leu Val
        35                  40                  45
Pro Gly Phe Val Phe Gly Ala Ala Thr Ala Ser Tyr Gln Val Glu Gly
    50                  55                  60
Ala Ala Asn Leu Asp Gly Arg Gly Pro Ser Ile Trp Asp Thr Phe Thr
65                  70                  75                  80
His Lys His Pro Glu Lys Ile Ala Asp Gly Ser Asn Gly Asp Val Ala
                85                  90                  95
Ile Asp Gln Tyr His Arg Tyr Lys Glu Asp Val Ala Ile Met Lys Asp
            100                 105                 110
Met Gly Leu Glu Ser Tyr Arg Phe Ser Ile Ser Trp Ser Arg Val Leu
        115                 120                 125
Pro Asn Gly Thr Leu Ser Gly Gly Ile Asn Lys Lys Gly Ile Glu Tyr
    130                 135                 140
Tyr Asn Asn Leu Ile Asn Glu Leu Leu His Asn Gly Ile Glu Pro Leu
145                 150                 155                 160
Val Thr Leu Phe His Trp Asp Val Pro Gln Thr Leu Glu Asp Glu Tyr
                165                 170                 175
Gly Gly Phe Leu Ser Asn Arg Ile Val Asn Asp Phe Glu Glu Tyr Ala
            180                 185                 190
Glu Leu Cys Phe Lys Lys Phe Gly Asp Arg Val Lys His Trp Thr Thr
        195                 200                 205
Leu Asn Glu Pro Tyr Thr Phe Ser Ser His Gly Tyr Ala Lys Gly Thr
    210                 215                 220
His Ala Pro Gly Arg Cys Ser Ala Trp Tyr Asn Gln Thr Cys Phe Gly
225                 230                 235                 240
Gly Asp Ser Ala Thr Glu Pro Tyr Leu Val Thr His Asn Leu Leu Leu
                245                 250                 255
Ala His Ala Ala Ala Val Lys Leu Tyr Lys Thr Lys Tyr Gln Ala Tyr
            260                 265                 270
Gln Lys Gly Val Ile Gly Ile Thr Val Val Thr Pro Trp Phe Glu Pro
        275                 280                 285
Ala Ser Glu Ala Lys Glu Asp Ile Asp Ala Val Phe Arg Ala Leu Asp
    290                 295                 300
Phe Ile Tyr Gly Trp Phe Met Asp Pro Leu Thr Arg Gly Asp Tyr Pro
305                 310                 315                 320
Gln Ser Met Arg Ser Leu Val Gly Glu Arg Leu Pro Asn Phe Thr Lys
                325                 330                 335
Lys Glu Ser Lys Ser Leu Ser Gly Ser Phe Asp Tyr Ile Gly Ile Asn
            340                 345                 350
Tyr Tyr Ser Ala Arg Tyr Ala Ser Ala Ser Lys Asn Tyr Ser Gly His
        355                 360                 365
Pro Ser Tyr Leu Asn Asp Val Asn Val Asp Val Lys Thr Glu Leu Asn
    370                 375                 380
Gly Val Pro Ile Gly Pro Gln Ala Ala Ser Ser Trp Leu Tyr Phe Tyr

385 390 395 400
Pro Lys Gly Leu Tyr Asp Leu Leu Cys Tyr Thr Lys Glu Lys Tyr Asn
405 410 415
Asp Pro Ile Ile Tyr Ile Thr Glu Asn Gly Val Asp Glu Phe Asn Gln
420 425 430
Pro Asn Pro Lys Leu Ser Leu Cys Gln Leu Leu Asp Asp Ser Asn Arg
435 440 445
Ile Tyr Tyr Tyr Tyr His His Leu Cys Tyr Leu Gln Ala Ala Ile Lys
450 455 460
Glu Gly Val Lys Val Lys Gly Tyr Phe Ala Trp Ser Leu Leu Asp Asn
465 470 475 480
Phe Glu Trp Asp Asn Gly Tyr Thr Val Arg Phe Gly Ile Asn Tyr Val
485 490 495
Asp Tyr Asp Asn Gly Leu Lys Arg His Ser Lys His Ser Thr His Trp
500 505 510
Phe Lys Ser Phe Leu Lys Lys Ser Ser Arg Asn Thr Lys Lys Ile Arg
515 520 525
Arg Cys Gly Asn Asn Asn Thr Ser Ala Thr Lys Phe Val Phe
530 535 540

<210> 103
<211> 1381
<212> PRT
<213> Artificial Sequence

<220>
<223> DexT Native host Leuconostoc citreum ATCC 11449

<400> 103
Met Pro Ala Asn Ala Pro Asp Lys Gln Ser Val Thr Asn Ala Pro Val
1 5 10 15
Val Pro Pro Lys His Asp Thr Asp Gln Gln Asp Asp Ser Leu Glu Lys
20 25 30
Gln Gln Val Leu Glu Pro Ser Val Asn Ser Asn Ile Pro Lys Lys Gln
35 40 45
Thr Asn Gln Gln Leu Ala Val Val Thr Ala Pro Ala Asn Ser Ala Pro
50 55 60
Gln Thr Lys Thr Thr Ala Glu Ile Ser Ala Gly Thr Glu Leu Asp Thr
65 70 75 80
Met Pro Asn Val Lys His Val Asp Gly Lys Val Tyr Phe Tyr Gly Asp
85 90 95
Asp Gly Gln Pro Lys Lys Asn Phe Thr Thr Ile Ile Asp Gly Lys Pro
100 105 110
Tyr Tyr Phe Asp Lys Asp Thr Gly Ala Leu Ser Asn Asn Asp Lys Gln
115 120 125
Tyr Val Ser Glu Leu Phe Ser Ile Gly Asn Lys His Asn Ala Val Tyr
130 135 140
Asn Thr Ser Ser Asp Asn Phe Thr Gln Leu Glu Gly His Leu Thr Ala
145 150 155 160
Ser Ser Trp Tyr Arg Pro Lys Asp Ile Leu Lys Asn Gly Lys Arg Trp
165 170 175
Ala Pro Ser Thr Val Thr Asp Phe Arg Pro Leu Leu Met Ala Trp Trp
180 185 190

```
Pro Asp Lys Ser Thr Gln Val Thr Tyr Leu Asn Tyr Met Lys Asp Gln
        195                 200                 205
Gly Leu Leu Ser Gly Thr His His Phe Ser Asp Asn Glu Asn Met Arg
    210                 215                 220
Thr Leu Thr Ala Ala Ala Met Gln Ala Gln Val Asn Ile Glu Lys Lys
225                 230                 235                 240
Ile Gly Gln Leu Gly Asn Thr Asp Trp Leu Lys Thr Ala Met Thr Gln
                245                 250                 255
Tyr Ile Asp Ala Gln Pro Asn Trp Asn Ile Asp Ser Glu Ala Lys Gly
            260                 265                 270
Asp Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Thr Asn Ser Asp Met
        275                 280                 285
Ser Pro Lys Ala Asn Ser Asp Tyr Arg Lys Leu Ser Arg Thr Pro Lys
    290                 295                 300
Asn Gln Lys Gly Gln Ile Ala Asp Lys Tyr Lys Gln Gly Gly Phe Glu
305                 310                 315                 320
Leu Leu Leu Ala Asn Asp Val Asp Asn Ser Asn Pro Val Val Gln Ala
                325                 330                 335
Glu Gln Leu Asn Trp Leu His Tyr Met Met Asn Ile Gly Ser Ile Leu
            340                 345                 350
Gln Asn Asp Asp Gln Ala Asn Phe Asp Gly Tyr Arg Val Asp Ala Val
        355                 360                 365
Asp Asn Val Asp Ala Asp Leu Leu Gln Ile Ala Gly Glu Tyr Ala Lys
    370                 375                 380
Ala Ala Tyr Gly Val Asp Lys Asn Asp Ala Arg Ala Asn Gln His Leu
385                 390                 395                 400
Ser Ile Leu Glu Asp Trp Gly Asp Glu Asp Pro Asp Tyr Val Lys Ala
                405                 410                 415
His Gly Asn Gln Gln Ile Thr Met Asp Phe Pro Leu His Leu Ala Ile
            420                 425                 430
Lys Tyr Ala Leu Asn Met Pro Asn Asp Lys Arg Ser Gly Leu Glu Pro
        435                 440                 445
Thr Arg Glu His Ser Leu Val Lys Arg Ile Thr Asp Asp Lys Glu Asn
    450                 455                 460
Val Ala Gln Pro Asn Tyr Ser Phe Ile Arg Ala His Asp Ser Glu Val
465                 470                 475                 480
Gln Thr Ile Ile Ala Asp Ile Ile Lys Asp Lys Ile Asn Pro Ala Ser
                485                 490                 495
Thr Gly Leu Asp Ser Thr Val Thr Leu Asp Gln Ile Lys Gln Ala Phe
            500                 505                 510
Asp Ile Tyr Asn Ala Asp Glu Leu Lys Ala Asp Lys Val Tyr Thr Pro
        515                 520                 525
Tyr Asn Ile Pro Ala Ser Tyr Ala Leu Leu Leu Thr Asn Lys Asp Thr
    530                 535                 540
Ile Pro Arg Val Tyr Tyr Gly Asp Met Phe Thr Asp Asp Gly Gln Tyr
545                 550                 555                 560
Met Ala Lys Gln Ser Pro Tyr Tyr Gln Ala Ile Asp Ala Leu Leu Lys
                565                 570                 575
Ala Arg Ile Lys Tyr Ala Ala Gly Gly Gln Thr Met Lys Met Asn Tyr
            580                 585                 590
Phe Pro Asp Glu Gln Ser Val Met Thr Ser Val Arg Tyr Gly Lys Gly
        595                 600                 605
Ala Met Thr Ala Ser Asp Ser Gly Asn Gln Glu Thr Arg Tyr Gln Gly
    610                 615                 620
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```
Ile Gly Leu Val Val Asn Asn Arg Pro Asp Leu Lys Leu Ser Asp Lys
625                 630                 635                 640
Asp Glu Val Lys Met Asp Met Gly Ala Ala His Lys Asn Gln Asp Tyr
                645                 650                 655
Arg Pro Val Leu Leu Thr Thr Lys Ser Gly Leu Lys Val Tyr Ser Thr
            660                 665                 670
Asp Ala Asn Ala Pro Val Val Arg Thr Asp Ala Asn Gly Gln Leu Thr
        675                 680                 685
Phe Lys Ala Asp Met Val Tyr Gly Val Asn Asp Pro Gln Val Ser Gly
    690                 695                 700
Tyr Ile Ala Ala Trp Val Pro Val Gly Ala Ser Glu Asn Gln Asp Ala
705                 710                 715                 720
Arg Thr Lys Ser Glu Thr Thr Gln Ser Thr Asp Gly Ser Val Tyr His
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Phe Gln Asp Phe Pro Thr Thr Pro Asp Glu Phe Thr Asn Ile Lys Ile
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785                 790                 795                 800
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Gly Gly Ala Phe Leu Glu Gln Leu Lys Thr Gln Tyr Pro Gln Leu Phe
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His Tyr Phe Asp Gly Ala Ser Gly Asn Met Leu Phe Lys Ser Trp Gly
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1170 1175 1180
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1315 1320 1325
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<213> Artificial Sequence

<220>
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<220>
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Thr Glu Ser Gln Ala Ser Leu Val Thr Thr Ser Glu Ala Ala Lys Glu
    50                  55                  60
Thr Leu Thr Ala Thr Asp Thr Ser Thr Ala Thr Ser Ala Thr Ser Gln
65                  70                  75                  80
Pro Thr Ala Thr Val Thr Asp Asn Val Ser Thr Thr Asn Gln Ser Thr
                85                  90                  95
Asn Thr Thr Ala Asn Thr Ala Asn Phe Asp Val Lys Pro Thr Thr Thr
            100                 105                 110
Ser Glu Gln Ser Lys Thr Asp Asn Ser Asp Lys Ile Ile Ala Thr Ser
        115                 120                 125
Lys Ala Val Asn Arg Leu Thr Ala Thr Gly Lys Phe Val Pro Ala Asn
    130                 135                 140
Asn Asn Thr Ala His Ser Arg Thr Val Thr Asp Lys Ile Val Pro Ile
145                 150                 155                 160
Lys Pro Lys Ile Gly Lys Leu Lys Gln Pro Ser Ser Leu Ser Gln Asp
                165                 170                 175
Asp Ile Ala Ala Leu Gly Asn Val Lys Asn Ile Arg Lys Val Asn Gly
            180                 185                 190
Lys Tyr Tyr Tyr Tyr Lys Glu Asp Gly Thr Leu Gln Lys Asn Tyr Ala
        195                 200                 205
Leu Asn Ile Asn Gly Lys Thr Phe Phe Phe Asp Glu Thr Gly Ala Leu
    210                 215                 220
Ser Asn Asn Thr Leu Pro Ser Lys Lys Gly Asn Ile Thr Asn Asn Asp
225                 230                 235                 240
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                245                 250                 255
Ala Asn Phe Glu His Val Asp His Tyr Leu Thr Ala Glu Ser Trp Tyr
            260                 265                 270
Arg Pro Lys Tyr Ile Leu Lys Asp Gly Lys Thr Trp Thr Gln Ser Thr
        275                 280                 285
Glu Lys Asp Phe Arg Pro Leu Leu Met Thr Trp Trp Pro Asp Gln Glu
    290                 295                 300
Thr Gln Arg Gln Tyr Val Asn Tyr Met Asn Ala Gln Leu Gly Ile His
305                 310                 315                 320
Gln Thr Tyr Asn Thr Ala Thr Ser Pro Leu Gln Leu Asn Leu Ala Ala
                325                 330                 335
Gln Thr Ile Gln Thr Lys Ile Glu Glu Lys Ile Thr Ala Glu Lys Asn
            340                 345                 350
Thr Asn Trp Leu Arg Gln Thr Ile Ser Ala Phe Val Lys Thr Gln Ser
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Ala Trp Asn Ser Asp Ser Glu Lys Pro Phe Asp Asp His Leu Gln Lys
    370                 375                 380
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Gln Leu Asn Trp Leu His Phe Leu Met Asn Phe Gly Asn Ile Tyr Ala
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465                 470                 475                 480
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Ala Lys Gly Ile His Lys Asn Asp Lys Ala Ala Asn Asp His Leu Ser
            500                 505                 510
Ile Leu Glu Ala Trp Ser Tyr Asn Asp Thr Pro Tyr Leu His Asp Asp
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Gly Asp Asn Met Ile Asn Met Asp Asn Arg Leu Arg Leu Ser Leu Leu
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Tyr Ser Leu Ala Lys Pro Leu Asn Gln Arg Ser Gly Met Asn Pro Leu
545                 550                 555                 560
Ile Thr Asn Ser Leu Val Asn Arg Thr Asp Asp Asn Ala Glu Thr Ala
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Ala Val Pro Ser Tyr Ser Phe Ile Arg Ala His Asp Ser Glu Val Gln
            580                 585                 590
Asp Leu Ile Arg Asn Ile Ile Arg Ala Glu Ile Asn Pro Asn Val Val
        595                 600                 605
Gly Tyr Ser Phe Thr Met Glu Glu Ile Lys Lys Ala Phe Glu Ile Tyr
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625                 630                 635                 640
Ala Leu Ser Tyr Ala Leu Leu Leu Thr Asn Lys Ser Ser Val Pro Arg
                645                 650                 655
Val Tyr Tyr Gly Asp Met Phe Thr Asp Asp Gly Gln Tyr Met Ala His
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Ser Glu Ile Ile Thr Ser Val Arg Tyr Gly Lys Gly Ala Leu Lys Ala
705                 710                 715                 720
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                725                 730                 735
Glu Gly Asn Asn Pro Ser Leu Arg Leu Lys Ala Ser Asp Arg Val Val
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Ala Gly Leu Val Arg Tyr Thr Asn Asp Arg Gly Glu Leu Ile Phe Thr
785                 790                 795                 800
Ala Ala Asp Ile Lys Gly Tyr Ala Asn Pro Gln Val Ser Gly Tyr Leu
                805                 810                 815
Gly Val Trp Val Pro Val Gly Ala Ala Ala Asp Gln Asp Val Arg Val
            820                 825                 830
Ala Ala Ser Thr Ala Pro Ser Thr Asp Gly Lys Ser Val His Gln Asn
```

```
        835                 840                 845
Ala Ala Leu Asp Ser Arg Val Met Phe Glu Gly Phe Ser Asn Phe Gln
    850                 855                 860
Ala Phe Ala Thr Lys Lys Glu Glu Tyr Thr Asn Val Val Ile Ala Lys
865                 870                 875                 880
Asn Val Asp Lys Phe Ala Glu Trp Gly Val Thr Asp Phe Glu Met Ala
                885                 890                 895
Pro Gln Tyr Val Ser Ser Thr Asp Gly Ser Phe Leu Asp Ser Val Ile
            900                 905                 910
Gln Asn Gly Tyr Ala Phe Thr Asp Arg Tyr Asp Leu Gly Ile Ser Lys
        915                 920                 925
Pro Asn Lys Tyr Gly Thr Ala Asp Asp Leu Val Lys Ala Ile Lys Ala
    930                 935                 940
Leu His Ser Lys Gly Ile Lys Val Met Ala Asp Trp Val Pro Asp Gln
945                 950                 955                 960
Met Tyr Ala Leu Pro Glu Lys Glu Val Val Thr Ala Thr Arg Val Asp
                965                 970                 975
Lys Tyr Gly Thr Pro Val Ala Gly Ser Gln Ile Lys Asn Thr Leu Tyr
            980                 985                 990
Val Val Asp Gly Lys Ser Ser Gly Lys Asp Gln Gln Ala Lys Tyr Gly
        995                 1000                1005
Gly Ala Phe Leu Glu Glu Leu Gln Ala Lys Tyr Pro Glu Leu Phe Ala
    1010                1015                1020
Arg Lys Gln Ile Ser Thr Gly Val Pro Met Asp Pro Ser Val Lys Ile
1025                1030                1035                1040
Lys Gln Trp Ser Ala Lys Tyr Phe Asn Gly Thr Asn Ile Leu Gly Arg
                1045                1050                1055
Gly Ala Gly Tyr Val Leu Lys Asp Gln Ala Thr Asn Thr Tyr Phe Ser
            1060                1065                1070
Leu Val Ser Asp Asn Thr Phe Leu Pro Lys Ser Leu Val Asn Pro Asn
        1075                1080                1085
His Gly Thr Ser Ser Ser Val Thr Gly Leu Val Phe Asp Gly Lys Gly
    1090                1095                1100
Tyr Val Tyr Tyr Ser Thr Ser Gly Asn Gln Ala Lys Asn Ala Phe Ile
1105                1110                1115                1120
Ser Leu Gly Asn Asn Trp Tyr Tyr Phe Asp Asn Asn Gly Tyr Met Val
                1125                1130                1135
Thr Gly Ala Gln Ser Ile Asn Gly Ala Asn Tyr Tyr Phe Leu Ser Asn
            1140                1145                1150
Gly Ile Gln Leu Arg Asn Ala Ile Tyr Asp Asn Gly Asn Lys Val Leu
        1155                1160                1165
Ser Tyr Tyr Gly Asn Asp Gly Arg Arg Tyr Glu Asn Gly Tyr Tyr Leu
    1170                1175                1180
Phe Gly Gln Gln Trp Arg Tyr Phe Gln Asn Gly Ile Met Ala Val Gly
1185                1190                1195                1200
Leu Thr Arg Ile His Gly Ala Val Gln Tyr Phe Asp Ala Ser Gly Phe
                1205                1210                1215
Gln Ala Lys Gly Gln Phe Ile Thr Thr Ala Asp Gly Lys Leu Arg Tyr
            1220                1225                1230
Phe Asp Arg Asp Ser Gly Asn Gln Ile Ser Asn Arg Phe Val Arg Asn
        1235                1240                1245
Ser Lys Gly Glu Trp Phe Leu Phe Asp His Asn Gly Val Ala Val Thr
    1250                1255                1260
Gly Thr Val Thr Phe Asn Gly Gln Arg Leu Tyr Phe Lys Pro Asn Gly
```

1265 1270 1275 1280
Val Gln Ala Lys Gly Glu Phe Ile Arg Asp Ala Asp Gly His Leu Arg
1285 1290 1295
Tyr Tyr Asp Pro Asn Ser Gly Asn Glu Val Arg Asn Arg Phe Val Arg
1300 1305 1310
Asn Ser Lys Gly Glu Trp Phe Leu Phe Asp His Asn Gly Ile Ala Val
1315 1320 1325
Thr Gly Thr Arg Val Val Asn Gly Gln Arg Leu Tyr Phe Lys Ser Asn
1330 1335 1340
Gly Val Gln Ala Lys Gly Glu Leu Ile Thr Glu Arg Lys Gly Arg Ile
1345 1350 1355 1360
Lys Tyr Tyr Asp Pro Asn Ser Gly Asn Glu Val Arg Asn Arg Tyr Val
1365 1370 1375
Arg Thr Ser Ser Gly Asn Trp Tyr Tyr Phe Gly Asn Asp Gly Tyr Ala
1380 1385 1390
Leu Ile Gly Trp His Val Val Glu Gly Arg Arg Val Tyr Phe Asp Glu
1395 1400 1405
Asn Gly Val Tyr Arg Tyr Ala Ser His Asp Gln Arg Asn His Trp Asp
1410 1415 1420
Tyr Asp Tyr Arg Arg Asp Phe Gly Arg Gly Ser Ser Ser Ala Val Arg
1425 1430 1435 1440
Phe Arg His Ser Arg Asn Gly Phe Phe Asp Asn Phe Phe Arg Phe
1445 1450 1455

<210> 107
<211> 1476
<212> PRT
<213> Artificial Sequence

<220>
<223> Dextransucrase

<400> 107
Met Asp Lys Lys Val Arg Tyr Lys Leu Arg Lys Val Lys Lys Arg Trp
1 5 10 15
Val Thr Val Ser Val Ala Ser Ala Val Met Thr Leu Thr Thr Leu Ser
20 25 30
Gly Gly Leu Val Lys Ala Asp Ser Asn Glu Ser Lys Ser Gln Ile Ser
35 40 45
Asn Asp Ser Asn Thr Ser Val Val Thr Ala Asn Glu Glu Ser Asn Val
50 55 60
Thr Thr Glu Val Thr Ser Lys Gln Glu Ala Ala Ser Ser Gln Thr Asn
65 70 75 80
His Thr Val Thr Thr Ile Ser Ser Ser Thr Ser Val Val Asn Pro Lys
85 90 95
Glu Val Val Ser Asn Pro Tyr Thr Val Gly Glu Thr Ala Ser Asn Gly
100 105 110
Glu Lys Leu Gln Asn Gln Thr Thr Thr Val Asp Lys Thr Ser Glu Ala
115 120 125
Ala Ala Asn Asn Ile Ser Lys Gln Thr Thr Glu Ala Asp Thr Asp Val
130 135 140
Ile Asp Asp Ser Asn Ala Ala Asn Leu Gln Ile Leu Glu Lys Leu Pro
145 150 155 160

```
Asn Val Lys Glu Ile Asp Gly Lys Tyr Tyr Tyr Tyr Asp Asn Asn Gly
                165                 170                 175
Lys Val Arg Thr Asn Phe Thr Leu Ile Ala Asp Gly Lys Ile Leu His
            180                 185                 190
Phe Asp Glu Thr Gly Ala Tyr Thr Asp Thr Ser Ile Asp Thr Val Asn
        195                 200                 205
Lys Asp Ile Val Thr Thr Arg Ser Asn Leu Tyr Lys Lys Tyr Asn Gln
    210                 215                 220
Val Tyr Asp Arg Ser Ala Gln Ser Phe Glu His Val Asp His Tyr Leu
225                 230                 235                 240
Thr Ala Glu Ser Trp Tyr Arg Pro Lys Tyr Ile Leu Lys Asp Gly Lys
                245                 250                 255
Thr Trp Thr Gln Ser Thr Glu Lys Asp Phe Arg Pro Leu Leu Met Thr
            260                 265                 270
Trp Trp Pro Ser Gln Glu Thr Gln Arg Gln Tyr Val Asn Tyr Met Asn
        275                 280                 285
Ala Gln Leu Gly Ile Asn Lys Thr Tyr Asp Asp Thr Ser Asn Gln Leu
    290                 295                 300
Gln Leu Asn Ile Ala Ala Ala Thr Ile Gln Ala Lys Ile Glu Ala Lys
305                 310                 315                 320
Ile Thr Thr Leu Lys Asn Thr Asp Trp Leu Arg Gln Thr Ile Ser Ala
                325                 330                 335
Phe Val Lys Thr Gln Ser Ala Trp Asn Ser Asp Ser Glu Lys Pro Phe
            340                 345                 350
Asp Asp His Leu Gln Asn Gly Ala Val Leu Tyr Asp Asn Glu Gly Lys
        355                 360                 365
Leu Thr Pro Tyr Ala Asn Ser Asn Tyr Arg Ile Leu Asn Arg Thr Pro
    370                 375                 380
Thr Asn Gln Thr Gly Lys Lys Asp Pro Arg Tyr Thr Ala Asp Asn Thr
385                 390                 395                 400
Ile Gly Gly Tyr Glu Phe Leu Leu Ala Asn Asp Val Asp Asn Ser Asn
                405                 410                 415
Pro Val Val Gln Ala Glu Gln Leu Asn Trp Leu His Phe Leu Met Asn
            420                 425                 430
Phe Gly Asn Ile Tyr Ala Asn Asp Pro Asp Ala Asn Phe Asp Ser Ile
        435                 440                 445
Arg Val Asp Ala Val Asp Asn Val Asp Ala Asp Leu Leu Gln Ile Ala
    450                 455                 460
Gly Asp Tyr Leu Lys Ala Ala Lys Gly Ile His Lys Asn Asp Lys Ala
465                 470                 475                 480
Ala Asn Asp His Leu Ser Ile Leu Glu Ala Trp Ser Asp Asn Asp Thr
                485                 490                 495
Pro Tyr Leu His Asp Asp Gly Asp Asn Met Ile Asn Met Asp Asn Lys
            500                 505                 510
Leu Arg Leu Ser Leu Leu Phe Ser Leu Ala Lys Pro Leu Asn Gln Arg
        515                 520                 525
Ser Gly Met Asn Pro Leu Ile Thr Asn Ser Leu Val Asn Arg Thr Asp
    530                 535                 540
Asp Asn Ala Glu Thr Ala Ala Val Pro Ser Tyr Ser Phe Ile Arg Ala
545                 550                 555                 560
His Asp Ser Glu Val Gln Asp Leu Ile Arg Asp Ile Ile Lys Ala Glu
                565                 570                 575
Ile Asn Pro Asn Val Val Gly Tyr Ser Phe Thr Met Glu Glu Ile Lys
            580                 585                 590
```

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Lys Ala Phe Glu Ile Tyr Asn Lys Asp Leu Leu Ala Thr Glu Lys Lys
        595                 600                 605
Tyr Thr His Tyr Asn Thr Ala Leu Ser Tyr Ala Leu Leu Leu Thr Asn
    610                 615                 620
Lys Ser Ser Val Pro Arg Val Tyr Tyr Gly Asp Met Phe Thr Asp Asp
625                 630                 635                 640
Gly Gln Tyr Met Ala His Lys Thr Ile Asn Tyr Glu Ala Ile Glu Thr
                645                 650                 655
Leu Leu Lys Ala Arg Ile Lys Tyr Val Ser Gly Gly Gln Ala Met Arg
            660                 665                 670
Asn Gln Gln Val Gly Asn Ser Glu Ile Ile Thr Ser Val Arg Tyr Gly
        675                 680                 685
Lys Gly Ala Leu Lys Ala Thr Asp Thr Gly Asp Arg Thr Thr Arg Thr
    690                 695                 700
Ser Gly Val Ala Val Ile Glu Gly Asn Asn Pro Ser Leu Arg Leu Lys
705                 710                 715                 720
Ala Ser Asp Arg Val Val Val Asn Met Gly Ala Ala His Lys Asn Gln
                725                 730                 735
Ala Tyr Arg Pro Leu Leu Leu Thr Thr Asp Asn Gly Ile Lys Ala Tyr
            740                 745                 750
His Ser Asp Gln Glu Ala Ala Gly Leu Val Arg Tyr Thr Asn Asp Arg
        755                 760                 765
Gly Glu Leu Ile Phe Thr Ala Ala Asp Ile Lys Gly Tyr Ala Asn Pro
    770                 775                 780
Gln Val Ser Gly Tyr Leu Gly Val Trp Val Pro Val Gly Ala Ala Ala
785                 790                 795                 800
Asp Gln Asp Val Arg Val Ala Ala Ser Thr Ala Pro Ser Thr Asp Gly
                805                 810                 815
Lys Ser Val His Gln Asn Ala Ala Leu Asp Ser Arg Val Met Phe Glu
            820                 825                 830
Gly Phe Ser Asn Phe Gln Ala Phe Ala Thr Lys Lys Glu Glu Tyr Thr
        835                 840                 845
Asn Val Val Ile Ala Lys Asn Val Asp Lys Phe Ala Glu Trp Gly Val
    850                 855                 860
Thr Asp Phe Glu Met Ala Pro Gln Tyr Val Ser Ser Thr Asp Gly Ser
865                 870                 875                 880
Phe Leu Asp Ser Val Ile Gln Asn Gly Tyr Ala Phe Thr Asp Arg Tyr
                885                 890                 895
Asp Leu Gly Ile Ser Lys Pro Asn Lys Tyr Gly Thr Ala Asp Asp Leu
            900                 905                 910
Val Lys Ala Ile Lys Ala Leu His Ser Lys Gly Ile Lys Val Met Ala
        915                 920                 925
Asp Trp Val Pro Asp Gln Met Tyr Ala Phe Pro Glu Lys Glu Val Val
    930                 935                 940
Thr Ala Thr Arg Val Asp Lys Phe Gly Lys Pro Val Glu Gly Ser Gln
945                 950                 955                 960
Ile Lys Ser Val Leu Tyr Val Ala Asp Ser Lys Ser Ser Gly Lys Asp
                965                 970                 975
Gln Gln Ala Lys Tyr Gly Gly Ala Phe Leu Glu Glu Leu Gln Ala Lys
            980                 985                 990
Tyr Pro Glu Leu Phe Ala Arg Lys Gln Ile Ser Thr Gly Val Pro Met
        995                 1000                1005
Asp Pro Ser Val Lys Ile Lys Gln Trp Ser Ala Lys Tyr Phe Asn Gly
    1010                1015                1020
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```
Thr Asn Ile Leu Gly Arg Gly Ala Gly Tyr Val Leu Lys Asp Gln Ala
1025                1030                1035                1040
Thr Asn Thr Tyr Phe Asn Ile Ser Asp Asn Lys Glu Ile Asn Phe Leu
                1045                1050                1055
Pro Lys Thr Leu Leu Asn Gln Asp Ser Gln Val Gly Phe Ser Tyr Asp
            1060                1065                1070
Gly Lys Gly Tyr Val Tyr Tyr Ser Thr Ser Gly Tyr Gln Ala Lys Asn
        1075                1080                1085
Thr Phe Ile Ser Glu Gly Asp Lys Trp Tyr Tyr Phe Asp Asn Asn Gly
    1090                1095                1100
Tyr Met Val Thr Gly Ala Gln Ser Ile Asn Gly Val Asn Tyr Tyr Phe
1105                1110                1115                1120
Leu Ser Asn Gly Leu Gln Leu Arg Asp Ala Ile Leu Lys Asn Glu Asp
                1125                1130                1135
Gly Thr Tyr Ala Tyr Tyr Gly Asn Asp Gly Arg Arg Tyr Glu Asn Gly
            1140                1145                1150
Tyr Tyr Gln Phe Met Ser Gly Val Trp Arg His Phe Asn Asn Gly Glu
        1155                1160                1165
Met Ser Val Gly Leu Thr Val Ile Asp Gly Gln Val Gln Tyr Phe Asp
    1170                1175                1180
Glu Met Gly Tyr Gln Ala Lys Gly Lys Phe Val Thr Thr Ala Asp Gly
1185                1190                1195                1200
Lys Ile Arg Tyr Phe Asp Lys Gln Ser Gly Asn Met Tyr Arg Asn Arg
                1205                1210                1215
Phe Ile Glu Asn Glu Glu Gly Lys Trp Leu Tyr Leu Gly Glu Asp Gly
            1220                1225                1230
Ala Ala Val Thr Gly Ser Gln Thr Ile Asn Gly Gln His Leu Tyr Phe
        1235                1240                1245
Arg Ala Asn Gly Val Gln Val Lys Gly Glu Phe Val Thr Asp Arg Tyr
    1250                1255                1260
Gly Arg Ile Ser Tyr Tyr Asp Ser Asn Ser Gly Asp Gln Ile Arg Asn
1265                1270                1275                1280
Arg Phe Val Arg Asn Ala Gln Gly Gln Trp Phe Tyr Phe Asp Asn Asn
                1285                1290                1295
Gly Tyr Ala Val Thr Gly Ala Arg Thr Ile Asn Gly Gln His Leu Tyr
            1300                1305                1310
Phe Arg Ala Asn Gly Val Gln Val Lys Gly Glu Phe Val Thr Asp Arg
        1315                1320                1325
His Gly Arg Ile Ser Tyr Tyr Asp Gly Asn Ser Gly Asp Gln Ile Arg
    1330                1335                1340
Asn Arg Phe Val Arg Asn Ala Gln Gly Gln Trp Phe Tyr Phe Asp Asn
1345                1350                1355                1360
Asn Gly Tyr Ala Val Thr Gly Ala Arg Thr Ile Asn Gly Gln His Leu
                1365                1370                1375
Tyr Phe Arg Ala Asn Gly Val Gln Val Lys Gly Glu Phe Val Thr Asp
            1380                1385                1390
Arg Tyr Gly Arg Ile Ser Tyr Tyr Asp Ser Asn Ser Gly Asp Gln Ile
        1395                1400                1405
Arg Asn Arg Phe Val Arg Asn Ala Gln Gly Gln Trp Phe Tyr Phe Asp
    1410                1415                1420
Asn Asn Gly Tyr Ala Val Thr Gly Ala Arg Thr Ile Asn Gly Gln His
1425                1430                1435                1440
Leu Tyr Phe Arg Ala Asn Gly Val Gln Val Lys Gly Glu Phe Val Thr
                1445                1450                1455
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Asp Arg Tyr Gly Arg Ile Ser Tyr Tyr Asp Ala Asn Ser Gly Glu Arg
            1460                1465                1470
Val Arg Ile Asn
        1475


<210> 108
<211> 1462
<212> PRT
<213> Artificial Sequence

<220>
<223> Glucosyltransferase-S

<400> 108
Met Glu Thr Lys Arg Arg Tyr Lys Met Tyr Lys Val Lys Lys His Trp
 1               5                  10                  15
Val Thr Ile Ala Val Ala Ser Gly Leu Ile Thr Leu Gly Thr Thr Thr
            20                  25                  30
Leu Gly Ser Ser Val Ser Ala Glu Thr Glu Gln Gln Thr Ser Asp Lys
        35                  40                  45
Val Val Thr Gln Lys Ser Glu Asp Asp Lys Ala Ala Ser Glu Ser Ser
    50                  55                  60
Gln Thr Asp Ala Pro Lys Thr Lys Gln Ala Gln Thr Glu Gln Thr Gln
65                  70                  75                  80
Ala Gln Ser Gln Ala Asn Val Ala Asp Thr Ser Thr Ser Ile Thr Lys
                85                  90                  95
Glu Thr Pro Ser Gln Asn Ile Thr Thr Gln Ala Asn Ser Asp Asp Lys
            100                 105                 110
Thr Val Thr Asn Thr Lys Ser Glu Glu Ala Gln Thr Ser Glu Glu Arg
        115                 120                 125
Thr Lys Gln Ala Glu Glu Ala Gln Ala Thr Ala Ser Ser Gln Ala Leu
    130                 135                 140
Thr Gln Ala Lys Ala Glu Leu Thr Lys Gln Arg Gln Thr Ala Ala Gln
145                 150                 155                 160
Glu Asn Lys Asn Pro Val Asp Leu Ala Ala Ile Pro Asn Val Lys Gln
                165                 170                 175
Ile Asp Gly Lys Tyr Tyr Tyr Ile Gly Ser Asp Gly Gln Pro Lys Lys
            180                 185                 190
Asn Phe Ala Leu Thr Val Asn Asn Lys Val Leu Tyr Phe Asp Lys Asn
        195                 200                 205
Thr Gly Ala Leu Thr Asp Thr Ser Gln Tyr Gln Phe Lys Gln Gly Leu
    210                 215                 220
Thr Lys Leu Asn Asn Asp Tyr Thr Pro His Asn Gln Ile Val Asn Phe
225                 230                 235                 240
Glu Asn Thr Ser Leu Glu Thr Ile Asp Asn Tyr Val Thr Ala Asp Ser
                245                 250                 255
Trp Tyr Arg Pro Lys Asp Ile Leu Lys Asn Gly Lys Thr Trp Thr Ala
            260                 265                 270
Ser Ser Glu Ser Asp Leu Arg Pro Leu Leu Met Ser Trp Trp Pro Asp
        275                 280                 285
Lys Gln Thr Gln Ile Ala Tyr Leu Asn Tyr Met Asn Gln Gln Gly Leu
    290                 295                 300
Gly Thr Gly Glu Asn Tyr Thr Ala Asp Ser Ser Gln Glu Ser Leu Asn
```

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305                 310                 315                 320
Leu Ala Ala Gln Thr Val Gln Val Lys Ile Glu Thr Lys Ile Ser Gln
                325                 330                 335
Thr Gln Gln Thr Gln Trp Leu Arg Asp Ile Ile Asn Ser Phe Val Lys
            340                 345                 350
Thr Gln Pro Asn Trp Asn Ser Gln Thr Glu Ser Asp Thr Ser Ala Gly
        355                 360                 365
Glu Lys Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Ser Asn Ser Asp
    370                 375                 380
Lys Thr Ala Tyr Ala Asn Ser Asp Tyr Arg Leu Leu Asn Arg Thr Pro
385                 390                 395                 400
Thr Ser Gln Thr Gly Lys Pro Lys Tyr Phe Glu Asp Asn Ser Ser Gly
                405                 410                 415
Gly Tyr Asp Phe Leu Leu Ala Asn Asp Ile Asp Asn Ser Asn Pro Val
            420                 425                 430
Val Gln Ala Glu Gln Leu Asn Trp Leu His Tyr Leu Met Asn Tyr Gly
        435                 440                 445
Ser Ile Val Ala Asn Asp Pro Glu Ala Asn Phe Asp Gly Val Arg Val
    450                 455                 460
Asp Ala Val Asp Asn Val Asn Ala Asp Leu Leu Gln Ile Ala Ser Asp
465                 470                 475                 480
Tyr Leu Lys Ala His Tyr Gly Val Asp Lys Ser Glu Lys Asn Ala Ile
                485                 490                 495
Asn His Leu Ser Ile Leu Glu Ala Trp Ser Asp Asn Asp Pro Gln Tyr
            500                 505                 510
Asn Lys Asp Thr Lys Gly Ala Gln Leu Pro Ile Asp Asn Lys Leu Arg
        515                 520                 525
Leu Ser Leu Leu Tyr Ala Leu Thr Arg Pro Leu Glu Lys Asp Ala Ser
    530                 535                 540
Asn Lys Asn Glu Ile Arg Ser Gly Leu Glu Pro Val Ile Thr Asn Ser
545                 550                 555                 560
Leu Asn Asn Arg Ser Ala Glu Gly Lys Asn Ser Glu Arg Met Ala Asn
                565                 570                 575
Tyr Ile Phe Ile Arg Ala His Asp Ser Glu Val Gln Thr Val Ile Ala
            580                 585                 590
Lys Ile Ile Lys Ala Gln Ile Asn Pro Lys Thr Asp Gly Leu Thr Phe
        595                 600                 605
Thr Leu Asp Glu Leu Lys Gln Ala Phe Lys Ile Tyr Asn Glu Asp Met
    610                 615                 620
Arg Gln Ala Lys Lys Lys Tyr Thr Gln Ser Asn Ile Pro Thr Ala Tyr
625                 630                 635                 640
Ala Leu Met Leu Ser Asn Lys Asp Ser Ile Thr Arg Leu Tyr Tyr Gly
                645                 650                 655
Asp Met Tyr Ser Asp Asp Gly Gln Tyr Met Ala Thr Lys Ser Pro Tyr
            660                 665                 670
Tyr Asp Ala Ile Asp Thr Leu Leu Lys Ala Arg Ile Lys Tyr Ala Ala
        675                 680                 685
Gly Gly Gln Asp Met Lys Ile Thr Tyr Val Glu Gly Asp Lys Ser His
    690                 695                 700
Met Asp Trp Asp Tyr Thr Gly Val Leu Thr Ser Val Arg Tyr Gly Thr
705                 710                 715                 720
Gly Ala Asn Glu Ala Thr Asp Gln Gly Ser Glu Ala Thr Lys Thr Gln
                725                 730                 735
Gly Met Ala Val Ile Thr Ser Asn Asn Pro Ser Leu Lys Leu Asn Gln
```

```
            740                 745                 750
Asn Asp Lys Val Ile Val Asn Met Gly Thr Ala His Lys Asn Gln Glu
        755                 760                 765
Tyr Arg Pro Leu Leu Leu Thr Thr Lys Asp Gly Leu Thr Ser Tyr Thr
    770                 775                 780
Ser Asp Ala Ala Ala Lys Ser Leu Tyr Arg Lys Thr Asn Asp Lys Gly
785                 790                 795                 800
Glu Leu Val Phe Asp Ala Ser Asp Ile Gln Gly Tyr Leu Asn Pro Gln
                805                 810                 815
Val Ser Gly Tyr Leu Ala Val Trp Val Pro Val Gly Ala Ser Asp Asn
            820                 825                 830
Gln Asp Val Arg Val Ala Ala Ser Asn Lys Ala Asn Ala Thr Gly Gln
        835                 840                 845
Val Tyr Glu Ser Ser Ser Ala Leu Asp Ser Gln Leu Ile Tyr Glu Gly
    850                 855                 860
Phe Ser Asn Phe Gln Asp Phe Val Thr Lys Asp Ser Asp Tyr Thr Asn
865                 870                 875                 880
Lys Lys Ile Ala Gln Asn Val Gln Leu Phe Lys Ser Trp Gly Val Thr
                885                 890                 895
Ser Phe Glu Met Ala Pro Gln Tyr Val Ser Ser Glu Asp Gly Ser Phe
            900                 905                 910
Leu Asp Ser Ile Ile Gln Asn Gly Tyr Ala Phe Glu Asp Arg Tyr Asp
        915                 920                 925
Leu Ala Met Ser Lys Asn Asn Lys Tyr Gly Ser Gln Gln Asp Met Ile
    930                 935                 940
Asn Ala Val Lys Ala Leu His Lys Ser Gly Ile Gln Val Ile Ala Asp
945                 950                 955                 960
Trp Val Pro Asp Gln Ile Tyr Asn Leu Pro Gly Lys Glu Val Val Thr
                965                 970                 975
Ala Thr Arg Val Asn Asp Tyr Gly Glu Tyr Arg Lys Asp Ser Glu Ile
            980                 985                 990
Lys Asn Thr Leu Tyr Ala Ala Asn Thr Lys Ser Asn Gly Lys Asp Tyr
        995                 1000                1005
Gln Ala Lys Tyr Gly Gly Ala Phe Leu Ser Glu Leu Ala Ala Lys Tyr
    1010                1015                1020
Pro Ser Ile Phe Asn Arg Thr Gln Ile Ser Asn Gly Lys Lys Ile Asp
1025                1030                1035                1040
Pro Ser Glu Lys Ile Thr Ala Trp Lys Ala Lys Tyr Phe Asn Gly Thr
                1045                1050                1055
Asn Ile Leu Gly Arg Gly Val Gly Tyr Val Leu Lys Asp Asn Ala Ser
            1060                1065                1070
Asp Lys Tyr Phe Glu Leu Lys Gly Asn Gln Thr Tyr Leu Pro Lys Gln
        1075                1080                1085
Met Thr Asn Lys Glu Ala Ser Thr Gly Phe Val Asn Asp Gly Asn Gly
    1090                1095                1100
Met Thr Phe Tyr Ser Thr Ser Gly Tyr Gln Ala Lys Asn Ser Phe Val
1105                1110                1115                1120
Gln Asp Ala Lys Gly Asn Trp Tyr Tyr Phe Asp Asn Asn Gly His Met
                1125                1130                1135
Val Tyr Gly Leu Gln His Leu Asn Gly Glu Val Gln Tyr Phe Leu Ser
            1140                1145                1150
Asn Gly Val Gln Leu Arg Glu Ser Phe Leu Glu Asn Ala Asp Gly Ser
        1155                1160                1165
Lys Asn Tyr Phe Gly His Leu Gly Asn Arg Tyr Ser Asn Gly Tyr Tyr
```

```
    1170                1175                1180
Ser Phe Asp Asn Asp Ser Lys Trp Arg Tyr Phe Asp Ala Ser Gly Val
1185                1190                1195                1200
Met Ala Val Gly Leu Lys Thr Ile Asn Gly Asn Thr Gln Tyr Phe Asp
                1205                1210                1215
Gln Asp Gly Tyr Gln Val Lys Gly Ala Trp Ile Thr Gly Ser Asp Gly
            1220                1225                1230
Lys Lys Arg Tyr Phe Asp Asp Gly Ser Gly Asn Met Ala Val Asn Arg
        1235                1240                1245
Phe Ala Asn Asp Lys Asn Gly Asp Trp Tyr Tyr Leu Asn Ser Asp Gly
    1250                1255                1260
Ile Ala Leu Val Gly Val Gln Thr Ile Asn Gly Lys Thr Tyr Tyr Phe
1265                1270                1275                1280
Gly Gln Asp Gly Lys Gln Ile Lys Gly Lys Ile Ile Thr Asp Asn Gly
                1285                1290                1295
Lys Leu Lys Tyr Phe Leu Ala Asn Ser Gly Glu Leu Ala Arg Asn Ile
            1300                1305                1310
Phe Ala Thr Asp Ser Gln Asn Asn Trp Tyr Tyr Phe Gly Ser Asp Gly
        1315                1320                1325
Val Ala Val Thr Gly Ser Gln Thr Ile Ala Gly Lys Lys Leu Tyr Phe
    1330                1335                1340
Ala Ser Asp Gly Lys Gln Val Lys Gly Ser Phe Val Thr Tyr Asn Gly
1345                1350                1355                1360
Lys Val His Tyr Tyr His Ala Asp Ser Gly Glu Leu Gln Val Asn Arg
                1365                1370                1375
Phe Glu Ala Asp Lys Asp Gly Asn Trp Tyr Tyr Leu Asp Ser Asn Gly
            1380                1385                1390
Glu Ala Leu Thr Gly Ser Gln Arg Ile Asn Gly Gln Arg Val Phe Phe
        1395                1400                1405
Thr Arg Glu Gly Lys Gln Val Lys Gly Asp Val Ala Tyr Asp Glu Arg
    1410                1415                1420
Gly Leu Leu Arg Tyr Tyr Asp Lys Asn Ser Gly Asn Met Val Tyr Asn
1425                1430                1435                1440
Lys Val Val Thr Leu Ala Asn Gly Arg Arg Ile Gly Ile Asp Arg Trp
                1445                1450                1455
Gly Ile Ala Arg Tyr Tyr
            1460
```

<210> 109
<211> 1431
<212> PRT
<213> Artificial Sequence

<220>
<223> Dextransucrase

<400> 109

```
Met Glu Thr Lys Arg Arg Tyr Lys Met His Lys Val Lys Lys His Trp
 1               5                  10                  15
Val Thr Val Ala Val Ala Ser Gly Leu Ile Thr Leu Gly Thr Thr Thr
            20                  25                  30
Leu Gly Ser Ser Val Ser Ala Glu Thr Glu Gln Gln Thr Ser Asp Lys
        35                  40                  45
```

```
Val Val Thr Gln Lys Ser Glu Asp Asp Lys Ala Ala Ser Glu Ser Ser
    50                  55                  60
Gln Thr Asp Ala Pro Lys Thr Lys Gln Ala Gln Thr Glu Gln Thr Gln
65                  70                  75                  80
Ala Gln Ser Gln Ala Asn Val Ala Asp Thr Ser Thr Ser Ile Thr Lys
                85                  90                  95
Glu Thr Pro Ser Gln Asn Ile Thr Thr Gln Ala Asn Ser Asp Asp Lys
            100                 105                 110
Thr Val Thr Asn Thr Lys Ser Glu Glu Ala Gln Thr Ser Glu Glu Arg
        115                 120                 125
Thr Lys Gln Ser Glu Glu Ala Gln Thr Thr Ala Ser Ser Gln Ala Leu
    130                 135                 140
Thr Gln Ala Lys Ala Glu Leu Thr Lys Gln Arg Gln Thr Ala Ala Gln
145                 150                 155                 160
Glu Asn Lys Asn Pro Val Asp Leu Ala Ala Ile Pro Asn Val Lys Gln
                165                 170                 175
Ile Asp Gly Lys Tyr Tyr Tyr Ile Gly Ser Asp Gly Gln Pro Lys Lys
            180                 185                 190
Asn Phe Ala Leu Thr Val Asn Asn Lys Val Leu Tyr Phe Asp Lys Asn
        195                 200                 205
Thr Gly Ala Leu Thr Asp Thr Ser Gln Tyr Gln Phe Lys Gln Gly Leu
    210                 215                 220
Thr Lys Leu Asn Asn Asp Tyr Thr Pro His Asn Gln Ile Val Asn Phe
225                 230                 235                 240
Glu Asn Thr Ser Leu Glu Thr Ile Asp Asn Tyr Val Thr Ala Asp Ser
                245                 250                 255
Trp Tyr Arg Pro Lys Asp Ile Leu Lys Asn Gly Lys Thr Trp Thr Ala
            260                 265                 270
Ser Ser Glu Ser Asp Leu Arg Pro Leu Leu Met Ser Trp Trp Pro Asp
        275                 280                 285
Lys Gln Thr Gln Ile Ala Tyr Leu Asn Tyr Met Asn Gln Gln Gly Leu
    290                 295                 300
Gly Thr Gly Glu Asn Tyr Thr Ala Asp Ser Ser Gln Glu Ser Leu Asn
305                 310                 315                 320
Leu Ala Ala Gln Thr Val Gln Val Lys Ile Glu Thr Lys Ile Ser Gln
                325                 330                 335
Thr Gln Gln Thr Gln Trp Leu Arg Asp Ile Ile Asn Ser Phe Val Lys
            340                 345                 350
Thr Gln Pro Asn Trp Asn Ser Gln Thr Glu Ser Asp Thr Ser Ala Gly
        355                 360                 365
Glu Lys Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Ser Asn Ser Asp
    370                 375                 380
Lys Thr Ala Tyr Ala Asn Ser Asp Tyr Arg Leu Leu Asn Arg Thr Pro
385                 390                 395                 400
Thr Ser Gln Thr Gly Lys Pro Lys Tyr Phe Glu Asp Asn Ser Ser Gly
                405                 410                 415
Gly Tyr Asp Phe Leu Leu Ala Asn Asp Ile Asp Asn Ser Asn Pro Val
            420                 425                 430
Val Gln Ala Glu Gln Leu Asn Trp Leu His Tyr Leu Met Asn Tyr Gly
        435                 440                 445
Ser Ile Val Ala Asn Asp Pro Glu Ala Asn Phe Asp Gly Val Arg Val
    450                 455                 460
Asp Ala Val Asp Asn Val Asn Ala Asp Leu Leu Gln Ile Ala Ser Asp
465                 470                 475                 480
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Tyr Leu Lys Ala His Tyr Gly Val Asp Lys Ser Glu Lys Asn Ala Ile
                485                 490                 495
Asn His Leu Ser Ile Leu Glu Ala Trp Ser Asp Asn Asp Pro Gln Tyr
            500                 505                 510
Asn Lys Asp Thr Lys Gly Ala Gln Leu Pro Ile Asp Asn Lys Leu Arg
        515                 520                 525
Leu Ser Leu Leu Tyr Ala Leu Thr Arg Pro Leu Glu Lys Asp Ala Ser
    530                 535                 540
Asn Lys Asn Glu Ile Arg Ser Gly Leu Glu Pro Val Ile Thr Asn Ser
545                 550                 555                 560
Leu Asn Asn Arg Ser Ala Glu Gly Lys Asn Ser Glu Arg Met Ala Asn
                565                 570                 575
Tyr Ile Phe Ile Arg Ala His Asp Ser Glu Val Gln Thr Val Ile Ala
            580                 585                 590
Lys Ile Ile Lys Ala Gln Ile Asn Pro Lys Thr Asp Gly Leu Thr Phe
        595                 600                 605
Thr Leu Asp Glu Leu Lys Gln Ala Phe Lys Ile Tyr Asn Glu Asp Met
    610                 615                 620
Arg Gln Ala Lys Lys Lys Tyr Thr Gln Ser Asn Ile Pro Thr Ala Tyr
625                 630                 635                 640
Ala Leu Met Leu Ser Asn Lys Asp Ser Ile Thr Arg Leu Tyr Tyr Gly
                645                 650                 655
Asp Met Tyr Ser Asp Asp Gly Gln Tyr Met Ala Thr Lys Ser Pro Tyr
            660                 665                 670
Tyr Asp Ala Ile Asp Thr Leu Leu Lys Ala Arg Ile Lys Tyr Ala Ala
        675                 680                 685
Gly Gly Gln Asp Met Lys Ile Thr Tyr Val Glu Gly Asp Lys Ser His
    690                 695                 700
Met Asp Trp Asp Tyr Thr Gly Val Leu Thr Ser Val Arg Tyr Gly Thr
705                 710                 715                 720
Gly Ala Asn Glu Ala Thr Asp Gln Gly Ser Glu Ala Thr Lys Thr Gln
                725                 730                 735
Gly Met Ala Val Ile Thr Ser Asn Asn Pro Ser Leu Lys Leu Asn Gln
            740                 745                 750
Asn Asp Lys Val Ile Val Asn Met Gly Ala Ala His Lys Asn Gln Glu
        755                 760                 765
Tyr Arg Pro Leu Leu Leu Thr Thr Lys Asp Gly Leu Thr Ser Tyr Thr
    770                 775                 780
Ser Asp Ala Ala Ala Lys Ser Leu Tyr Arg Lys Thr Asn Asp Lys Gly
785                 790                 795                 800
Glu Leu Val Phe Asp Ala Ser Asp Ile Gln Gly Tyr Leu Asn Pro Gln
                805                 810                 815
Val Ser Gly Tyr Leu Ala Val Trp Val Pro Val Gly Ala Ser Asp Asn
            820                 825                 830
Gln Asp Val Arg Val Ala Ala Ser Asn Lys Ala Asn Ala Thr Gly Gln
        835                 840                 845
Val Tyr Glu Ser Ser Ser Ala Leu Asp Ser Gln Leu Ile Tyr Glu Gly
    850                 855                 860
Phe Ser Asn Phe Gln Asp Phe Val Thr Lys Asp Ser Asp Tyr Thr Asn
865                 870                 875                 880
Lys Lys Ile Ala Gln Asn Val Gln Leu Phe Lys Ser Trp Gly Val Thr
                885                 890                 895
Ser Phe Glu Met Ala Pro Gln Tyr Val Ser Ser Glu Asp Gly Ser Phe
            900                 905                 910
```

```
Leu Asp Ser Ile Ile Gln Asn Gly Tyr Ala Phe Glu Asp Arg Tyr Asp
        915                 920                 925
Leu Ala Met Ser Lys Asn Asn Lys Tyr Gly Ser Gln Gln Asp Met Ile
    930                 935                 940
Asn Ala Val Lys Ala Leu His Lys Ser Gly Ile Gln Val Ile Ala Asp
945                 950                 955                 960
Trp Val Pro Asp Gln Ile Tyr Asn Leu Pro Gly Lys Glu Val Val Thr
                965                 970                 975
Ala Thr Arg Val Asn Asp Tyr Gly Glu Tyr Arg Lys Asp Ser Glu Ile
            980                 985                 990
Lys Asn Thr Leu Tyr Ala Ala Asn Thr Lys Ser Asn Gly Lys Asp Tyr
        995                 1000                1005
Gln Ala Lys Tyr Gly Gly Ala Phe Leu Ser Glu Leu Ala Ala Lys Tyr
    1010                1015                1020
Pro Ser Ile Phe Asn Arg Thr Gln Ile Ser Asn Gly Lys Lys Ile Asp
1025                1030                1035                1040
Pro Ser Glu Lys Ile Thr Ala Trp Lys Ala Lys Tyr Phe Asn Gly Thr
                1045                1050                1055
Asn Ile Leu Gly Arg Gly Val Gly Tyr Val Leu Lys Asp Asn Ala Ser
            1060                1065                1070
Asp Lys Tyr Phe Glu Leu Lys Gly Asn Gln Thr Tyr Leu Pro Lys Gln
        1075                1080                1085
Met Thr Asn Lys Glu Ala Ser Thr Gly Phe Val Asn Asp Gly Asn Gly
    1090                1095                1100
Met Thr Phe Tyr Ser Thr Ser Gly Tyr Gln Ala Lys Asn Ser Phe Val
1105                1110                1115                1120
Gln Asp Ala Lys Gly Asn Trp Tyr Tyr Phe Asp Asn Asn Gly His Met
                1125                1130                1135
Val Tyr Gly Leu Gln Gln Leu Asn Gly Glu Val Gln Tyr Phe Leu Ser
            1140                1145                1150
Asn Gly Val Gln Leu Arg Glu Ser Phe Leu Glu Asn Ala Asp Gly Ser
        1155                1160                1165
Lys Asn Tyr Phe Gly His Leu Gly Asn Arg Tyr Ser Asn Gly Tyr Tyr
    1170                1175                1180
Ser Phe Asp Asn Asp Ser Lys Trp Arg Tyr Phe Asp Ala Ser Gly Val
1185                1190                1195                1200
Met Ala Val Gly Leu Lys Thr Ile Asn Gly Asn Thr Gln Tyr Phe Asp
                1205                1210                1215
Gln Asp Gly Tyr Gln Val Lys Gly Ala Trp Ile Thr Gly Ser Asp Gly
            1220                1225                1230
Lys Lys Arg Tyr Phe Asp Asp Gly Ser Gly Asn Met Ala Val Asn Arg
        1235                1240                1245
Phe Ala Asn Asp Lys Asn Gly Asp Trp Tyr Tyr Leu Asn Ser Asp Gly
    1250                1255                1260
Ile Ala Leu Val Gly Val Gln Thr Ile Asn Gly Lys Thr Tyr Tyr Phe
1265                1270                1275                1280
Gly Gln Asp Gly Lys Gln Ile Lys Gly Lys Ile Ile Thr Asp Asn Gly
                1285                1290                1295
Lys Leu Lys Tyr Phe Leu Ala Asn Ser Gly Glu Leu Ala Arg Asn Ile
            1300                1305                1310
Phe Ala Thr Asp Ser Gln Asn Asn Trp Tyr Tyr Phe Gly Ser Asp Gly
        1315                1320                1325
Val Ala Val Thr Gly Ser Gln Thr Ile Ala Gly Lys Lys Leu Tyr Phe
    1330                1335                1340
```

Ala Ser Asp Gly Lys Gln Val Lys Gly Ser Phe Val Thr Tyr Asn Gly
1345 1350 1355 1360
Lys Val His Tyr Tyr His Ala Asp Ser Gly Glu Leu Gln Val Asn Arg
1365 1370 1375
Phe Glu Ala Asp Lys Asp Gly Asn Trp Tyr Tyr Leu Asp Ser Asn Gly
1380 1385 1390
Glu Ala Leu Thr Gly Ser Gln Arg Ile Asn Asp Gln Arg Val Phe Phe
1395 1400 1405
Thr Arg Glu Gly Lys Gln Val Lys Gly Asp Val Ala Tyr Asp Glu Arg
1410 1415 1420
Gly Leu Leu Arg Tyr Tyr Asp
1425 1430

<210> 110
<211> 595
<212> PRT
<213> Artificial Sequence

<220>
<223> Hydrolyis of hyper-glycosylated Mogrosides from
DexT reaction Dextranase

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

```
Pro Gly Pro Ile Asn Gln Gly Asp Trp Gly Ser Ser Gly Ile Leu Tyr
                245                 250                 255
Phe Pro Pro Gly Val Tyr Trp Met Asn Ser Asn Gln Gln Gly Gln Thr
            260                 265                 270
Pro Lys Ile Gly Glu Asn His Ile Arg Leu His Pro Asn Thr Tyr Trp
        275                 280                 285
Ala Tyr Leu Ala Pro Gly Ala Tyr Val Lys Gly Ala Ile Glu Tyr Ser
    290                 295                 300
Thr Lys Ser Asp Phe Tyr Ala Thr Gly His Gly Val Leu Ser Gly Glu
305                 310                 315                 320
His Tyr Val Tyr Gln Ala Asn Pro Ala Thr Tyr Tyr Gln Ala Leu Lys
                325                 330                 335
Ser Asp Ala Thr Ser Leu Arg Met Trp Trp His Asn Asn Leu Gly Gly
            340                 345                 350
Gly Gln Thr Trp Tyr Cys Gln Gly Pro Thr Ile Asn Ala Pro Pro Phe
        355                 360                 365
Asn Thr Met Asp Phe His Gly Ser Ser Asp Ile Thr Thr Arg Ile Ser
    370                 375                 380
Asp Tyr Lys Gln Val Gly Ala Phe Phe Phe Gln Thr Asp Gly Pro Gln
385                 390                 395                 400
Met Tyr Pro Asn Ser Gln Val His Asp Val Phe Tyr His Val Asn Asp
                405                 410                 415
Asp Ala Ile Lys Thr Tyr Tyr Ser Gly Val Thr Val Thr Arg Ala Thr
            420                 425                 430
Ile Trp Lys Ala His Asn Asp Pro Ile Ile Gln Met Gly Trp Asp Thr
        435                 440                 445
Arg Asp Val Thr Gly Val Thr Leu Gln Asp Leu Tyr Ile Ile His Thr
    450                 455                 460
Arg Tyr Ile Lys Ser Glu Thr Tyr Val Pro Ser Ala Ile Ile Gly Ala
465                 470                 475                 480
Ser Pro Phe Tyr Met Pro Gly Arg Ser Val Asp Pro Ala Lys Ser Ile
                485                 490                 495
Ser Met Thr Ile Ser Asn Leu Val Cys Glu Gly Leu Cys Pro Ala Leu
            500                 505                 510
Met Arg Ile Thr Pro Leu Gln Asn Tyr Arg Asp Phe Arg Ile Gln Asn
        515                 520                 525
Val Ala Phe Pro Asp Gly Leu Gln Ala Asn Ser Ile Gly Thr Gly Lys
    530                 535                 540
Ser Ile Val Pro Ala Ser Ser Gly Leu Lys Phe Gly Val Ala Ile Ser
545                 550                 555                 560
Asn Trp Thr Val Gly Gly Glu Gln Val Thr Met Ser Asn Phe Gln Ser
                565                 570                 575
Asp Ser Leu Gly Gln Leu Asp Ile Asp Val Ser Tyr Trp Gly Gln Trp
            580                 585                 590
Val Ile Arg
        595
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<210> 111
<211> 731
<212> PRT
<213> Artificial Sequence

<220>

<223> Amino acid sequence of S. cerevisiae lanosterol
synthase

<400> 111

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Met Thr Glu Phe Tyr Ser Asp Thr Ile Gly Leu Pro Lys Thr Asp Pro
 1               5                  10                  15
Arg Leu Trp Arg Leu Arg Thr Asp Glu Leu Gly Arg Glu Ser Trp Glu
            20                  25                  30
Tyr Leu Thr Pro Gln Gln Ala Ala Asn Asp Pro Pro Ser Thr Phe Thr
        35                  40                  45
Gln Trp Leu Leu Gln Asp Pro Lys Phe Pro Gln Pro His Pro Glu Arg
    50                  55                  60
Asn Lys His Ser Pro Asp Phe Ser Ala Phe Asp Ala Cys His Asn Gly
65                  70                  75                  80
Ala Ser Phe Phe Lys Leu Leu Gln Glu Pro Asp Ser Gly Ile Phe Pro
                85                  90                  95
Cys Gln Tyr Lys Gly Pro Met Phe Met Thr Ile Gly Tyr Val Ala Val
            100                 105                 110
Asn Tyr Ile Ala Gly Ile Glu Ile Pro Glu His Glu Arg Ile Glu Leu
        115                 120                 125
Ile Arg Tyr Ile Val Asn Thr Ala His Pro Val Asp Gly Gly Trp Gly
    130                 135                 140
Leu His Ser Val Asp Lys Ser Thr Val Phe Gly Thr Val Leu Asn Tyr
145                 150                 155                 160
Val Ile Leu Arg Leu Leu Gly Leu Pro Lys Asp His Pro Val Cys Ala
                165                 170                 175
Lys Ala Arg Ser Thr Leu Leu Arg Leu Gly Gly Ala Ile Gly Ser Pro
            180                 185                 190
His Trp Gly Lys Ile Trp Leu Ser Ala Leu Asn Leu Tyr Lys Trp Glu
        195                 200                 205
Gly Val Asn Pro Ala Pro Pro Glu Thr Trp Leu Leu Pro Tyr Ser Leu
    210                 215                 220
Pro Met His Pro Gly Arg Trp Trp Val His Thr Arg Gly Val Tyr Ile
225                 230                 235                 240
Pro Val Ser Tyr Leu Ser Leu Val Lys Phe Ser Cys Pro Met Thr Pro
                245                 250                 255
Leu Leu Glu Glu Leu Arg Asn Glu Ile Tyr Thr Lys Pro Phe Asp Lys
            260                 265                 270
Ile Asn Phe Ser Lys Asn Arg Asn Thr Val Cys Gly Val Asp Leu Tyr
        275                 280                 285
Tyr Pro His Ser Thr Thr Leu Asn Ile Ala Asn Ser Leu Val Val Phe
    290                 295                 300
Tyr Glu Lys Tyr Leu Arg Asn Arg Phe Ile Tyr Ser Leu Ser Lys Lys
305                 310                 315                 320
Lys Val Tyr Asp Leu Ile Lys Thr Glu Leu Gln Asn Thr Asp Ser Leu
                325                 330                 335
Cys Ile Ala Pro Val Asn Gln Ala Phe Cys Ala Leu Val Thr Leu Ile
            340                 345                 350
Glu Glu Gly Val Asp Ser Glu Ala Phe Gln Arg Leu Gln Tyr Arg Phe
        355                 360                 365
Lys Asp Ala Leu Phe His Gly Pro Gln Gly Met Thr Ile Met Gly Thr
    370                 375                 380
Asn Gly Val Gln Thr Trp Asp Cys Ala Phe Ala Ile Gln Tyr Phe Phe
385                 390                 395                 400
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```
Val Ala Gly Leu Ala Glu Arg Pro Glu Phe Tyr Asn Thr Ile Val Ser
                405                 410                 415
Ala Tyr Lys Phe Leu Cys His Ala Gln Phe Asp Thr Glu Cys Val Pro
            420                 425                 430
Gly Ser Tyr Arg Asp Lys Arg Lys Gly Ala Trp Gly Phe Ser Thr Lys
        435                 440                 445
Thr Gln Gly Tyr Thr Val Ala Asp Cys Thr Ala Glu Ala Ile Lys Ala
    450                 455                 460
Ile Ile Met Val Lys Asn Ser Pro Val Phe Ser Glu Val His His Met
465                 470                 475                 480
Ile Ser Ser Glu Arg Leu Phe Glu Gly Ile Asp Val Leu Leu Asn Leu
                485                 490                 495
Gln Asn Ile Gly Ser Phe Glu Tyr Gly Ser Phe Ala Thr Tyr Glu Lys
            500                 505                 510
Ile Lys Ala Pro Leu Ala Met Glu Thr Leu Asn Pro Ala Glu Val Phe
        515                 520                 525
Gly Asn Ile Met Val Glu Tyr Pro Tyr Val Glu Cys Thr Asp Ser Ser
    530                 535                 540
Val Leu Gly Leu Thr Tyr Phe His Lys Tyr Phe Asp Tyr Arg Lys Glu
545                 550                 555                 560
Glu Ile Arg Thr Arg Ile Arg Ile Ala Ile Glu Phe Ile Lys Lys Ser
                565                 570                 575
Gln Leu Pro Asp Gly Ser Trp Tyr Gly Ser Trp Gly Ile Cys Phe Thr
            580                 585                 590
Tyr Ala Gly Met Phe Ala Leu Glu Ala Leu His Thr Val Gly Glu Thr
        595                 600                 605
Tyr Glu Asn Ser Ser Thr Val Arg Lys Gly Cys Asp Phe Leu Val Ser
    610                 615                 620
Lys Gln Met Lys Asp Gly Gly Trp Gly Glu Ser Met Lys Ser Ser Glu
625                 630                 635                 640
Leu His Ser Tyr Val Asp Ser Glu Lys Ser Leu Val Val Gln Thr Ala
                645                 650                 655
Trp Ala Leu Ile Ala Leu Leu Phe Ala Glu Tyr Pro Asn Lys Glu Val
            660                 665                 670
Ile Asp Arg Gly Ile Asp Leu Leu Lys Asn Arg Gln Glu Glu Ser Gly
        675                 680                 685
Glu Trp Lys Phe Glu Ser Val Glu Gly Val Phe Asn His Ser Cys Ala
    690                 695                 700
Ile Glu Tyr Pro Ser Tyr Arg Phe Leu Phe Pro Ile Lys Ala Leu Gly
705                 710                 715                 720
Met Tyr Ser Arg Ala Tyr Glu Thr His Thr Leu
                725                 730
```

<210> 112
<211> 2106
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA sequence encoding S. grosvenorii CPR4497

<400> 112
atgaaggtct ctccatttga gttcatgtcg gcaataatta agggcaggat ggacccgtcc 60

aattcttcat ttgagtcgac tggcgaggtt gcctcagtta ttttcgagaa ccgtgagctg 120
gttgcgatct taaccacctc gatcgccgtc atgattggct gcttcgttgt tctcatgtgg 180
cgaagagccg gcagtcggaa agttaagaac gtggagctac ctaagccgtt gattgtgcac 240
gagccggagc ccgaagttga agacggcaag aagaaggttt caatcttctt cggtacacag 300
acaggcaccg ccgaaggatt tgcaaaggct ctagctgacg aggcgaaagc acgatacgag 360
aaggccacat ttagagttgt tgatttggat gattatgcag ctgatgacga tcagtatgaa 420
gagaagttga agaacgagtc tttcgctgtc ttcttattgg caacgtatgg cgatggagag 480
cccactgata atgccgcaag attctataaa tggttcgcgg aggggaaaga gagaggggag 540
tggcttcaga accttcatta tgcggtcttt ggccttggca accgacagta cgagcatttt 600
aataagattg caaaggtggc agatgagctg cttgaggcac agggaggcaa ccgccttgtt 660
aaagttggtc ttggagatga cgatcagtgc atagaggatg acttcagtgc ctggagagaa 720
tcattgtggc ctgagttgga tatgttgctt cgagatgagg atgatgcaac aacagtgacc 780
accccttaca cagctgccgt attagaatat cgagttgtat tccatgattc tgcagatgta 840
gctgctgagg acaagagctg gatcaatgca aacggtcatg ctgtacatga tgctcagcat 900
cccttcagat ctaatgtggt tgtgaggaag gagctccata cgtccgcatc tgatcgctcc 960
tgtagtcatc tagaatttaa tatttctggg tctgcactca attatgaaac aggggatcat 1020
gtcggtgttt actgtgaaaa cttaactgag actgtggacg aggcactaaa cttattgggt 1080
ttgtctcctg aaacgtattt ctccatatat actgataacg aggatggcac tccacttggt 1140
ggaagctctt taccacctcc ttttccatcc tgcaccctca gaacagcatt gactcgatat 1200
gcagatctct tgaattcacc caagaagtca gctttgcttg cattagcagc acatgcttca 1260
aatccagtag aggctgaccg attaagatat cttgcatcac ctgccgggaa ggatgaatac 1320
gcccagtctg tgattggtag ccagaaaagc cttcttgagg tcatggctga atttccttct 1380
gccaagcccc cacttggtgt cttcttcgca gctgttgcac cgcgcttgca gcctcgattc 1440
tactccatat catcatctcc aaggatggct ccatctagaa ttcatgttac ttgtgcttta 1500
gtctatgaca aaatgccaac aggacgtatt cataaaggag tgtgctcaac ttggatgaag 1560
aattctgtgc ccatggagaa aagccatgaa tgcagttggg ctccaatttt cgtgagacaa 1620
tcaaacttca agcttcctgc agagagtaaa gtgcccatta tcatggttgg tcctggaact 1680
ggattggctc ctttcagagg tttcttacag gaaagattag ctttgaagga atctggagta 1740
gaattggggc cttccatatt gttctttgga tgcagaaacc gtaggatgga ttacatatac 1800
gaggatgagc tgaacaactt tgttgagact ggtgctctct ctgagttggt tattgccttc 1860
tcacgcgaag ggccaactaa ggaatatgtg cagcataaaa tggcagagaa ggcttcggat 1920
atctggaatt tgatatcaga aggggcttac ttatatgtat gtggtgatgc aaagggcatg 1980
gctaaggatg tccaccgaac tctccatact atcatgcaag agcagggatc tcttgacagc 2040
tcaaaagctg agagcatggt gaagaatctg caaatgaatg gaaggtatct gcgtgatgtc 2100
tggtga 2106

<210> 113
<211> 701
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of S. grosvenorii CPR4497

<400> 113
Met Lys Val Ser Pro Phe Glu Phe Met Ser Ala Ile Ile Lys Gly Arg
 1               5                  10                  15
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
    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
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
    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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<210> 114
<211> 954
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon optimized nucleotide sequence of Epoxide
hydrolase 1 of S grosvenorii

<400> 114

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atggacgcga ttgaacatag aaccgtaagt gttaatggta tcaatatgca tgtggcagaa 60
aagggagagg gacctgtcgt gttgttgctt catggtttcc cagaattgtg gtacagttgg 120
agacatcaaa tattggctct ttcctcttta ggttacagag ctgtcgcacc agacttacga 180
ggctacgggg atacagatgc cccagggtca atttcatcat acacatgctt tcacatcgta 240
ggagatctcg tggctctagt tgagtctctg ggtatggaca gggtttttgt tgtagcccac 300
gattggggtg ccatgatcgc ttggtgtttg tgtctgttta gacctgaaat ggttaaagct 360
tttgtttgtc tctccgtccc attcagacag agaaacccta agatgaaacc agttcaaagt 420
atgagagcct ttttcggcga tgattactat atttgcagat ttcaaaatcc tggggaaatc 480
gaagaggaga tggctcaagt gggtgcaagg gaagtcttaa gaggaattct aacatctcgt 540
cgtcctggac caccaatctt accaaaaggg caagctttta gagcaagacc aggagcatcc 600
actgcattgc catcttggct atctgaaaaa gatctgtcat ttttcgcttc taagtatgat 660
caaaagggct ttacaggccc actaaactac tacagagcca tggatcttaa ttgggaattg 720
actgcgtcat ggactggtgt ccaagttaaa gtacctgtca aatacatcgt gggtgacgtt 780
gacatggttt ttacgactcc tggtgtaaag gaatatgtca acggcggtgg tttcaaaaag 840
gacgttccat ttttacagga agtggtaatc atggaaggcg ttggtcattt cattaatcag 900
gaaaaacctg aggagatttc atctcatata cacgatttca taagcaaatt ctaa       954
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<210> 115
<211> 951
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon optimized nucleotide sequence of Epoxide
hydrolase 2 of S grosvenorii

<400> 115
atggatgaaa tcgaacatat taccatcaat acaaatggaa tcaaaatgca tattgcgtca 60
gtcggcacag gaccagttgt tctcttgcta cacggctttc cagaattatg gtactcttgg 120
agacaccaac tactttacct gtcctccgtt gggtacagag caatagctcc agatttgaga 180
ggctatggcg atactgacag tccagctagt cctacctctt atactgctct tcatattgta 240
ggtgacctgg tcggcgcatt agacgaattg ggaatagaaa aggtcttttt agtgggtcat 300
gactggggtg ctattatcgc atggtacttt tgtttgttta gaccagatag aattaaagca 360
cttgtgaatt tgtctgtcca gtttatccca cgtaacccag caataccttt tatagaaggt 420
ttcagaacag cttttggtga tgacttctac atttgtagat ttcaagtacc tggggaagct 480
gaagaggatt tcgcgtctat cgatactgct caattgttta aaacttcatt atgcaataga 540
agctcagccc ctccttgttt gcctaaagag attggtttta gggctatccc accaccagaa 600
aatctgccat cttggctcac agaggaagat atcaacttct acgcagccaa gtttaaacaa 660
actggtttta ctggtgccct taactattat agagcattcg acttgacatg ggaattaaca 720
gccccatgga caggagccca gatccaagtt cctgtaaagt tcatagttgg tgattcagat 780
ctcacgtacc atttccctgg tgctaaggaa tacatccaca acggagggtt taaaagagat 840
gtgccactat tagaggaagt tgttgtggta aaagatgcct gccacttcat taaccaagag 900
cgaccacaag agattaatgc tcatattcat gacttcatca ataagttcta a 951

<210> 116
<211> 174
<212> DNA
<213> Artificial Sequence

<220>
<223> S grosvenorii UGT3494

<400> 116
atggcggatc ggaaagagag cgttgtgatg ttcccgttca tggggcaggg ccatatcatc 60
ccttttctag ctttggccct ccagattgag cacagaaaca gaaactacgc catatacttg 120
gtaaatactc ctctcaacgt taagaaaatg agatcttctc tccctccaga ttga 174

<210> 117
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Fragment of S grosvenorii UGT11789

<400> 117
ttctgctcca cgcctgtaaa tttggaagcc attaaaccaa agctttccaa aagctactct 60
gattcgatcc aactaatgga ggttcctctc gaatcgacgc cggagcttcc tcctcactat 120
catacagcca aaggccttcc gccgcattta atgcccaaac tcatgaatgc ctttaaaatg 180
gttgctccca atctcgaatc gatcctaaaa accctaaacc cagatctgct catcgtcgac 240
attctccttc catggatgct tccactcgct tcatcgctca aaattccgat ggttttcttc 300

actattttcg gtgccatggc catctccttt atgatttata atcgaaccgt ctcgaacgag 360
cttccatttc cagaatttga acttcacgag tgctggaaat cgaagtgccc ctatttgttc 420
aaggaccaag cggaaagtca atcgttctta gaatacttgg atcaatcttc aggcgtaatt 480
ttgatcaaaa cttccagaga gattgaggct aagtatgtag actttctcac ttcgtcgttt 540
acgaagaagg ttgtgaccac cggtcccctg gttcagcaac cttcttccgg cgaagacgag 600
aagcagtact ccgatatcat cgaatggcta gacaagaagg agccgttatc gacggtgctc 660
gtttcgtttg ggagcgagta ttatctgtca aaggaagaga tggaagaaat cgcctacggg 720
ctggagagcg ccagcgaggt gaatttcatc tggattgtta ggtttccgat gggacaggaa 780
acggaggtcg aggcggcgct gccggagggg ttcatccaga gggcaggaga gagagggaaa 840
gtggtcgagg gctgggctcc gcaggcgaaa atattggcgc atccgagcac cggcggccat 900
gtgagccaca acgggtggag ctcgattgtg gagtgcttga tgtccggtgt accggtgatc 960
ggcgcgccga tgcaacttga cgggccaatc gtcgcaaggc tggtggagga gatcggcgtg 1020
ggtttggaaa tcaagagaga tgaggaaggg agaatcacga ggggcgaagt tgccgatgca 1080
atcaagacgg tggcggtggg caaaaccggg gaagatttta gaaggaaagc aaaaaaaatc 1140
agcagcattt tgaagatgaa agatgaagaa gaggttgaca ctttggcaat ggaattagtg 1200
aggttatgcc aaatgaaaag agggcaggag tctcaggact aa 1242

<210> 118
<211> 912
<212> DNA
<213> Artificial Sequence

<220>
<223> S. grosvenorii UGT11999

<400> 118
tcccggtcaa cggtagagga cttcacggag cttcgagagt ggatgccttc tggatcgaac 60
atggtctacc ggtaccacga gattaaaaaa tccttagatg gagcaaccgg caacgaatcg 120
gggacgtctg attcggtccg attcggaatt gtgattgagg agagtgttgc tgtggctgta 180
agaagctccc ctgaactgga accggaatgg ttcgatttgc tcgcgaagct ttaccagaag 240
ccagttgttc cggtaggatt tctacctcca gtaattgaag atgcggaaga attgagcagc 300
gatatcaagg aatggttaga caaacagagc tcaaactcgg tcctttacgt cgcattcggg 360
accgaggcga ctctgagtca agatgacgtc actgagttag ccatggggct tgagcaatct 420
gggataccat ttttctgggt actgagaacc tcacctcggg acgagtcaga catgttaccg 480
gccgggttca aggagcgagt cgaaggtcga ggaagtgttc acgtgggatg ggtctcgcag 540
gtgaagatac tgagtcacga ctcggttggc ggttgtttga cacactgtgg atggaactcg 600
atcatagagg ggctcggatt cgggcgcgtt atggtattgt ttccagtcgt gaacgaccag 660
ggattgaacg ctagattgtt gggggagaag aagctcggga tagagataga aagggacgag 720
cgagatggat cgttcacacg cgactcggtg tcggaatcgg tgaggtcggc aatggcggaa 780
agttcaggcg aggccttgag agtgagggcc agggaaatga aggggttgtt tggaaacgga 840
gatgagaacg agcatcaact gaacaagttt gtacaatttc tcgaggcaaa caggaatagg 900
cagtccgagt aa 912

<210> 119
<211> 1125
<212> DNA
<213> Artificial Sequence

<220>
<223> Partial sequence from Siraitia grosvenorii
UGT13679

<400> 119
ctgctgccga ttccgctgcc gaaaccggcc gccgatctct tgccggaagg tgcagaggcg 60

acggtggata ttccgtccga caagattccg tatctgaaat tggccctcga tctcgccgag 120
cagccgtttc ggaagttcgt cgttgatcgt ccgccggatt ggatgatcgt cgattttaat 180
gctacttggg tctgcgatat ttctcgggag cttcaaatcc caatcgtttt ctttcgtgtt 240
ctttcgcctg gatttcttgc tttctttgcg catgttcttg ggagtggtct gccgctgtcg 300
gagatcgaaa gcctgatgac tccgccggtg atcgacgggt cgacggtggc gtaccgccgg 360
catgaagctg ccgttatttg tgctgggttt tttgagaaga acgcttctgg tatgagtgat 420
cgcgatcggg taaccaaaat tctctctgcc agtcaagcaa tcgcagttcg ttcttgctac 480
gaatttgacg ttgagtattt gaaattgtac gagaaatatt gtggaaaaag agtgattcct 540
ctagggtttc tccctccaga aaagccccaa aagtccgagt tcgccgccga ttcgccatgg 600
aaaccgacct tcgagtggct tgacaaacaa aagccccgat cagtggtgtt cgtcggattc 660
ggcagcgaat gcaaactcac gaaagatgat gtttacgaga tagcgcgcgg ggtggagctg 720
tcggagctgc cattttgtg ggctctgaga aaaccgatct gggcggcggc ggacgattcc 780
gacgctctgc ctgccggatt cctcgagcgg acggcggaga gagggattgt gagcatgggg 840
tgggcgccgc agatggagat tttaacgcac ccgtcgattg gcggctctct gtttcacgcc 900
gggtggggat ccgccattga agctctgcaa ttcgggcatt gccttgttct gttgccattc 960
atcgtggatc agccactgaa tgcaaggctt ctggtggaga agggtgttgc agtcgaagtt 1020
ggaagaaagg aagacgggtc ttttagtgga gaagacatag ctaaagctct gagagaagct 1080
atggtttcag aagaaggtga gcagatgagg aggcaagcga gaaag 1125

<210> 120
<211> 486
<212> DNA
<213> Artificial Sequence

<220>
<223> Partial sequence of S grosvenorii UGT 15423

<400> 120
atggaaaacg acggcgtttt gcacgtggtg gtattcccat ggctagcctt gggtcatctc 60
attcctttcg ctcgactcgc cacctgctta gcccacaagg gtctcagggt ttcgttcgta 120
tcaaccacaa ggaacctgag cagaattccc aaaatacccc cacatctctc ctcctccgtc 180
aacctcgtcg gctttcctct gccccacgtc gacggccttc cggacgccgc cgaggcttcc 240
tccgacgtgc cttacaacaa gcaacagtta ctgaagaagg ccttcgactc tctggaatca 300
ccgctcgccg atttgcttcg tgatttgaat cccgattgga ttatctacga ttacgcctct 360
cattggcttc cgcagctcgc ggcggagctc cgtatctcgt ctgttttctt cagcctcttc 420
accgcggcgt ttcttgcttt tcttggccca ccgtcggcgt tgtccggcga cggcagttcc 480
cggtga 486

<210> 121
<211> 1491
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding S grosvenorii UGT1576

<400> 121
atggcttctc ctcgccacac tcctcacttt ctgctcttcc ctttcatggc tcaaggccac 60
atgatcccca tgattgacct tgccaggctt ctggctcagc gaggagttat catcactatt 120
atcaccacgc cccacaatgc tgctcgctac cactctgttc ttgctcgcgc catcgattct 180
gggttacaca tccatgtcct ccaactgcag tttccatgta aggaaggtgg gctgccagaa 240
gggtgcgaga atgtggactt gctaccttca cttgcttcca tacccagatt ctacagagca 300
gcaagtgatc tcctttacga accatctgaa aaactgtttg aggaactcat cccccggccg 360
acctgcataa tctccgatat gtgcctgccc tggaccatgc gaattgctct gaaatatcac 420

gtcccaaggc tcgttttcta cagtttgagc tgcttctttc ttctctgtat gcggagttta 480
aaaaacaatc tagcgcttat aagctccaag tctgattctg agttcgtaac tttctctgac 540
ttgcctgatc cagtcgagtt tctcaagtcg gagctaccta aatccaccga tgaagacttg 600
gtgaagttta gttatgaaat gggggaggcc gatcggcagt catacggcgt tattttaaat 660
ctatttgagg agatggaacc aaagtatctt gcagaatatg aaaaggaaag agaatcgccg 720
gaaagagtct ggtgcgtcgg cccagtttcg ctttgcaacg acaacaaact cgacaaagct 780
gaaagaggca acaaagcctc catcgacgaa tacaaatgca tcaggtggct cgacgggcag 840
cagccatctt cggtggttta cgtctcttta ggaagcttgt gcaatctggt gacggcgcag 900
atcatagagc tgggtttggg tttggaggca tcaaagaaac ccttcatttg ggtcataaga 960
agaggaaaca taacagagga gttacagaaa tggcttgtgg agtacgattt cgaggagaaa 1020
attaaaggga gagggctggt gattcttggc tgggctcccc aagttctgat actgtcacac 1080
cctgcaatcg gatgcttttt gacgcactgc ggttggaact caagcatcga agggatatcg 1140
gccggcgtgc caatggtcac ctggccgctt tttgcggatc aagtcttcaa cgagaagcta 1200
attgtacaaa tactcagaat cggcgtaagt gtaggcacgg aaactactat gaactgggga 1260
gaggaagagg agaaaggggt ggttgtgaag agagagaaag tgagggaagc catagaaata 1320
gtgatggatg gagatgagag agaagagagg agagagagat gcaaagagct tgctgaaacg 1380
gcgaagagag ctatagaaga agggggctcg tctcaccgga acctcacgat gttgattgaa 1440
gatataattc atggaggagg tttgagttat gagaaaggaa gttgtcgctg a 1491

<210> 122
<211> 1380
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding S grosvenorii UGT
SK98

<400> 122
atggatgccc agcgaggtca caccaccacc attttgatgc ttccatgggt cggctacggc 60
catctcttgc ctttcctcga gctggccaaa agcctctcca ggaggaaatt attccacatc 120
tacttctgtt caacgtctgt tagcctcgac gccattaaac caaagcttcc tccttctatc 180
tcttctgatg attccatcca acttgtggaa cttcgtctcc cttcttctcc tgagttacct 240
cctcatcttc acacaaccaa cggccttccc tctcacctca tgcccgctct ccaccaagcc 300
ttcgtcatgg ccgcccaaca ctttcaggtc attttacaaa cacttgcccc gcatctcctc 360
atttatgaca ttctccaacc ttgggctcct caagtggctt catccctcaa cattccagcc 420
atcaacttca gtactaccgg agcttcaatg ctttctcgaa cgcttcaccc tactcactac 480
ccaagttcta aattcccaat ctcagagttt gttcttcaca atcactggag agccatgtac 540
accaccgccg atggggctct tacagaagaa ggccacaaaa ttgaagaaac acttgcgaat 600
tgcttgcata cttcttgcgg ggtagttttg gtcaatagtt tcagagagct tgagacgaaa 660
tatatcgatt atctctctgt tctcttgaac aagaaagttg ttccggtcgg tcctttggtt 720
tacgaaccga atcaagaagg ggaagatgaa ggttattcaa gcatcaaaaa ttggcttgac 780
aaaaaggaac cgtcctcaac cgtcttcgtt tcatttggaa ccgaatactt cccgtcaaag 840
gaagaaatgg aagagatagc gtatgggtta gagctgagcg aggttaattt catctgggtc 900
cttagatttc ctcaaggaga cagcaccagc accattgaag acgccttgcc gaaggggttt 960
ctggagagag cgggagagag ggcgatggtg gtgaagggtt gggctcctca ggcgaagata 1020
ctgaagcatt ggagcacagg ggggcttgtg agtcactgtg gatggaactc gatgatggag 1080
ggcatgatgt ttggcgtacc cataatagcg gtcccgatgc atctggacca gccctttaac 1140
gccggactct tggaagaagc tggcgtcggc gtggaagcca agcgaggttc ggacggcaaa 1200
attcaaagag aagaagttgc aaagtcgatc aaagaagtgg tgattgagaa aaccagggaa 1260
gacgtgagga agaaagcaag agaaatgggt gagattttga ggagtaaagg agatgagaaa 1320
attgatgagt tggtggctga aatttctctt ttgcgcaaaa aggctccatg ttcaatttaa 1380

<210> 123
<211> 1377
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding S grosvenorii UG98

<400> 123
atggatgccc agcgaggtca caccacaacc attttgatgt ttccatggct cggctatggc 60
catctttcgg ctttcctaga gttggccaaa agcctctcaa ggaggaactt ccatatctac 120
ttctgttcaa cctctgttaa cctcgacgcc attaaaccaa agcttccttc ttcttcctct 180
tctgattcca tccaacttgt ggaactttgt cttccatctt ctcctgatca gctccctcct 240
catcttcaca caaccaacgc cctcccccct cacctcatgc ccactctcca ccaagccttc 300
tccatggctg cccaacactt tgctgccatt ttacacacac ttgctccgca tctcctcatt 360
tacgactctt tccaaccttg ggctcctcaa ctagcttcat ccctcaacat tccagccatc 420
aacttcaata ctacgggagc ttcagtcctg acccgaatgc ttcacgctac tcactaccca 480
agttctaaat tcccaatttc agagtttgtt ctccacgatt attggaaagc catgtacagc 540
gccgccggtg gggctgttac aaaaaaagac cacaaaattg gagaaacact tgcgaattgc 600
ttgcatgctt cttgtagtgt aattctaatc aatagtttca gagagctcga ggagaaatat 660
atggattatc tctccgttct cttgaacaag aaagttgttc cggttggtcc tttggtttac 720
gaaccgaatc aagacgggga agatgaaggt tattcaagca tcaaaaattg gcttgacaaa 780
aaggaaccgt cctccaccgt cttcgtttca tttggaagcg aatacttccc gtcaaaggaa 840
gaaatggaag agatagccca tgggttagag gcgagcgagg ttcatttcat ctgggtcgtt 900
aggtttcctc aaggagacaa caccagcgcc attgaagatg ccttgccgaa ggggtttctg 960
gagagggtgg gagagagagg gatggtggtg aagggttggg ctcctcaggc gaagatactg 1020
aagcattgga gcacaggggg attcgtgagc cactgtggat ggaactcggt gatggaaagc 1080
atgatgtttg gcgttcccat aataggggtt ccgatgcatc tggaccagcc ctttaacgcc 1140
ggactcgcgg aagaagctgg cgtcggcgtg gaagccaagc gagattcgga cggcaaaatt 1200
caaagagaag aagttgcaaa gtcgatcaaa gaagtggtga ttgagaaaac cagggaagac 1260
gtgaggaaga aagcaagaga aatgggtgag attttgagga gtaaaggaga tgagaaaatt 1320
gatgagttgg tggctgaaat ttctcttttg cgcaaaaagg ctccatgttc aatttaa    1377

<210> 124
<211> 419
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding codon optimized UGT
SK98

<400> 124
catttgtctg ctttttgga attggccaag tccttgtcta gaagaaactt ccatatctac 60
ttttgctcca cctccgttaa tttggatgct attaagccaa agttgccatc ctcttcatcc 120
tccgattcta ttcaattggt tgaattgtgc ttgccatctt ccccagatca attgccacca 180
cacttgcata caactaatgc tttaccacca catttgatgc caacattgca tcaagctttt 240
tctatggctg ctcaacattt tgctgctatc ttgcatactt ggctcctcat ttgttgatct 300
acgattcttt tcaaccatgg gctccacaat tggcttcatc tttgaatatt ccagccatca 360
acttcaacac tactggtgct tcagttttga ccagaatgtt gcatgctact cattaccca  419

<210> 125
<211> 453
<212> PRT

<213> Artificial Sequence

<220>
<223> UGT polypeptide is also referred to as UGT94A9, A9
or UGT94-289-1

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

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


<210> 126
<211> 316
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT polypeptide is also referred to as EH1, EPH1
      and contig 73966

<400> 126
Met Glu Asn Ile Glu His Thr Thr Val Gln Thr Asn Gly Ile Lys Met
 1               5                  10                  15
His Val Ala Ala Ile Gly Thr Gly Pro Pro Val Leu Leu Leu His Gly
            20                  25                  30
Phe Pro Glu Leu Trp Tyr Ser Trp Arg His Gln Leu Leu Tyr Leu Ser
        35                  40                  45
Ser Ala Gly Tyr Arg Ala Ile Ala Pro Asp Leu Arg Gly Tyr Gly Asp
    50                  55                  60
Thr Asp Ala Pro Pro Ser Pro Ser Ser Tyr Thr Ala Leu His Ile Val
65                  70                  75                  80
Gly Asp Leu Val Gly Leu Leu Asp Val Leu Gly Ile Glu Lys Val Phe
                85                  90                  95
Leu Ile Gly His Asp Trp Gly Ala Ile Ile Ala Trp Tyr Phe Cys Leu
            100                 105                 110
Phe Arg Pro Asp Arg Ile Lys Ala Leu Val Asn Leu Ser Val Gln Phe
        115                 120                 125
Phe Pro Arg Asn Pro Thr Thr Pro Phe Val Lys Gly Phe Arg Ala Val
    130                 135                 140
Leu Gly Asp Gln Phe Tyr Met Val Arg Phe Gln Glu Pro Gly Lys Ala
145                 150                 155                 160
Glu Glu Glu Phe Ala Ser Val Asp Ile Arg Glu Phe Phe Lys Asn Val
                165                 170                 175
Leu Ser Asn Arg Asp Pro Gln Ala Pro Tyr Leu Pro Asn Glu Val Lys
            180                 185                 190
Phe Glu Gly Val Pro Pro Pro Ala Leu Ala Pro Trp Leu Thr Pro Glu
        195                 200                 205
Asp Ile Asp Val Tyr Ala Asp Lys Phe Ala Glu Thr Gly Phe Thr Gly
    210                 215                 220
Gly Leu Asn Tyr Tyr Arg Ala Phe Asp Arg Thr Trp Glu Leu Thr Ala
225                 230                 235                 240
Pro Trp Thr Gly Ala Arg Ile Gly Val Pro Val Lys Phe Ile Val Gly
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                245                 250                 255
Asp Leu Asp Leu Thr Tyr His Phe Pro Gly Ala Gln Lys Tyr Ile His
            260                 265                 270
Gly Glu Gly Phe Lys Lys Ala Val Pro Gly Leu Glu Glu Val Val Val
        275                 280                 285
Met Glu Asp Thr Ser His Phe Ile Asn Gln Glu Arg Pro His Glu Ile
    290                 295                 300
Asn Ser His Ile His Asp Phe Phe Ser Lys Phe Cys
305                 310                 315
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<210> 127
<211> 1425
<212> DNA
<213> Artificial Sequence

<220>
<223> Gene encoding UGT UCT85E5

<400> 127
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ttatcactgg cggagctgct ttccgacgcc ggcatagacg tcgtcttcct cagcaccgag 120
tataaccacc gtcggatctc caacactgaa gccctagcct cccgcttccc gacgcttcat 180
ttcgaaacta taccggatgg cctgccgcct aatgagtcgc gcgctcttgc cgacggccca 240
ctgtatttct ccatgcgtga gggaactaaa ccgagattcc ggcaactgat tcaatctctt 300
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<213> Artificial Sequence

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<223> UGT protein

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Asp Val Val Phe Leu Ser Thr Glu Tyr Asn His Arg Arg Ile Ser Asn
        35                  40                  45
Thr Glu Ala Leu Ala Ser Arg Phe Pro Thr Leu His Phe Glu Thr Ile
    50                  55                  60
Pro Asp Gly Leu Pro Pro Asn Glu Ser Arg Ala Leu Ala Asp Gly Pro
65                  70                  75                  80
Leu Tyr Phe Ser Met Arg Glu Gly Thr Lys Pro Arg Phe Arg Gln Leu
                85                  90                  95
Ile Gln Ser Leu Asn Asp Gly Arg Trp Pro Ile Thr Cys Ile Ile Thr
            100                 105                 110
Asp Ile Met Leu Ser Ser Pro Ile Glu Val Ala Glu Glu Phe Gly Ile
        115                 120                 125
Pro Val Ile Ala Phe Cys Pro Cys Ser Ala Arg Tyr Leu Ser Ile His
    130                 135                 140
Phe Phe Ile Pro Lys Leu Val Glu Glu Gly Gln Ile Pro Tyr Ala Asp
145                 150                 155                 160
Asp Asp Pro Ile Gly Glu Ile Gln Gly Val Pro Leu Phe Glu Gly Leu
                165                 170                 175
Leu Arg Arg Asn His Leu Pro Gly Ser Trp Ser Asp Lys Ser Ala Asp
            180                 185                 190
Ile Ser Phe Ser His Gly Leu Ile Asn Gln Thr Leu Ala Ala Gly Arg
        195                 200                 205
Ala Ser Ala Leu Ile Leu Asn Thr Phe Asp Glu Leu Glu Ala Pro Phe
    210                 215                 220
Leu Thr His Leu Ser Ser Ile Phe Asn Lys Ile Tyr Thr Ile Gly Pro
225                 230                 235                 240
Leu His Ala Leu Ser Lys Ser Arg Leu Gly Asp Ser Ser Ser Ser Ala
                245                 250                 255
Ser Ala Leu Ser Gly Phe Trp Lys Glu Asp Arg Ala Cys Met Ser Trp
            260                 265                 270
Leu Asp Cys Gln Pro Pro Arg Ser Val Val Phe Val Ser Phe Gly Ser
        275                 280                 285
Thr Met Lys Met Lys Ala Asp Glu Leu Arg Glu Phe Trp Tyr Gly Leu
    290                 295                 300
Val Ser Ser Gly Lys Pro Phe Leu Cys Val Leu Arg Ser Asp Val Val
305                 310                 315                 320
Ser Gly Gly Glu Ala Ala Glu Leu Ile Glu Gln Met Ala Glu Glu Glu
                325                 330                 335
Gly Ala Gly Gly Lys Leu Gly Met Val Val Glu Trp Ala Ala Gln Glu
            340                 345                 350
Lys Val Leu Ser His Pro Ala Val Gly Gly Phe Leu Thr His Cys Gly
        355                 360                 365
Trp Asn Ser Thr Val Glu Ser Ile Ala Ala Gly Val Pro Met Met Cys
    370                 375                 380
Trp Pro Ile Leu Gly Asp Gln Pro Ser Asn Ala Thr Trp Ile Asp Arg
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<210> 129
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<212> PRT
<213> Artificial Sequence

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UGT94-289-3

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

Lys Ile Leu Lys His Trp Ser Thr Gly Gly Phe Val Ser His Cys Gly
340 345 350
Trp Asn Ser Val Met Glu Ser Met Met Phe Gly Val Pro Ile Ile Gly
355 360 365
Val Pro Met His Val Asp Gln Pro Phe Asn Ala Gly Leu Val Glu Glu
370 375 380
Ala Gly Val Gly Val Glu Ala Lys Arg Asp Pro Asp Gly Lys Ile Gln
385 390 395 400
Arg Asp Glu Val Ala Lys Leu Ile Lys Glu Val Val Val Glu Lys Thr
405 410 415
Arg Glu Asp Val Arg Lys Lys Ala Arg Glu Met Ser Glu Ile Leu Arg
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Ser Lys Gly Glu Glu Lys Phe Asp Glu Met Val Ala Glu Ile Ser Leu
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<210> 130
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<212> DNA
<213> Artificial Sequence

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

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Thr Phe Ser Asn Leu Glu Asp Gly Ile Tyr Arg Asn Leu Phe Asp Leu
    210                 215                 220
Ala Asp Phe Asn His Gln Asn Gln Phe Ile Asp Lys Tyr Leu Lys Asp
225                 230                 235                 240
Ala Ile Lys Leu Trp Leu Asp Met Gly Ile Asp Gly Ile Arg Met Asp
                245                 250                 255
Ala Val Lys His Met Pro Phe Gly Trp Gln Lys Ser Phe Met Asp Glu
            260                 265                 270
Val Tyr Asp Tyr Arg Pro Val Phe Thr Phe Gly Glu Trp Phe Leu Ser
        275                 280                 285
Glu Asn Glu Val Asp Ser Asn Asn His Phe Phe Ala Asn Glu Ser Gly
    290                 295                 300
Met Ser Leu Leu Asp Phe Arg Phe Gly Gln Lys Leu Arg Gln Val Leu
305                 310                 315                 320
Arg Asn Asn Ser Asp Asp Trp Tyr Gly Phe Asn Gln Met Ile Gln Asp
                325                 330                 335
Thr Ala Ser Ala Tyr Asp Glu Val Ile Asp Gln Val Thr Phe Ile Asp
            340                 345                 350
Asn His Asp Met Asp Arg Phe Met Ala Asp Glu Gly Asp Pro Arg Lys
        355                 360                 365
Val Asp Ile Ala Leu Ala Val Leu Leu Thr Ser Arg Gly Val Pro Asn
    370                 375                 380
Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asn Gly Asp Pro Asn
385                 390                 395                 400
Asn Arg Lys Met Met Thr Ser Phe Asn Lys Asn Thr Arg Ala Tyr Gln
                405                 410                 415
Val Ile Gln Lys Leu Ser Ser Leu Arg Arg Ser Asn Pro Ala Leu Ser
            420                 425                 430
Tyr Gly Asp Thr Glu Gln Arg Trp Ile Asn Ser Asp Val Tyr Ile Tyr
        435                 440                 445
Glu Arg Gln Phe Gly Lys Asp Val Val Leu Val Ala Val Asn Arg Ser
    450                 455                 460
Leu Ser Lys Ser Tyr Ser Ile Thr Gly Leu Phe Thr Ala Leu Pro Ser
465                 470                 475                 480
Gly Thr Tyr Thr Asp Gln Leu Gly Ala Leu Leu Asp Gly Asn Thr Ile
                485                 490                 495
Gln Val Gly Ser Asn Gly Ala Val Asn Ala Phe Asn Leu Gly Pro Gly
            500                 505                 510
Glu Val Gly Val Trp Thr Tyr Ser Ala Ala Glu Ser Val Pro Ile Ile
        515                 520                 525
Gly His Ile Gly Pro Met Met Gly Gln Val Gly His Lys Leu Thr Ile
    530                 535                 540
Asp Gly Glu Gly Phe Gly Thr Asn Val Gly Thr Val Lys Phe Gly Asn
545                 550                 555                 560
Thr Val Ala Ser Val Val Ser Trp Ser Asn Asn Gln Ile Thr Val Thr
                565                 570                 575
Val Pro Asn Ile Pro Ala Gly Lys Tyr Asn Ile Thr Val Gln Thr Ser
            580                 585                 590
Gly Gly Gln Val Ser Ala Ala Tyr Asp Asn Phe Glu Val Leu Thr Asn
        595                 600                 605
Asp Gln Val Ser Val Arg Phe Val Val Asn Asn Ala Asn Thr Asn Trp
    610                 615                 620
Gly Glu Asn Ile Tyr Leu Val Gly Asn Val His Glu Leu Gly Asn Trp
625                 630                 635                 640
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Asn Thr Ser Lys Ala Ile Gly Pro Leu Phe Asn Gln Val Ile Tyr Ser
                645                 650                 655
Tyr Pro Thr Trp Tyr Val Asp Val Ser Val Pro Glu Gly Lys Thr Ile
            660                 665                 670
Glu Phe Lys Phe Ile Lys Lys Asp Gly Ser Gly Asn Val Ile Trp Glu
        675                 680                 685
Ser Gly Ser Asn His Val Tyr Thr Thr Pro Thr Ser Thr Thr Gly Thr
    690                 695                 700
Val Asn Val Asn Trp Gln Tyr
705                 710
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 154

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

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

<220>
<223> DexT protein [Leuconostoc citreum]

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            20                  25                  30
Gln Gln Val Leu Glu Pro Ser Val Asn Ser Asn Ile Pro Lys Lys Gln
        35                  40                  45
Thr Asn Gln Gln Leu Ala Val Val Thr Ala Pro Ala Asn Ser Ala Pro
    50                  55                  60
Gln Thr Lys Thr Thr Ala Glu Ile Ser Ala Gly Thr Glu Leu Asp Thr
65                  70                  75                  80
Met Pro Asn Val Lys His Val Asp Gly Lys Val Tyr Phe Tyr Gly Asp
                85                  90                  95
Asp Gly Gln Pro Lys Lys Asn Phe Thr Thr Ile Ile Asp Gly Lys Pro
            100                 105                 110
Tyr Tyr Phe Asp Lys Asp Thr Gly Ala Leu Ser Asn Asn Asp Lys Gln
        115                 120                 125
Tyr Val Ser Glu Leu Phe Ser Ile Gly Asn Lys His Asn Ala Val Tyr
    130                 135                 140
Asn Thr Ser Ser Asp Asn Phe Thr Gln Leu Glu Gly His Leu Thr Ala
145                 150                 155                 160
Ser Ser Trp Tyr Arg Pro Lys Asp Ile Leu Lys Asn Gly Lys Arg Trp
                165                 170                 175
Ala Pro Ser Thr Val Thr Asp Phe Arg Pro Leu Leu Met Ala Trp Trp
            180                 185                 190
Pro Asp Lys Ser Thr Gln Val Thr Tyr Leu Asn Tyr Met Lys Asp Gln
        195                 200                 205
Gly Leu Leu Ser Gly Thr His His Phe Ser Asp Asn Glu Asn Met Arg
    210                 215                 220
Thr Leu Thr Ala Ala Ala Met Gln Ala Gln Val Asn Ile Glu Lys Lys
225                 230                 235                 240
Ile Gly Gln Leu Gly Asn Thr Asp Trp Leu Lys Thr Ala Met Thr Gln
                245                 250                 255
Tyr Ile Asp Ala Gln Pro Asn Trp Asn Ile Asp Ser Glu Ala Lys Gly
            260                 265                 270
Asp Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Thr Asn Ser Asp Met
        275                 280                 285
Ser Pro Lys Ala Asn Ser Asp Tyr Arg Lys Leu Ser Arg Thr Pro Lys
    290                 295                 300
Asn Gln Lys Gly Gln Ile Ala Asp Lys Tyr Lys Gln Gly Gly Phe Glu
305                 310                 315                 320
Leu Leu Leu Ala Asn Asp Val Asp Asn Ser Asn Pro Val Val Gln Ala
                325                 330                 335
Glu Gln Leu Asn Trp Leu His Tyr Met Met Asn Ile Gly Ser Ile Leu
            340                 345                 350
Gln Asn Asp Asp Gln Ala Asn Phe Asp Gly Tyr Arg Val Asp Ala Val
        355                 360                 365
Asp Asn Val Asp Ala Asp Leu Leu Gln Ile Ala Gly Glu Tyr Ala Lys
    370                 375                 380
Ala Ala Tyr Gly Val Asp Lys Asn Asp Ala Arg Ala Asn Gln His Leu
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Ser Ile Leu Glu Asp Trp Gly Asp Glu Asp Pro Asp Tyr Val Lys Ala
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His Gly Asn Gln Gln Ile Thr Met Asp Phe Pro Leu His Leu Ala Ile
            420                 425                 430
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Thr Arg Glu His Ser Leu Val Lys Arg Ile Thr Asp Asp Lys Glu Asn
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Val Ala Gln Pro Asn Tyr Ser Phe Ile Arg Ala His Asp Ser Glu Val
465                 470                 475                 480
Gln Thr Ile Ile Ala Asp Ile Ile Lys Asp Lys Ile Asn Pro Ala Ser
                485                 490                 495
Thr Gly Leu Asp Ser Thr Val Thr Leu Asp Gln Ile Lys Gln Ala Phe
            500                 505                 510
Asp Ile Tyr Asn Ala Asp Glu Leu Lys Ala Asp Lys Val Tyr Thr Pro
        515                 520                 525
Tyr Asn Ile Pro Ala Ser Tyr Ala Leu Leu Leu Thr Asn Lys Asp Thr
    530                 535                 540
Ile Pro Arg Val Tyr Tyr Gly Asp Met Phe Thr Asp Asp Gly Gln Tyr
545                 550                 555                 560
Met Ala Lys Gln Ser Pro Tyr Tyr Gln Ala Ile Asp Ala Leu Leu Lys
                565                 570                 575
Ala Arg Ile Lys Tyr Ala Ala Gly Gly Gln Thr Met Lys Met Asn Tyr
            580                 585                 590
Phe Pro Asp Glu Gln Ser Val Met Thr Ser Val Arg Tyr Gly Lys Gly
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Ala Met Thr Ala Ser Asp Ser Gly Asn Gln Glu Thr Arg Tyr Gln Gly
    610                 615                 620
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625                 630                 635                 640
Asp Glu Val Lys Met Asp Met Gly Ala Ala His Lys Asn Gln Asp Tyr
                645                 650                 655
Arg Pro Val Leu Leu Thr Thr Lys Ser Gly Leu Lys Val Tyr Ser Thr
            660                 665                 670
Asp Ala Asn Ala Pro Val Val Arg Thr Asp Ala Asn Gly Gln Leu Thr
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Phe Lys Ala Asp Met Val Tyr Gly Val Asn Asp Pro Gln Val Ser Gly
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Tyr Ile Ala Ala Trp Val Pro Val Gly Ala Ser Glu Asn Gln Asp Ala
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Arg Thr Lys Ser Glu Thr Thr Gln Ser Thr Asp Gly Ser Val Tyr His
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Ser Asn Ala Ala Leu Asp Ser Gln Val Ile Tyr Glu Gly Phe Ser Asn
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Phe Gln Asp Phe Pro Thr Thr Pro Asp Glu Phe Thr Asn Ile Lys Ile
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Ala Gln Asn Val Asn Leu Phe Lys Asp Trp Gly Ile Thr Ser Phe Glu
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Ile Val Gln Asn Gly Tyr Ala Phe Thr Asp Arg Tyr Asp Ile Gly Tyr
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Arg Ala Leu His Gly Gln Gly Ile Gln Ala Ile Asn Asp Trp Val Pro
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Asp Gln Ile Tyr Asn Leu Pro Asp Glu Gln Leu Val Thr Ala Ile Arg
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Gln Gln Lys Gln Ile Ser Thr Asp Gln Pro Met Asn Pro Asp Ile Gln
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Ser Thr Ser Gly Tyr Gln Ala Lys Ser Ala Phe Ile Cys Asp Asn Gly
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Ile Gly Lys Gln Leu His Asn Thr Tyr Tyr Gln Asp Lys Gln Lys Asn
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Trp Leu Tyr Leu Asn Asn Lys Gly Val Ala Val Thr Gly Glu Gln Ile
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Ile Asn Gly Gln Thr Leu Tyr Phe Gly Asn Asp Gly Arg Gln Phe Lys
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Gly Thr Thr His Ile Asn Ala Thr Gly Glu Ser Arg Tyr Tyr Asp Pro
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Gln Trp Ala Tyr Phe Gly Tyr Asp Gly Val Ala Val Thr Gly Asp Arg
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Ile Ile Lys Gly Gln Lys Leu Tyr Phe Asn Gln Asn Gly Ile Gln Met
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Lys Gly His Leu Arg Leu Glu Asn Gly Ile Met Arg Tyr Tyr Asp Ala
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Val Ile Asn Gly Gln Thr Leu Tyr Phe Asp Ala Asp Gly Arg Gln Val
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Lys Gly Gln Gln Arg Val Ile Gly Asn Gln Arg Tyr Trp Met Asp Lys
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Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
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Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
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Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser
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Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
        355                 360                 365
Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr
    370                 375                 380
Gly Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala
385                 390                 395                 400
Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala
                405                 410                 415
Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu
            420                 425                 430
Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr
        435                 440                 445
Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr
    450                 455                 460
Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly
465                 470                 475                 480
Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr
                485                 490                 495
Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr
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            500                 505                 510
Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser Thr
        515                 520                 525
Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp
    530                 535                 540
Leu Thr Ala Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser
545                 550                 555                 560
Ile Ser Gln Leu Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser
                565                 570                 575
Ala Asp Lys Tyr Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr
            580                 585                 590
Leu Pro Ala Gly Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser
        595                 600                 605
Asp Asp Ser Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val
    610                 615                 620
Pro Gln Ala Cys Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
625                 630                 635                 640
Glu Tyr Thr Val Pro Gln Ala Cys Gly Thr Ser Thr Ala Thr Val Thr
                645                 650                 655
Asp Thr Trp Arg
            660


<210> 164
<211> 614
<212> PRT
<213> Artificial Sequence

<220>
<223> Glucoamylase G1 1008149A

<400> 164
Ala Thr Leu Asp Ser Trp Leu Ser Asn Glu Ala Thr Val Ala Arg Thr
 1               5                  10                  15
Ala Ile Leu Asn Asn Ile Gly Ala Asp Gly Ala Trp Val Ser Gly Ala
            20                  25                  30
Asp Ser Gly Ile Val Val Ala Ser Pro Ser Thr Asp Asn Pro Thr Tyr
        35                  40                  45
Phe Tyr Thr Arg Asp Ser Gly Leu Val Leu Lys Thr Leu Val Asp Leu
    50                  55                  60
Phe Arg Asn Gly Asp Thr Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile
65                  70                  75                  80
Ser Ala Gln Ala Ile Val Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu
                85                  90                  95
Ser Ser Gly Ala Gly Leu Gly Glu Pro Lys Phe Asn Val Asp Glu Thr
            100                 105                 110
Ala Tyr Thr Gly Ser Trp Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu
        115                 120                 125
Arg Ala Thr Ala Met Ile Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly
    130                 135                 140
Tyr Thr Ser Thr Ala Thr Asp Ile Val Trp Pro Leu Val Arg Asn Asp
145                 150                 155                 160
Leu Ser Tyr Val Ala Gln Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp
                165                 170                 175
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Glu Glu Val Asn Gly Ser Ser Phe Phe Thr Ile Ala Val Gln His Arg
            180                 185                 190
Ala Leu Val Glu Gly Ser Ala Phe Ala Thr Ala Val Gly Ser Ser Cys
        195                 200                 205
Ser Trp Cys Asp Ser Gln Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser
    210                 215                 220
Phe Trp Thr Gly Ser Phe Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser
225                 230                 235                 240
Gly Lys Asp Ala Asn Thr Leu Leu Gly Ser Ile His Thr Phe Asp Pro
                245                 250                 255
Glu Ala Ala Cys Asp Asp Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala
            260                 265                 270
Leu Ala Asn His Lys Glu Val Val Asp Ser Phe Arg Ser Ile Tyr Thr
        275                 280                 285
Leu Asn Asp Gly Leu Ser Asp Ser Glu Ala Val Ala Val Gly Arg Tyr
    290                 295                 300
Pro Glu Asp Thr Tyr Tyr Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu
305                 310                 315                 320
Ala Ala Ala Glu Gln Leu Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln
                325                 330                 335
Gly Ser Leu Glu Val Thr Asp Val Ser Leu Asp Phe Phe Lys Ala Leu
            340                 345                 350
Tyr Ser Asp Ala Ala Thr Gly Thr Tyr Ser Ser Ser Ser Ser Thr Tyr
        355                 360                 365
Ser Ser Ile Val Asp Ala Val Lys Thr Phe Ala Asp Gly Phe Val Ser
    370                 375                 380
Ile Val Glu Thr His Ala Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr
385                 390                 395                 400
Asp Lys Ser Asp Gly Glu Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser
                405                 410                 415
Tyr Ala Ala Leu Leu Thr Ala Asn Asn Arg Arg Asn Ser Val Val Pro
            420                 425                 430
Ala Ser Trp Gly Glu Thr Ser Ala Ser Ser Val Pro Gly Thr Cys Ala
        435                 440                 445
Ala Thr Ser Ala Ile Gly Thr Tyr Ser Ser Val Thr Val Thr Ser Trp
    450                 455                 460
Pro Ser Ile Val Ala Thr Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr
465                 470                 475                 480
Gly Ser Gly Ser Val Thr Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser
                485                 490                 495
Lys Thr Ser Thr Ser Thr Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala
            500                 505                 510
Val Ala Val Thr Phe Asp Leu Thr Ala Thr Thr Thr Tyr Gly Glu Asn
        515                 520                 525
Ile Tyr Leu Val Gly Ser Ile Ser Gln Leu Gly Asp Trp Glu Thr Ser
    530                 535                 540
Asp Gly Ile Ala Leu Ser Ala Asp Lys Tyr Thr Ser Ser Asp Pro Leu
545                 550                 555                 560
Trp Tyr Val Thr Val Thr Leu Pro Ala Gly Glu Ser Phe Glu Tyr Lys
                565                 570                 575
Phe Ile Arg Ile Glu Ser Asp Asp Ser Val Glu Trp Glu Ser Asp Pro
            580                 585                 590
Asn Arg Glu Tyr Thr Val Pro Gln Ala Cys Gly Thr Ser Thr Ala Thr
        595                 600                 605
```

Val Thr Asp Thr Trp Arg
610

<210> 165
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase

<220>
<221> VARIANT
<222> 11, 99, 118, 193
<223> Xaa = Any Amino Acid

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

<210> 166
<211> 719
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase AAB23581.1

<220>
<221> VARIANT
<222> 81, 156, 240, 268, 271, 279, 284, 293, 294, 295, 296, 305,
335, 357, 569, 615, 629, 633, 691, 704
<223> Xaa = Any Amino Acid

<400> 166
Ser Gln Asp Tyr Ile Ser Leu Ser His Gly Val Phe Leu Arg Asn Ser
 1               5                  10                  15
His Gly Leu Glu Ile Leu Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr
            20                  25                  30
Leu Gly Gly Gly Ile Asp Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala
        35                  40                  45
Asp Val Thr Arg Gln Tyr Leu Thr Ser Thr Val Gly Leu Pro Ala Met
    50                  55                  60
Gln Gln Tyr Asn Thr Leu Gly Phe His Gln Cys Arg Trp Gly Tyr Asn
65                  70                  75                  80
Xaa Trp Ser Asp Leu Ala Asp Val Val Ala Asn Phe Glu Lys Phe Glu
                85                  90                  95
Ile Pro Leu Glu Tyr Ile Trp Thr Asp Ile Asp Tyr Met His Gly Tyr
            100                 105                 110
Arg Asn Phe Asp Asn Asp Gln His Arg Phe Ser Tyr Ser Glu Gly Asp
        115                 120                 125
Glu Phe Leu Ser Lys Leu His Glu Ser Gly Arg Tyr Tyr Val Pro Ile
    130                 135                 140
Val Asp Ala Ala Leu Tyr Ile Pro Asn Pro Glu Xaa Ala Ser Asp Ala
145                 150                 155                 160
Tyr Ala Thr Tyr Asp Arg Gly Ala Ala Asp Asp Val Phe Leu Lys Asn
                165                 170                 175
Pro Asp Gly Ser Leu Tyr Ile Gly Ala Val Trp Pro Gly Tyr Thr Val
            180                 185                 190
Phe Pro Asp Trp His His Pro Lys Ala Val Asp Phe Trp Ala Asn Glu
        195                 200                 205
Leu Val Ile Trp Ser Lys Lys Val Ala Phe Asp Gly Val Trp Tyr Asp
    210                 215                 220
Met Ser Glu Val Ser Ser Phe Cys Val Gly Ser Cys Gly Thr Gly Xaa
225                 230                 235                 240
Leu Thr Leu Asn Pro Ala His Pro Ser Phe Leu Leu Pro Gly Glu Pro
                245                 250                 255
Gly Asp Ile Ile Tyr Asp Tyr Pro Glu Ala Phe Xaa Ile Thr Xaa Ala
            260                 265                 270
Thr Glu Ala Ala Ser Ala Xaa Ala Gly Ala Ser Xaa Gln Ala Ala Ala
        275                 280                 285
Thr Ala Thr Thr Xaa Xaa Xaa Xaa Val Ser Tyr Leu Arg Thr Thr Pro
    290                 295                 300
Xaa Pro Gly Val Arg Asn Val Glu His Pro Pro Tyr Val Ile Asn His
305                 310                 315                 320
Asp Gln Glu Gly His Asp Leu Ser Val His Ala Val Ser Pro Xaa Ala
                325                 330                 335
Thr His Val Asp Gly Val Glu Glu Tyr Asp Val His Gly Leu Tyr Gly

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            340                 345                 350
His Gln Gly Leu Xaa Ala Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser
        355                 360                 365
His Lys Arg Arg Pro Phe Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser
    370                 375                 380
Gly Lys Trp Ala Gly His Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp
385                 390                 395                 400
Ser Met Tyr Tyr Ser Ile Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly
                405                 410                 415
Ile Pro Met Phe Gly Ala Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp
            420                 425                 430
Glu Glu Leu Cys Asn Arg Trp Met Gln Leu Ser Ala Phe Phe Pro Phe
        435                 440                 445
Tyr Arg Asn His Asn Glu Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg
    450                 455                 460
Trp Ala Ser Val Ile Glu Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr
465                 470                 475                 480
Ala Ile Leu Pro Tyr Phe Tyr Thr Leu Phe Asp Leu Ala His Thr Thr
                485                 490                 495
Gly Ser Thr Val Met Arg Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro
            500                 505                 510
Thr Leu Ala Ala Val Glu Thr Gln Phe Met Val Gly Pro Ala Ile Met
        515                 520                 525
Val Val Pro Val Leu Glu Pro Leu Val Asn Thr Val Lys Gly Val Phe
    530                 535                 540
Pro Gly Val Gly His Gly Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala
545                 550                 555                 560
Ala Val Asp Ala Lys Pro Gly Val Xaa Thr Thr Ile Ser Ala Pro Leu
                565                 570                 575
Gly His Ile Pro Val Tyr Val Arg Gly Gly Asn Ile Leu Pro Met Gln
            580                 585                 590
Glu Pro Ala Leu Thr Thr Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu
        595                 600                 605
Leu Ala Ala Leu Gly Ser Xaa Gly Thr Ala Ser Gly Gln Leu Tyr Leu
    610                 615                 620
Asp Asp Gly Glu Xaa Ile Tyr Pro Xaa Ala Thr Leu His Val Asp Phe
625                 630                 635                 640
Thr Ala Ser Arg Ser Ser Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys
                645                 650                 655
Glu Arg Asn Pro Leu Ala Met Val Thr Val Leu Gly Val Asn Lys Glu
            660                 665                 670
Pro Ser Ala Val Thr Leu Asn Gly Gln Ala Val Phe Pro Gly Ser Val
        675                 680                 685
Thr Tyr Xaa Ser Thr Ser Gln Val Leu Phe Val Gly Gly Leu Gln Xaa
    690                 695                 700
Leu Thr Lys Gly Gly Ala Trp Ala Glu Asn Trp Val Leu Glu Trp
705                 710                 715
```

<210> 167
<211> 640
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAA25219.1

<400> 167
Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
 1               5                  10                  15
Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
            20                  25                  30
Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
        35                  40                  45
Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
    50                  55                  60
Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
65                  70                  75                  80
Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
                85                  90                  95
Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
            100                 105                 110
Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
        115                 120                 125
Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp
    130                 135                 140
Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile
145                 150                 155                 160
Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr
                165                 170                 175
Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln
            180                 185                 190
Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser
        195                 200                 205
Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser
    210                 215                 220
Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln
225                 230                 235                 240
Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe
                245                 250                 255
Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr
            260                 265                 270
Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp
        275                 280                 285
Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu
    290                 295                 300
Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
305                 310                 315                 320
Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
                325                 330                 335
Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
            340                 345                 350
Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
        355                 360                 365
Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr
    370                 375                 380
Gly Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala
385                 390                 395                 400

Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala
405 410 415
Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu
420 425 430
Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr
435 440 445
Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr
450 455 460
Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly
465 470 475 480
Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr
485 490 495
Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr
500 505 510
Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser Thr
515 520 525
Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp
530 535 540
Leu Thr Ala Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser
545 550 555 560
Ile Ser Gln Leu Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser
565 570 575
Ala Asp Lys Tyr Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr
580 585 590
Leu Pro Ala Gly Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser
595 600 605
Asp Asp Ser Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val
610 615 620
Pro Gln Ala Cys Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
625 630 635 640

<210> 168
<211> 985
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase BAA23616.1

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

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            100                 105                 110
Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
        115                 120                 125
Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
    130                 135                 140
Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
145                 150                 155                 160
Phe Asn Phe Lys Val Ile Arg Lys Ala Thr Gly Asp Ala Leu Phe Ser
                165                 170                 175
Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
            180                 185                 190
Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
        195                 200                 205
Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
    210                 215                 220
Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
225                 230                 235                 240
Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
                245                 250                 255
Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
            260                 265                 270
Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
        275                 280                 285
Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
    290                 295                 300
Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
305                 310                 315                 320
Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
                325                 330                 335
Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
            340                 345                 350
Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
        355                 360                 365
Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
    370                 375                 380
Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
385                 390                 395                 400
His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
                405                 410                 415
Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
            420                 425                 430
Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
        435                 440                 445
Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
    450                 455                 460
Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
465                 470                 475                 480
Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
                485                 490                 495
Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
            500                 505                 510
His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
        515                 520                 525
Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
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    530                 535                 540
Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
545                 550                 555                 560
Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
                565                 570                 575
Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
            580                 585                 590
Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
        595                 600                 605
Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
    610                 615                 620
Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
625                 630                 635                 640
Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
                645                 650                 655
Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
            660                 665                 670
Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
        675                 680                 685
Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
    690                 695                 700
Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
705                 710                 715                 720
Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
                725                 730                 735
Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
            740                 745                 750
Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
        755                 760                 765
Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
    770                 775                 780
Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
785                 790                 795                 800
Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
                805                 810                 815
Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
            820                 825                 830
Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
        835                 840                 845
Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
    850                 855                 860
Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865                 870                 875                 880
Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
                885                 890                 895
Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
            900                 905                 910
Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
        915                 920                 925
Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
    930                 935                 940
Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945                 950                 955                 960
Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
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```
                965                 970                 975
Trp Ala Glu Asn Trp Val Leu Glu Trp
            980                 985


<210> 169
<211> 985
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase P56526.1

<400> 169
Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
 1               5                  10                  15
Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
            20                  25                  30
Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
        35                  40                  45
Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
    50                  55                  60
Gly Tyr Lys Ala Ser Lys Val Gln His Asn Ser Arg Gly Phe Thr Ala
65                  70                  75                  80
Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
                85                  90                  95
Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
            100                 105                 110
Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
        115                 120                 125
Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
    130                 135                 140
Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
145                 150                 155                 160
Phe Asn Phe Lys Val Ile Arg Lys Ala Thr Gly Asp Ala Leu Phe Ser
                165                 170                 175
Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
            180                 185                 190
Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
        195                 200                 205
Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
    210                 215                 220
Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
225                 230                 235                 240
Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
                245                 250                 255
Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
            260                 265                 270
Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
        275                 280                 285
Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
    290                 295                 300
Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
305                 310                 315                 320
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Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
                325                 330                 335
Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
            340                 345                 350
Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
        355                 360                 365
Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
    370                 375                 380
Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
385                 390                 395                 400
His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
                405                 410                 415
Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
            420                 425                 430
Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
        435                 440                 445
Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
    450                 455                 460
Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
465                 470                 475                 480
Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
                485                 490                 495
Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
            500                 505                 510
His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
        515                 520                 525
Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
    530                 535                 540
Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
545                 550                 555                 560
Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
                565                 570                 575
Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
            580                 585                 590
Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
        595                 600                 605
Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
    610                 615                 620
Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
625                 630                 635                 640
Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
                645                 650                 655
Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
            660                 665                 670
Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
        675                 680                 685
Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
    690                 695                 700
Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
705                 710                 715                 720
Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
                725                 730                 735
Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
            740                 745                 750
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Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
        755                 760                 765
Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
    770                 775                 780
Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
785                 790                 795                 800
Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
                805                 810                 815
Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
            820                 825                 830
Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
        835                 840                 845
Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
    850                 855                 860
Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865                 870                 875                 880
Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
                885                 890                 895
Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
            900                 905                 910
Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
        915                 920                 925
Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
    930                 935                 940
Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945                 950                 955                 960
Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
                965                 970                 975
Trp Ala Glu Asn Trp Val Leu Glu Trp
            980                 985


<210> 170
<211> 639
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase AAP04499.1

<400> 170
Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
 1               5                  10                  15
Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Trp Asp Ser Trp Leu Ser
            20                  25                  30
Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
        35                  40                  45
Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
    50                  55                  60
Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
65                  70                  75                  80
Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
                85                  90                  95
Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
```

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            100                 105                 110
Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
        115                 120                 125
Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp
    130                 135                 140
Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile
145                 150                 155                 160
Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr
                165                 170                 175
Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln
            180                 185                 190
Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Val Asn Gly Ser Ser
        195                 200                 205
Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser Ala
    210                 215                 220
Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln Ala
225                 230                 235                 240
Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe Ile
                245                 250                 255
Leu Ala Asn Phe Asp Ser Ser Arg Ser Ala Lys Asp Ala Asn Thr Leu
            260                 265                 270
Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp
        275                 280                 285
Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu
    290                 295                 300
Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
305                 310                 315                 320
Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
                325                 330                 335
Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
            340                 345                 350
Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
        355                 360                 365
Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Thr Gly
    370                 375                 380
Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala Val
385                 390                 395                 400
Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala Ala
                405                 410                 415
Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu Gln
            420                 425                 430
Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr Ala
        435                 440                 445
Asn Asn Arg Arg Asn Val Val Pro Ser Ala Ser Trp Gly Glu Thr Ser
    450                 455                 460
Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly Thr
465                 470                 475                 480
Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr Gly
                485                 490                 495
Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr Ser
            500                 505                 510
Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser Thr Ser
        515                 520                 525
Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu
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    530                 535                 540
Thr Ala Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser Ile
545                 550                 555                 560
Ser Gln Leu Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser Ala
                565                 570                 575
Asp Lys Tyr Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr Leu
            580                 585                 590
Pro Ala Gly Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser Asp
        595                 600                 605
Asp Ser Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro
    610                 615                 620
Gln Ala Cys Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
625                 630                 635


<210> 171
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase AAM18050.2

<400> 171
Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp
 1               5                  10                  15
Leu Thr Ala Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser
            20                  25                  30
Ile Ser Gln Leu Gly Asp Trp Asp Thr Ser Asp Gly Ile Ala Leu Ser
        35                  40                  45
Ala Asp Lys Tyr Thr Ser Ser Asn Pro Leu Trp Tyr Val Thr Val Thr
    50                  55                  60
Leu Pro Ala Gly Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser
65                  70                  75                  80
Asp Asp Ser Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val
                85                  90                  95
Pro Gln Val Cys Gly Glu Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
            100                 105                 110


<210> 172
<211> 640
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase AAT67041.1

<400> 172
Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
 1               5                  10                  15
Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
            20                  25                  30
Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
```

```
        35                  40                  45
Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
    50                  55                  60
Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
65                  70                  75                  80
Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
                85                  90                  95
Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
            100                 105                 110
Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
        115                 120                 125
Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp
    130                 135                 140
Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile
145                 150                 155                 160
Gly Phe Arg Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr
                165                 170                 175
Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln
            180                 185                 190
Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser
        195                 200                 205
Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser
    210                 215                 220
Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln
225                 230                 235                 240
Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe
                245                 250                 255
Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr
            260                 265                 270
Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp
        275                 280                 285
Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu
    290                 295                 300
Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
305                 310                 315                 320
Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
                325                 330                 335
Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
            340                 345                 350
Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
        355                 360                 365
Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr
    370                 375                 380
Gly Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala
385                 390                 395                 400
Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala
                405                 410                 415
Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu
            420                 425                 430
Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr
        435                 440                 445
Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr
    450                 455                 460
Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly
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465                 470                 475                 480
Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr
                485                 490                 495
Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr
            500                 505                 510
Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser Thr
        515                 520                 525
Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp
    530                 535                 540
Leu Thr Ala Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser
545                 550                 555                 560
Ile Ser Gln Leu Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser
                565                 570                 575
Ala Asp Lys Tyr Thr Ser Gly Asp Pro Leu Trp Tyr Val Thr Val Thr
            580                 585                 590
Leu Pro Ala Gly Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser
        595                 600                 605
Asp Asp Ser Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val
    610                 615                 620
Pro Gln Ala Cys Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
625                 630                 635                 640
```

<210> 173
<211> 640
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase P69328.1

<400> 173

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

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Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln
            180                 185                 190
Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser
        195                 200                 205
Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser
    210                 215                 220
Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln
225                 230                 235                 240
Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe
                245                 250                 255
Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr
            260                 265                 270
Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp
        275                 280                 285
Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu
    290                 295                 300
Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
305                 310                 315                 320
Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
                325                 330                 335
Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
            340                 345                 350
Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
        355                 360                 365
Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr
    370                 375                 380
Gly Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala
385                 390                 395                 400
Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala
                405                 410                 415
Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu
            420                 425                 430
Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr
        435                 440                 445
Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr
    450                 455                 460
Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly
465                 470                 475                 480
Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr
                485                 490                 495
Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr
            500                 505                 510
Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser Thr
        515                 520                 525
Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp
    530                 535                 540
Leu Thr Ala Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser
545                 550                 555                 560
Ile Ser Gln Leu Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser
                565                 570                 575
Ala Asp Lys Tyr Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr
            580                 585                 590
Leu Pro Ala Gly Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser
        595                 600                 605
```

Asp Asp Ser Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val
    610                 615                 620
Pro Gln Ala Cys Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
625                 630                 635                 640

<210> 174
<211> 985
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase BAF37801.1

<400> 174
Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
 1               5                  10                  15
Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
            20                  25                  30
Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
        35                  40                  45
Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
    50                  55                  60
Gly Tyr Lys Ala Ser Lys Val Gln His Asn Ser Arg Gly Phe Thr Ala
65                  70                  75                  80
Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
                85                  90                  95
Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
            100                 105                 110
Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
        115                 120                 125
Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
    130                 135                 140
Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
145                 150                 155                 160
Phe Asn Phe Lys Val Ile Arg Lys Ala Thr Gly Asp Ala Leu Phe Ser
                165                 170                 175
Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
            180                 185                 190
Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
        195                 200                 205
Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
    210                 215                 220
Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
225                 230                 235                 240
Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
                245                 250                 255
Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
            260                 265                 270
Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
        275                 280                 285
Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
    290                 295                 300
Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr

```
305                 310                 315                 320
Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
                325                 330                 335
Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
            340                 345                 350
Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
        355                 360                 365
Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
    370                 375                 380
Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
385                 390                 395                 400
His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
                405                 410                 415
Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
            420                 425                 430
Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
        435                 440                 445
Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
    450                 455                 460
Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
465                 470                 475                 480
Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
                485                 490                 495
Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
            500                 505                 510
His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
        515                 520                 525
Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
    530                 535                 540
Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
545                 550                 555                 560
Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
                565                 570                 575
Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
            580                 585                 590
Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
        595                 600                 605
Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
    610                 615                 620
Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
625                 630                 635                 640
Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
                645                 650                 655
Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
            660                 665                 670
Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
        675                 680                 685
Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
    690                 695                 700
Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
705                 710                 715                 720
Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
                725                 730                 735
Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
```

```
            740                 745                 750
Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
        755                 760                 765
Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
    770                 775                 780
Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
785                 790                 795                 800
Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
                805                 810                 815
Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
            820                 825                 830
Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
        835                 840                 845
Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
    850                 855                 860
Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865                 870                 875                 880
Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
                885                 890                 895
Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
            900                 905                 910
Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
        915                 920                 925
Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
    930                 935                 940
Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945                 950                 955                 960
Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
                965                 970                 975
Trp Ala Glu Asn Trp Val Leu Glu Trp
            980                 985


<210> 175
<211> 655
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK37022.1

<400> 175
Met Leu Tyr Ala Glu Asp Asn Lys Leu Ile Phe Arg Phe Asp Asp His
 1               5                  10                  15
Leu Leu Trp Ile Gln Pro Trp Gly Glu Asn Ala Leu Arg Val Arg Ala
            20                  25                  30
Thr Lys Leu Ala Ser Met Pro Thr Glu Asp Trp Ala Leu Ser Ser Lys
        35                  40                  45
Val Thr Ser Ile Glu Pro Thr Ile Ser Ile Glu Glu His Lys Asp Ser
    50                  55                  60
Ser Ile Thr Asn Gly Lys Ile Lys Ala Thr Val Ser Gln Arg Gly Lys
65                  70                  75                  80
Ile Thr Ile Tyr Asn Gln Lys Gly Glu Lys Leu Leu Glu Glu Tyr Ala
                85                  90                  95
```

```
Arg Asn Arg Arg Asp Leu Lys Asp Pro Lys Cys Ser Ala Leu Glu Val
            100                 105                 110
Glu Ala Arg Glu Leu Arg Pro Ile Leu Gly Gly Asp Phe His Leu Thr
        115                 120                 125
Met Arg Phe Glu Ser Leu Asp Pro Lys Glu Lys Ile Tyr Gly Met Gly
    130                 135                 140
Gln Tyr Gln Gln Pro Phe Leu Asn Leu Lys Gly Val Asp Ile Glu Leu
145                 150                 155                 160
Ala His Arg Asn Ser Gln Ala Ser Val Pro Phe Ala Leu Ser Ser Leu
                165                 170                 175
Gly Tyr Gly Phe Leu Trp Asn Asn Pro Ala Ile Gly Arg Ala Val Leu
            180                 185                 190
Gly Thr Asn Thr Met Ser Phe Glu Ala Tyr Ser Thr Lys Val Leu Asp
        195                 200                 205
Tyr Trp Val Val Ala Gly Asp Ser Pro Ala Glu Ile Glu Glu Ala Tyr
    210                 215                 220
Ser Lys Val Thr Gly Tyr Val Pro Met Met Pro Glu Tyr Gly Leu Gly
225                 230                 235                 240
Phe Trp Gln Cys Lys Leu Arg Tyr Trp Asn Gln Glu Gln Leu Leu Asp
                245                 250                 255
Val Ala Arg Glu Tyr Lys Arg Arg Asn Ile Pro Leu Asp Leu Ile Val
            260                 265                 270
Val Asp Phe Phe His Trp Lys His Gln Gly Glu Trp Ser Phe Asp Pro
        275                 280                 285
Glu Phe Trp Pro Asp Pro Asp Ala Met Ile Lys Glu Leu Gln Ser Leu
    290                 295                 300
Asn Val Glu Leu Met Val Ser Val Trp Pro Thr Val Glu Asn Ala Ser
305                 310                 315                 320
Thr Asn Tyr Pro Glu Met Leu Glu Lys Gly Leu Leu Ile Arg His Asp
                325                 330                 335
Arg Gly Leu Arg Val Ser Met Gln Cys Asn Gly Asp Ile Thr His Phe
            340                 345                 350
Asp Ala Thr Asn Pro Ser Ala Arg Ala Tyr Val Trp Ser Lys Ala Lys
        355                 360                 365
Gln Asn Tyr Tyr Asp Lys Gly Ile Lys Val Phe Trp Leu Asp Glu Ala
    370                 375                 380
Glu Pro Glu Tyr Ser Val Tyr Asp Phe Asp Leu Tyr Arg Tyr His Ala
385                 390                 395                 400
Gly Ser Asn Leu Gln Ile Gly Asn Ile Phe Pro Lys Glu Tyr Ala Arg
                405                 410                 415
Gly Phe Tyr Glu Gly Met Glu Ser Ala Gly Gln Thr Asn Ile Val Asn
            420                 425                 430
Leu Leu Arg Cys Ala Trp Ala Gly Ser Gln Lys Tyr Gly Ala Leu Val
        435                 440                 445
Trp Ser Gly Asp Ile Ala Ser Ser Trp Ser Ser Phe Arg Asn Gln Leu
    450                 455                 460
Ala Ala Gly Leu Asn Met Gly Leu Ala Gly Ile Pro Trp Trp Thr Thr
465                 470                 475                 480
Asp Ile Gly Gly Phe His Gly Gly Asp Pro Ser Asp Pro Ala Phe Arg
                485                 490                 495
Glu Leu Phe Thr Arg Trp Phe Gln Trp Gly Ala Phe Cys Pro Val Met
            500                 505                 510
Arg Leu His Gly Asp Arg Glu Pro Lys Pro Glu Asn Arg Pro Thr Asp
        515                 520                 525
```

```
Ser Gly Ser Asp Asn Glu Ile Trp Ser Tyr Gly Glu Glu Val Tyr Glu
    530                 535                 540
Ile Cys Lys Lys Tyr Ile Gly Ile Arg Glu Glu Leu Arg Asp Tyr Thr
545                 550                 555                 560
Arg Gly Leu Met Lys Glu Ala His Glu Lys Gly Thr Pro Val Met Arg
                565                 570                 575
Thr Leu Phe Tyr Glu Phe Pro Ala Asp Lys Lys Ala Trp Asp Val Glu
            580                 585                 590
Thr Glu His Leu Phe Gly Ser Lys Tyr Leu Val Val Pro Val Phe Glu
        595                 600                 605
Ala Gly Lys Arg Ser Val Glu Val Tyr Leu Pro Ala Gly Ala Ser Trp
    610                 615                 620
Lys Val Trp Gly Gln Glu Asp Val Ile His Glu Gly Gly Lys Glu Ile
625                 630                 635                 640
Gln Val Asp Cys Pro Ile Glu Thr Met Pro Val Phe Val Arg Val
                645                 650                 655


<210> 176
<211> 1539
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK37087.1

<400> 176
Met Ser Ser Pro Gln Gln Val Tyr Leu Leu Pro Leu Lys Asp Asp Gly
 1               5                  10                  15
Ser Pro Asp Val Pro Gly Gly Tyr Ile Tyr Leu Pro Ala Pro Thr Asn
            20                  25                  30
Pro Pro Tyr Leu Leu Arg Phe Val Ile Glu Gly Ser Ser Ser Ile Cys
        35                  40                  45
Arg Glu Gly Ala Leu Trp Val Asn Ile Pro Glu Lys Gly Glu Ser Phe
    50                  55                  60
Asn Arg Ser Ala Phe Arg Ser Phe Ser Leu Ser Pro Asp Phe Asn Lys
65                  70                  75                  80
Asn Ile Gln Ile Asp Val Pro Ile Thr Ser Ala Gly Ser Phe Ala Phe
                85                  90                  95
Tyr Val Thr Phe Ser Pro Leu Pro Glu Phe Ser Val Leu Ser Thr Pro
            100                 105                 110
Thr Pro Glu Pro Thr Arg Thr Pro Thr His Tyr Ile Asp Val Ser Pro
        115                 120                 125
Lys Leu Thr Leu Arg Gly Gln Asp Leu Pro Leu Asn Ala Leu Ser Ile
    130                 135                 140
Tyr Ser Val Ile Ser Lys Phe Met Gly Gln Tyr Pro Lys Glu Trp Glu
145                 150                 155                 160
Lys His Leu Asn Gly Ile Ser Gln Arg Asn Tyr Asn Met Val His Phe
                165                 170                 175
Thr Pro Leu Met Lys Arg Gly Ala Ser Asn Ser Pro Tyr Ser Ile Phe
            180                 185                 190
Asp Gln Leu Gln Phe Asp Asp Ala Val Phe Pro Asn Gly Glu Asp Asp
        195                 200                 205
Val Ala Arg Leu Ile Ser Lys Met Glu Asn Glu Tyr Gly Leu Leu Ser
```

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    210                 215                 220
Leu Thr Asp Val Val Trp Asn His Thr Ala His Asn Ser Lys Trp Leu
225                 230                 235                 240
Glu Glu His Pro Glu Ala Gly Tyr Ser Val Glu Thr Ala Pro Trp Leu
                245                 250                 255
Glu Ala Ala Leu Glu Leu Asp Thr Ala Leu Leu Lys Phe Gly Gln Asp
            260                 265                 270
Leu Gln Asn Leu Gly Leu Pro Thr Glu Phe Gln Thr Val Asp Glu Leu
        275                 280                 285
Met Lys Val Met Asn Val Met Arg Asp Lys Val Ile Ala Gly Ile Arg
    290                 295                 300
Leu Trp Glu Phe Tyr Ala Ile Asp Val Lys Ser Asp Thr His Lys Ile
305                 310                 315                 320
Leu Asp Lys Trp Lys Thr Ser Lys Asp Ile Asp Leu Thr Asp Thr Asn
                325                 330                 335
Trp Ala Gln Leu Asn Leu Gln Asp Tyr Lys Asn Trp Thr Leu Lys Gln
            340                 345                 350
Gln Ala Thr Phe Ile Arg Asp His Ala Ile Pro Thr Ser Lys Gln Val
        355                 360                 365
Leu Gly Arg Phe Ser Arg Ala Val Asp Leu Gln Phe Gly Ala Ala Ile
    370                 375                 380
Leu Thr Ala Leu Phe Gly Pro His Asn Pro Ser Thr Ser Asp Thr Ser
385                 390                 395                 400
Ile Val Glu Glu Ser Leu Ser Lys Ile Leu Asp Glu Val Asn Leu Pro
                405                 410                 415
Phe Tyr Glu Glu Tyr Asp Gly Asp Val Ser Glu Ile Met Asn Gln Val
            420                 425                 430
Phe Asn Arg Ile Lys Tyr Leu Arg Ile Asp Asp His Gly Pro Lys Leu
        435                 440                 445
Gly Ala Val Thr Ala Gln Ser Pro Leu Ile Glu Thr Tyr Phe Thr Arg
    450                 455                 460
Leu Pro Leu Asn Asp Val Thr Lys Lys His Lys Lys Glu Ala Leu Ala
465                 470                 475                 480
Leu Val Asn Asn Gly Trp Ile Trp Asn Ala Asp Ala Leu Arg Asp Asn
                485                 490                 495
Ala Gly Pro Asp Ser Arg Ala Tyr Leu Arg Arg Glu Val Ile Val Trp
            500                 505                 510
Gly Asp Cys Val Lys Leu Arg Tyr Gly Ser Cys Arg Asp Asp Asn Pro
        515                 520                 525
Phe Leu Trp Asp Phe Met Thr Asp Tyr Thr Arg Leu Met Ala Lys Tyr
    530                 535                 540
Phe Ser Gly Phe Arg Ile Asp Asn Cys His Ser Thr Pro Leu Val Val
545                 550                 555                 560
Ala Glu Tyr Leu Leu Asp Glu Ala Arg Lys Val Arg Pro Asn Leu Thr
                565                 570                 575
Val Phe Ala Glu Leu Phe Thr Gly Ser Glu Glu Ala Asp Tyr Ile Phe
            580                 585                 590
Val Lys Arg Leu Gly Ile Asn Ala Leu Ile Arg Glu Ala Met Gln Ala
        595                 600                 605
Trp Ser Thr Gly Glu Leu Ser Arg Leu Val His Arg His Gly Gly Arg
    610                 615                 620
Pro Ile Gly Ser Phe Asp Leu Asp Leu Pro Ser Ser Gly Ser Ser His
625                 630                 635                 640
Ala Ile Ala Ser Ser Gly Leu Asp Ser Gly Lys Glu Lys Val Val His
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                645                 650                 655
Ile Arg Pro Thr Pro Val Gln Ala Leu Phe Met Asp Cys Thr His Asp
            660                 665                 670
Asn Glu Met Pro Ala Gln Lys Arg Thr Ala Lys Asp Thr Leu Pro Asn
        675                 680                 685
Gly Ala Leu Val Ala Met Cys Ala Ser Ala Ile Gly Ser Val Ile Gly
    690                 695                 700
Tyr Asp Glu Val Tyr Pro Arg Leu Val Asp Leu Val His Glu His Arg
705                 710                 715                 720
Leu Tyr Phe Ser Glu Phe Ser Glu Ala Pro Glu Thr Gly Leu Asn Ser
                725                 730                 735
Leu Glu Gly Gly Ile Gly Gly Ile Lys Lys Leu Leu Asn Glu Leu His
            740                 745                 750
Thr Lys Met Gly Ile Glu Gly Tyr Asp Glu Thr His Ile His His Asp
        755                 760                 765
Gly Glu Tyr Ile Thr Val His Arg Val His Pro Arg Thr Arg Lys Gly
    770                 775                 780
Val Phe Leu Ile Ala His Thr Ala Phe Pro Gly Gln Asp Ser Arg Ser
785                 790                 795                 800
Val Leu Ala Pro Thr His Leu Val Gly Thr Gln Val Lys His Ile Gly
                805                 810                 815
Thr Trp Leu Leu Glu Val Asp Thr Ser Gln Thr Thr Lys Glu Arg Ile
            820                 825                 830
Gln Ala Asp Lys Ser Tyr Leu Arg Gly Leu Pro Ser Gln Val Lys Thr
        835                 840                 845
Phe Glu Gly Thr Lys Ile Glu Glu Ser Gly Lys Asp Thr Ile Ile Ser
    850                 855                 860
Val Leu Asn Ser Phe Val Ala Gly Ser Ile Ala Leu Phe Glu Thr Ser
865                 870                 875                 880
Met Pro Ser Val Glu His Ala Ser Gly Leu Asp Asn Tyr Ile Thr Glu
                885                 890                 895
Gly Val Asp His Ala Phe Ser Asp Leu Ser Leu Val Asp Leu Asn Phe
            900                 905                 910
Ala Leu Tyr Arg Cys Glu Ala Glu Glu Arg Asp Ser Ser Lys Gly Gln
        915                 920                 925
Asp Gly Ala Tyr Asp Ile Pro Gly His Gly Pro Leu Val Tyr Ala Gly
    930                 935                 940
Leu Gln Gly Trp Trp Ser Val Leu Glu Asn Ile Ile Lys Tyr Asn Glu
945                 950                 955                 960
Leu Gly His Pro Leu Cys Asp His Leu Arg Asn Gly Gln Trp Ala Leu
                965                 970                 975
Asp Tyr Ile Val Ala Arg Leu Glu Lys Leu Ser His Lys Glu Glu His
            980                 985                 990
Pro Ala Leu Gly Arg Pro Ala Ala Trp Leu Gln Glu Lys Phe Gln Ala
        995                 1000                1005
Val Arg Gln Leu Pro Ser Phe Leu Leu Pro Arg Tyr Phe Ala Ile Ile
    1010                1015                1020
Val Gln Val Ala Tyr Asn Ala Ala Trp Lys Arg Gly Ile Gln Leu Leu
1025                1030                1035                1040
Gly Pro His Ile Gln Lys Gly Gln Glu Phe Ile His Gln Leu Gly Met
                1045                1050                1055
Val Ser Val Gln Gln Thr Gly Tyr Val Asn Ser Ala Ser Leu Trp Pro
            1060                1065                1070
Thr Lys Lys Val Pro Ser Leu Ala Ala Gly Leu Pro His Phe Ala Val
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        1075                1080                1085
Asp Trp Ala Arg Cys Trp Gly Arg Asp Val Phe Ile Ser Leu Arg Gly
    1090                1095                1100
Leu Leu Leu Cys Thr Gly Arg Phe Glu Asp Ala Lys Glu His Ile Thr
1105                1110                1115                1120
Ala Phe Ala Ser Val Leu Lys His Gly Met Ile Pro Asn Leu Leu Ser
                1125                1130                1135
Ser Gly Lys Leu Pro Arg Tyr Asn Ser Arg Asp Ser Val Trp Phe Phe
            1140                1145                1150
Leu Gln Ser Ile Gln Asp Tyr Thr Glu Met Ala Pro Asp Gly Leu Glu
        1155                1160                1165
Ile Leu Asp His Lys Val Pro Arg Arg Phe Leu Pro Tyr Asp Asp Val
    1170                1175                1180
Trp Phe Pro Phe Asp Asp Pro Arg Ala Tyr Ser Gln Gln Ser Thr Ile
1185                1190                1195                1200
Ser Glu Ile Ile Gln Glu Val Phe Gln Arg His Ala Gln Gly Leu Ser
                1205                1210                1215
Phe Arg Glu Tyr Asn Ala Gly Pro Asp Leu Asp Met Gln Met Thr Gln
            1220                1225                1230
Asp Gly Phe Gln Ile Asp Val Lys Val Asp Trp Glu Thr Gly Leu Ile
        1235                1240                1245
Phe Gly Gly Ser Gln Tyr Asn Cys Gly Thr Trp Gln Asp Lys Met Gly
    1250                1255                1260
Glu Ser Ala Lys Ala Gly Asn Lys Gly Val Pro Gly Thr Pro Arg Asp
1265                1270                1275                1280
Gly Ala Ala Ile Glu Ile Thr Gly Leu Val Tyr Ser Ala Leu Thr Trp
                1285                1290                1295
Val Ala Lys Leu His Glu Arg Gly Ile Tyr Lys His Asp Gly Val Asp
            1300                1305                1310
Ile Gly Gly Gly Lys Ser Ile Ser Phe Glu Asp Trp Ala Ser Arg Ile
        1315                1320                1325
Arg Ala Asn Phe Glu Arg Cys Tyr Tyr Val Pro Leu Gln Pro Lys Asp
    1330                1335                1340
Asp Gly Gln Tyr Asp Ile Asp Ala Asn Ile Ile Asn Arg Arg Gly Ile
1345                1350                1355                1360
Tyr Lys Asp Leu Tyr Arg Ser Gly Lys Pro Tyr Glu Asp Tyr Gln Leu
                1365                1370                1375
Arg Ser Asn Phe Pro Ile Ala Met Thr Val Ala Pro Asp Leu Phe Thr
            1380                1385                1390
Ala Ser Lys Ala Leu Ala Ala Leu Ala Leu Ala Asp Glu Val Leu Val
        1395                1400                1405
Gly Pro Val Gly Met Ala Thr Leu Asp Pro Ser Asp Leu Asn Tyr Arg
    1410                1415                1420
Pro Asn Tyr Asn Asn Ser Glu Asp Ser Thr Asp Phe Ala Thr Ala Lys
1425                1430                1435                1440
Gly Arg Asn Tyr His Gln Gly Pro Glu Trp Val Trp Gln Arg Gly Tyr
                1445                1450                1455
Phe Leu Arg Ala Phe Leu His Phe Asp Leu Ala Arg Arg Thr Thr Pro
            1460                1465                1470
Ala Glu Arg Thr Glu Thr Tyr Gln Gln Ile Thr Arg Arg Leu Glu Gly
        1475                1480                1485
Cys Lys Arg Ala Leu Arg Glu Ser Pro Trp Lys Gly Leu Thr Glu Leu
    1490                1495                1500
Thr Asn Lys Asn Gly Ala Tyr Cys Ala Asp Ser Ser Pro Thr Gln Ala
```

1505 1510 1515 1520
Trp Ser Ala Gly Cys Leu Leu Asp Leu Tyr Tyr Asp Ala Ser Arg His
1525 1530 1535
Ser Gln Ser

<210> 177
<211> 656
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK43781.1

<400> 177
Met Trp Ser Ser Trp Leu Leu Ser Ala Leu Leu Ala Thr Glu Ala Leu
1 5 10 15
Ala Val Pro Tyr Glu Glu Tyr Ile Leu Ala Pro Ser Ser Arg Asp Leu
20 25 30
Ala Pro Ala Ser Val Arg Gln Val Asn Gly Ser Val Thr Asn Ala Ala
35 40 45
Ala Leu Thr Gly Ala Gly Gly Gln Ala Thr Phe Asn Gly Val Ser Ser
50 55 60
Val Thr Tyr Asp Phe Gly Ile Asn Val Ala Gly Ile Val Ser Val Asp
65 70 75 80
Val Ala Ser Ala Ser Ser Asp Ser Ala Phe Ile Gly Val Thr Phe Thr
85 90 95
Glu Ser Ser Met Trp Ile Ser Ser Glu Ala Cys Asp Ala Thr Gln Asp
100 105 110
Ala Gly Leu Asp Thr Pro Leu Trp Phe Ala Val Gly Gln Gly Ala Gly
115 120 125
Leu Tyr Thr Val Glu Lys Lys Tyr Asn Arg Gly Ala Phe Arg Tyr Met
130 135 140
Thr Val Val Ser Asn Thr Thr Ala Thr Val Ser Leu Asn Ser Val Lys
145 150 155 160
Ile Asn Tyr Thr Ala Ser Pro Thr Gln Asp Leu Arg Ala Tyr Thr Gly
165 170 175
Tyr Phe His Ser Asn Asp Glu Leu Leu Asn Arg Ile Trp Tyr Ala Gly
180 185 190
Ala Tyr Thr Leu Gln Leu Cys Ser Ile Asp Pro Thr Thr Gly Asp Ala
195 200 205
Leu Val Gly Leu Gly Val Ile Thr Ser Ser Glu Thr Ile Ser Leu Pro
210 215 220
Gln Thr Asp Lys Trp Trp Thr Asn Tyr Thr Ile Thr Asn Gly Ser Ser
225 230 235 240
Thr Leu Thr Asp Gly Ala Lys Arg Asp Arg Leu Val Trp Pro Gly Asp
245 250 255
Met Ser Ile Ala Leu Glu Ser Val Ala Val Ser Thr Glu Asp Leu Tyr
260 265 270
Ser Val Arg Thr Ala Leu Glu Ser Leu Tyr Ala Leu Gln Lys Pro Asp
275 280 285
Gly Arg Leu Pro Tyr Ala Gly Lys Pro Phe Phe Asp Thr Val Ser Phe
290 295 300

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Thr Tyr His Leu His Ser Leu Val Gly Ala Ala Ser Tyr Tyr Gln Tyr
305                 310                 315                 320
Thr Gly Asp Arg Ala Trp Leu Thr Arg Tyr Trp Gly Gln Tyr Lys Lys
                325                 330                 335
Gly Val Gln Trp Ala Leu Ser Ser Val Asp Ser Thr Gly Leu Ala Asn
            340                 345                 350
Ile Thr Ala Ser Ala Asp Trp Leu Arg Phe Gly Met Gly Ala His Asn
        355                 360                 365
Ile Glu Ala Asn Ala Ile Leu Tyr Tyr Val Leu Asn Asp Ala Ile Ser
    370                 375                 380
Leu Ala Gln Thr Leu Asn Asp Asn Ala Pro Ile Arg Asn Trp Thr Thr
385                 390                 395                 400
Thr Ala Ala Arg Ile Lys Thr Val Ala Asn Glu Leu Leu Trp Asp Asp
                405                 410                 415
Lys Asn Gly Leu Tyr Thr Asp Asn Glu Thr Thr Thr Leu His Pro Gln
            420                 425                 430
Asp Gly Asn Ser Trp Ala Val Lys Ala Asn Leu Thr Leu Ser Ala Asn
        435                 440                 445
Gln Ser Ala Ile Val Ser Glu Ser Leu Ala Ala Arg Trp Gly Pro Tyr
    450                 455                 460
Gly Ala Pro Ala Pro Glu Ala Gly Ala Thr Val Ser Pro Phe Ile Gly
465                 470                 475                 480
Gly Phe Glu Leu Gln Ala His Tyr Gln Ala Gly Gln Pro Asp Arg Ala
                485                 490                 495
Leu Asp Leu Leu Arg Leu Gln Trp Gly Phe Met Leu Asp Asp Pro Arg
            500                 505                 510
Met Thr Asn Ser Thr Phe Ile Glu Gly Tyr Ser Thr Asp Gly Ser Leu
        515                 520                 525
Ala Tyr Ala Pro Tyr Thr Asn Thr Pro Arg Val Ser His Ala His Gly
    530                 535                 540
Trp Ala Thr Gly Pro Thr Ser Ala Leu Thr Ile Tyr Thr Ala Gly Leu
545                 550                 555                 560
Arg Val Thr Gly Pro Ala Gly Ala Thr Trp Leu Tyr Lys Pro Gln Pro
                565                 570                 575
Gly Asn Leu Thr Gln Val Glu Ala Gly Phe Ser Thr Arg Leu Gly Ser
            580                 585                 590
Phe Ala Ser Ser Phe Ser Arg Ser Gly Gly Arg Tyr Gln Glu Leu Ser
        595                 600                 605
Phe Ser Thr Pro Asn Gly Thr Thr Gly Ser Val Glu Leu Gly Asp Val
    610                 615                 620
Ser Gly Gln Leu Val Ser Asp Arg Gly Val Lys Val Gln Leu Val Gly
625                 630                 635                 640
Gly Lys Ala Ser Gly Leu Gln Gly Gly Lys Trp Lys Leu Ser Asn Asn
                645                 650                 655
```

<210> 178
<211> 1202
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK37133.1

<400> 178
Met Ser Ser Asp Ser Gln Leu Ser Arg Ser His Phe Leu Ala Pro Pro
 1               5                  10                  15
Thr Val Ile Pro Ala Pro Ser Tyr Ile Ala Ser Ser Ala Ala Ala Gln
            20                  25                  30
Ile Ile Thr Ala Asp Gln Glu Phe Asn Ala Ala Asp Phe Val Ala Asp
        35                  40                  45
Asp Glu Gly His Asp Ser Ser Ala Ser Ala Leu Val Thr Pro Glu Ala
    50                  55                  60
Leu Ser Ser Leu Asn Ala Phe Leu Asp Asn Ile Leu Phe Asn Ile Leu
65                  70                  75                  80
Ala Ala Ala Lys Ser Thr Gln Leu Val Lys Ile Arg Pro Ala Val Ala
                85                  90                  95
Glu Val Leu Lys Pro Arg Leu Ala Lys Glu Met Val Ser Ala Ala Asp
            100                 105                 110
Asp Glu Leu Ser Glu Tyr Leu Gly Gly Pro Glu Asp Glu Gln Leu Glu
        115                 120                 125
Phe Arg Ser Gly Gln Thr Ser Ile Gly Glu Phe Asp Leu Val Arg Ser
    130                 135                 140
Trp Lys Leu Thr Arg Leu Arg Cys Met Val Tyr Thr Arg Leu Gly Asp
145                 150                 155                 160
Met Glu Glu Asp Asp Glu Glu Glu Tyr Ile Asn Gln Glu Ile Ile Gly
                165                 170                 175
Glu Asp Gly Gly Gly Leu Arg Arg Leu Ala Ser His Val Gly His Ile
            180                 185                 190
Thr Pro Ala Ala Ser Ile Phe Leu Thr Ser Ile Ile Glu His Met Gly
        195                 200                 205
Glu Gln Ala Leu Ile Ile Ala Gly Glu Ile Ala Arg Ser Arg Leu Ser
    210                 215                 220
Ala Asn Leu Glu Asp Glu Asp Asp Leu Ala Gly Thr Gly Ala Asn Arg
225                 230                 235                 240
Ala Ser Met Asp Arg Leu Val Val Glu Asp His Asp Met Glu Arg Leu
                245                 250                 255
Ala Leu Asn Pro Thr Leu Gly Arg Leu Trp Arg Thr Trp Arg Lys Arg
            260                 265                 270
Val Arg Gly Ser Asn Leu Ser Arg Ala Val Ser Arg Glu Ser Leu Arg
        275                 280                 285
Asn Arg Gln Ser Leu Val Phe Gly Pro Gly Ser Arg Lys Ser Ser Ala
    290                 295                 300
Ile Thr Ile Asp Glu Ile Ser Pro Arg Thr Ala Ser Ser Arg Ser Val
305                 310                 315                 320
Asn Glu Pro Leu Pro Glu Thr Glu Asp Glu Val Asp Pro Ala Ser Val
                325                 330                 335
Pro Leu Pro Met Ser Glu His Asp Ile Gln Glu Ile Glu Ile Pro Cys
            340                 345                 350
Phe Leu Pro Glu Leu Asp Thr Gly Asp Ile Gln Thr Met Gln Ala Val
        355                 360                 365
Val Ala His Lys Val Arg Pro His Ser Leu Met Val Leu Thr Leu Pro
    370                 375                 380
Ser Pro Arg Ser Pro Ser Ser Asn Gly Asn Ser Pro Ile Thr Pro Arg
385                 390                 395                 400
Leu Val Asn Ile Lys Ser Pro Arg His Val Arg Ser Arg Ser Leu Pro
                405                 410                 415
Asn Thr Ala Pro Ala Asp Glu Gln Pro Ser Glu Val Glu Gln Pro Ala

```
            420                 425                 430
Glu Arg Thr Ser Pro Thr Pro Ser Glu Glu Arg Arg Arg Leu Glu Thr
        435                 440                 445
Met Tyr Glu His Asp Glu Asp Asp Glu Arg His Gly Glu Ala Ala Thr
    450                 455                 460
Lys Pro Glu Ala Val Glu Gln Asn Glu Pro Val Val Pro Ser Ala Gly
465                 470                 475                 480
Gln Gly Ala Ala Ala Thr Pro Ser Thr Ser Val Ala Ser Val Glu Val
                485                 490                 495
Ala Met Ser Asp Ala Ser Ser Thr Pro Val Ser Ser Pro Ser Leu Ser
            500                 505                 510
Asp Arg Asp Tyr Pro Glu Thr Asp Glu Val Glu Lys His Glu Arg Val
        515                 520                 525
Glu Lys Ala Gln Leu Ala Pro Gly Val Glu Thr Ala Pro Gly Pro Leu
    530                 535                 540
Ala Pro Arg Thr Gln Gly Val Val Asp Ser Thr Pro Ala Gln Pro Thr
545                 550                 555                 560
Ala Ala Ala Asp Gln Asp Ala Ser Lys Ala Ala Asp Cys Asp Gln Ser
                565                 570                 575
Thr Pro Glu Asp Ser Thr Pro Pro Thr Val Pro Ser Ser Ala Glu Asp
            580                 585                 590
Thr Ala Val Glu Lys Ala Ser Arg Pro Val Ser Thr Ser Gly Glu Ser
        595                 600                 605
Ala Ile Ser Asp Ser Ser Arg Ser Leu Pro Gly Lys Arg Gly Ser Ser
    610                 615                 620
Val Pro Gly Val Gln His Gln Tyr Gly Arg Ser Ser Pro Gly Ile Ala
625                 630                 635                 640
Ser Val Ser Ser Gly Val Glu Arg Ala Ala Val Gln Arg Leu Pro Ala
                645                 650                 655
Arg Pro Ser Thr Ser Val Ala Ser Ser Val Tyr Ser Lys Ser Arg Arg
            660                 665                 670
Ser Gly Ser Phe Ser Ser Ser Arg Glu Lys Arg Pro Val Thr Ala Gly
        675                 680                 685
Ser Thr Thr Ser Gln Val Ser Ser Lys Leu Lys Gly Leu Ile Gly Arg
    690                 695                 700
Pro Ala Asp Thr Gly Ser Leu Arg Leu Arg Thr Ser Ser Glu Val Ser
705                 710                 715                 720
Arg Val Ser Thr Arg Glu Ser Ala Tyr Asp Asp Thr Ser Gly Leu Asp
                725                 730                 735
Glu Leu Ile Arg Ser Glu Glu Thr Ile His Phe Thr Leu Thr Pro Arg
            740                 745                 750
Ser Met Arg Glu Met Glu Leu Pro Asp Ser Pro Arg Trp Arg Ala Gln
        755                 760                 765
Gln Ala Ser Thr Asp Pro Thr Asp Leu Pro Lys Ser Val Glu Pro Ile
    770                 775                 780
Pro Asp Asp Met Ser Arg Ser Arg His Ser Thr Thr Ser Ser Lys Ser
785                 790                 795                 800
Thr Val Asp Leu Pro Pro Val Pro Lys Tyr Ile Gln Ser Lys Pro Lys
                805                 810                 815
Ser Ile Glu Ile Pro Thr Thr Gly Leu Gln Gln Lys Pro Ala Val Gly
            820                 825                 830
Gln Ala Arg Asp Ala Lys His Ser Met Glu Ser Thr Arg Asp Phe Ala
        835                 840                 845
Asn Phe Leu Lys Ser Thr Gly Pro Asn Thr Pro Thr Thr Pro Ala Thr
```

```
    850                 855                 860
Val Asp Gly Ser Pro Ala Lys Ser Ser Arg Leu Arg Arg Leu Ser Asp
865                 870                 875                 880
Ala Thr Glu Ile Ser Lys Lys Leu Ser Arg Pro Ala Ser Ser Thr Val
                885                 890                 895
Ser Val Ala Asn Ser Ala Arg Ser Gly Pro Arg Leu Glu Ala Arg Ser
            900                 905                 910
Ala Val Ala Pro Arg Gly Asp Gln Thr Ser Asp Leu Ile Asp Phe Ile
        915                 920                 925
Arg Glu Gly Pro Pro Thr Ala Gly Ala His Arg Ile Pro Arg Thr Val
    930                 935                 940
Ala Pro Phe Arg Asp Thr Met Asp Ser Asp Glu Leu Gln Ala Ile Glu
945                 950                 955                 960
Pro Gly Arg Thr Ala Lys Gly Ala Pro Ser Val Ala Ser Thr Gln Ser
                965                 970                 975
Val Ala Glu Thr Ser Leu Val Ser Val Gly Ser Arg Thr Gly Leu Leu
            980                 985                 990
Glu Ser Thr Ser Arg Thr Ser Thr Pro Thr Ala Leu Ala Lys Glu Thr
        995                 1000                1005
Lys Thr Thr Phe Ala Ala Pro Val Ser Val Ser Asp Asp His Arg Pro
    1010                1015                1020
Pro Arg Thr Arg Arg Arg Val Pro Asp Pro Tyr Ala Ile Asp Leu Asp
1025                1030                1035                1040
Asp Asp Asp Glu Leu Asp Glu Leu Leu Glu Glu Pro Lys Pro Lys Arg
                1045                1050                1055
Asp Glu Glu Ser Leu Ile Asp Phe Leu Arg Asn Val Pro Pro Pro Glu
            1060                1065                1070
Pro Thr Pro Pro Gln Gln Pro Leu Ala Ala Thr Ala Asn Ser Arg Arg
        1075                1080                1085
Gly Ser Ala Ser Val Lys Ala Arg Leu Arg Arg Asn Thr Ala Ser Glu
    1090                1095                1100
Lys Thr Leu Met Ala Lys Pro Ser Lys Thr Ser Leu His Gln Gln Pro
1105                1110                1115                1120
Asp Asn Tyr Met Gly Gly Ala Ser Asn Tyr Thr Val Lys Val Gly Met
                1125                1130                1135
Glu Arg Asn Ala Gly Ala Met Asn Gly Ala Tyr Asp Leu Lys Thr Pro
            1140                1145                1150
Ser Val Arg Gln Thr Glu Thr Ser Ala Leu Ala Asp Phe Leu Lys Asn
        1155                1160                1165
Thr Gly Pro Pro Glu Pro Pro Val Thr Lys Ala Pro Ala Ala Thr Lys
    1170                1175                1180
Ser Lys Asp Ser Gly Phe Ser Arg Leu Phe Met Arg Arg Lys Lys Val
1185                1190                1195                1200
Glu Ala
```

<210> 179
<211> 759
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK37219.1

<400> 179
```
Met Ala Ala Leu Val Gln Thr Ile Pro Gln Gln Ser Gly Thr Val Ser
 1               5                  10                  15
Val Leu Gln Thr Arg Pro Ser Ser Ser Ser Gly Thr Phe Thr Thr Ser
            20                  25                  30
Ser Gln Pro Gly Gln Gln Gln Asn Pro Arg Asn Ser Thr Met Ser Trp
        35                  40                  45
Asn Pro Tyr Asn Asn Ser Gly Ser Ser Gly Asn Tyr Arg Val Gly His
    50                  55                  60
Gln Val Val Ala Pro Tyr Ala Phe Thr Ser Thr Pro Asn Pro Ser Asn
65                  70                  75                  80
Pro Thr Asn Met Gln Ser Arg Gln Ser Leu Ser Pro His Leu Arg Pro
                85                  90                  95
Glu His Arg Thr Ser Ser Ala Pro Ser Val Pro Gln Gly Ser Ala Ser
            100                 105                 110
Pro Ala Asn Val Gly Val Asn Ser Arg Phe Ala His Pro Ala Ala Gly
        115                 120                 125
Ser Val Ser Thr Ser Ser Ser Asn Ser Ser Val His Ser Tyr Met Ser
    130                 135                 140
Lys Asp Asp Ser Ala Ile Pro Thr Arg Gln Ile Arg Thr Asp Ala Pro
145                 150                 155                 160
Leu Arg Pro Leu Ser Thr Val Asn Leu Pro Ser Pro Ser Ser Ser Asn
                165                 170                 175
Phe Met Asn Ile Ser Ser Pro Thr Val Ala Arg Pro Ser Pro Asp Arg
            180                 185                 190
Tyr Arg Arg Gly Asn Arg Arg Pro Glu Asn Ala Ala Gly Ala Gln Pro
        195                 200                 205
Ala Ser Thr Gln Pro Asn Gly Pro Ala Pro Ala Arg Ser Ala Thr Leu
    210                 215                 220
Ala Thr Asp Asp Ser Ser Leu His Met Ser Thr Pro Gly Leu Ala Gly
225                 230                 235                 240
Val Ser Leu Asp Ala Pro Arg Arg Pro Gly His Val Arg Val Pro Ser
                245                 250                 255
Ala Asp Asp Thr Thr Arg Ala Asp Lys Pro Gln Thr Glu Leu Ala Lys
            260                 265                 270
Arg Tyr Arg Arg Arg Ser Trp Gly Asn Ile Asp Asn Ala Gly Leu Ile
        275                 280                 285
Asn Met Gln Leu His Leu Pro Thr Ser Ser Pro Thr Pro Thr Ala Gly
    290                 295                 300
Gly His Asp Tyr Phe Asp Gln Ser Met Arg Pro Arg Ser Ala Gln Ser
305                 310                 315                 320
His Arg Glu Val Gln Gly Ser Ile Pro Ser Ala His Ser Ser Thr Ser
                325                 330                 335
Ser Val Arg Asp Ala Gly His Ser Glu Ser Ala Ser Ser Ser Lys Ser
            340                 345                 350
Gly Pro Lys Thr Asp Asp Ser Lys Arg Pro Asn Lys Pro Ser Pro Leu
        355                 360                 365
Ser Gln Pro Val Glu Val Asp Ala Lys Pro Pro Thr Pro Lys Ala Pro
    370                 375                 380
Gln Pro Ser Thr Thr Pro Gln Pro Ala Pro Thr Glu Ser Leu Ala Thr
385                 390                 395                 400
Gln Arg Leu Ala Glu Ile Thr Lys Gly Asp Pro Lys Arg Pro Gly Lys
                405                 410                 415
```

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

<210> 180
<211> 590
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK37226.1

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

```
            420                 425                 430
Asp Asp Asp Gln Ser Leu Pro Lys Cys Asn Thr Asn Asp Thr Gln Pro
        435                 440                 445
Thr Thr Cys Thr Thr Val Asn Pro Ser Leu Leu Met Phe Glu Ser Ser
    450                 455                 460
His Lys Thr Tyr Pro Thr Ile Glu Pro Ser Tyr Glu Val Ala Ala Ser
465                 470                 475                 480
Arg Pro Arg Ser Leu Ser Pro Val Gln Asn Leu Glu Asn Glu Leu Gln
                485                 490                 495
Val Gly Ser Ile Gly Gly Lys Asp Ala Glu Asp Ala Gly Ser Leu Ser
            500                 505                 510
Phe Asn Asp Glu Met Lys Glu Gly Ser Glu Met Asp Leu Phe Ser Ala
        515                 520                 525
Ser Leu Asp Gln Tyr Thr Ala Glu Gln Leu Ala Ser Arg Gln Leu Thr
    530                 535                 540
Arg Thr Pro Glu Leu Glu Glu Ser Asn Pro Asn Glu Tyr Gly Leu Gly
545                 550                 555                 560
Phe Gly Phe Gln His Asn Leu Phe Asp Gly Phe Asp Phe Phe Leu Pro
                565                 570                 575
Glu Asp Gln Ser Glu Leu Pro Leu Glu Ser Asn Met Ile Met
            580                 585                 590


<210> 181
<211> 865
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK37273.1

<400> 181
Met Leu Gly Ser Leu Leu Leu Leu Leu Pro Leu Val Gly Ala Ala Val
 1               5                  10                  15
Ile Gly Pro Arg Ala Asn Ser Gln Ser Cys Pro Gly Tyr Lys Ala Ser
            20                  25                  30
Asn Val Gln Lys Gln Ala Arg Ser Leu Thr Ala Asp Leu Thr Leu Ala
        35                  40                  45
Gly Thr Pro Cys Asn Ser Tyr Gly Lys Asp Leu Glu Asp Leu Lys Leu
    50                  55                  60
Leu Val Glu Tyr Gln Thr Asp Glu Arg Leu His Val Met Ile Tyr Asp
65                  70                  75                  80
Ala Asp Glu Glu Val Tyr Gln Val Pro Glu Ser Val Leu Pro Arg Val
                85                  90                  95
Gly Ser Asp Glu Asp Ser Glu Asp Ser Val Leu Glu Phe Asp Tyr Val
            100                 105                 110
Glu Glu Pro Phe Ser Phe Thr Ile Ser Lys Gly Asp Glu Val Leu Phe
        115                 120                 125
Asp Ser Ser Ala Ser Pro Leu Val Phe Gln Ser Gln Tyr Val Asn Leu
    130                 135                 140
Arg Thr Trp Leu Pro Asp Asp Pro Tyr Val Tyr Gly Leu Gly Glu His
145                 150                 155                 160
Ser Asp Pro Met Arg Leu Pro Thr Tyr Asn Tyr Thr Arg Thr Leu Trp
                165                 170                 175
```

```
Asn Arg Asp Ala Tyr Gly Thr Pro Asn Asn Thr Asn Leu Tyr Gly Ser
            180                 185                 190
His Pro Val Tyr Tyr Asp His Arg Gly Lys Ser Gly Thr Tyr Gly Val
        195                 200                 205
Phe Leu Leu Asn Ser Asn Gly Met Asp Ile Lys Ile Asn Gln Thr Thr
    210                 215                 220
Asp Gly Lys Gln Tyr Leu Glu Tyr Asn Leu Leu Gly Gly Val Leu Asp
225                 230                 235                 240
Phe Tyr Phe Phe Tyr Gly Glu Asp Pro Lys Gln Ala Ser Met Glu Tyr
                245                 250                 255
Ser Lys Ile Val Gly Leu Pro Ala Met Gln Ser Tyr Trp Thr Phe Gly
            260                 265                 270
Val Cys Pro Pro Pro Pro Asn Pro Ile Thr Val Arg Val Val Val Tyr
        275                 280                 285
Asn Tyr Ser Gln Ala Lys Ile Pro Leu Glu Thr Met Trp Thr Asp Ile
    290                 295                 300
Asp Tyr Met Asp Lys Arg Arg Val Phe Thr Leu Asp Pro Gln Arg Phe
305                 310                 315                 320
Pro Leu Glu Lys Met Arg Glu Leu Val Thr Tyr Leu His Asn His Asp
                325                 330                 335
Gln His Tyr Ile Val Met Val Asp Pro Ala Val Ser Val Ser Asn Asn
            340                 345                 350
Thr Ala Tyr Ile Thr Gly Val Arg Asp Asp Val Phe Leu His Asn Gln
        355                 360                 365
Asn Gly Ser Leu Tyr Glu Gly Ala Val Trp Pro Gly Val Thr Val Phe
    370                 375                 380
Pro Asp Trp Phe Asn Glu Gly Thr Gln Asp Tyr Trp Thr Ala Gln Phe
385                 390                 395                 400
Gln Gln Phe Phe Asp Pro Lys Ser Gly Val Asp Ile Asp Ala Leu Trp
                405                 410                 415
Ile Asp Met Asn Glu Ala Ser Asn Phe Cys Pro Tyr Pro Cys Leu Asp
            420                 425                 430
Pro Ala Ala Tyr Ala Ile Ser Ala Asp Leu Pro Pro Ala Ala Pro Pro
        435                 440                 445
Val Arg Pro Ser Ser Pro Ile Pro Leu Pro Gly Phe Pro Ala Asp Phe
    450                 455                 460
Gln Pro Ser Ser Lys Arg Ser Val Lys Arg Ala Gln Gly Asp Lys Gly
465                 470                 475                 480
Lys Lys Val Gly Leu Pro Asn Arg Asn Leu Thr Asp Pro Pro Tyr Thr
                485                 490                 495
Ile Arg Asn Ala Ala Gly Val Leu Ser Met Ser Thr Ile Glu Thr Asp
            500                 505                 510
Leu Ile His Ala Gly Glu Gly Tyr Ala Glu Tyr Asp Thr His Asn Leu
        515                 520                 525
Tyr Gly Thr Arg Leu Val Met Ser Ser Ala Ser Arg Thr Ala Met Gln
    530                 535                 540
Ala Arg Arg Pro Asp Val Arg Pro Leu Val Ile Thr Arg Ser Thr Phe
545                 550                 555                 560
Ala Gly Ala Gly Ala His Val Gly His Trp Leu Gly Asp Asn Phe Ser
                565                 570                 575
Asp Trp Val His Tyr Arg Ile Ser Ile Ala Gln Ile Leu Ser Phe Ala
            580                 585                 590
Ser Met Phe Gln Ile Pro Met Val Gly Ala Asp Val Cys Gly Phe Gly
        595                 600                 605
```

```
Ser Asn Thr Thr Glu Glu Leu Cys Ala Arg Trp Ala Ser Leu Gly Ala
    610                 615                 620
Phe Tyr Thr Phe Tyr Arg Asn His Asn Glu Leu Gly Asp Ile Ser Gln
625                 630                 635                 640
Glu Phe Tyr Arg Trp Pro Thr Val Ala Glu Ser Ala Arg Lys Ala Ile
                645                 650                 655
Asp Ile Arg Tyr Lys Leu Leu Asp Tyr Ile Tyr Thr Ala Leu His Arg
            660                 665                 670
Gln Ser Gln Thr Gly Glu Pro Phe Leu Gln Pro Gln Phe Tyr Leu Tyr
        675                 680                 685
Pro Glu Asp Ser Asn Thr Phe Ala Asn Asp Arg Gln Phe Phe Tyr Gly
    690                 695                 700
Asp Ala Leu Leu Val Ser Pro Val Leu Asn Glu Gly Ser Thr Ser Val
705                 710                 715                 720
Asp Ala Tyr Phe Pro Asp Asp Ile Phe Tyr Asp Trp Tyr Thr Gly Ala
                725                 730                 735
Val Val Arg Gly His Gly Glu Asn Ile Thr Leu Ser Asn Ile Asn Ile
            740                 745                 750
Thr His Ile Pro Leu His Ile Arg Gly Gly Asn Ile Ile Pro Val Arg
        755                 760                 765
Thr Ser Ser Gly Met Thr Thr Thr Glu Val Arg Lys Gln Gly Phe Glu
    770                 775                 780
Leu Ile Ile Ala Pro Asp Leu Asp Asp Thr Ala Ser Gly Ser Leu Tyr
785                 790                 795                 800
Leu Asp Asp Gly Asp Ser Leu Asn Pro Ser Ser Val Thr Glu Leu Glu
                805                 810                 815
Phe Thr Tyr Ser Lys Gly Glu Leu His Val Lys Gly Thr Phe Gly Gln
            820                 825                 830
Lys Ala Val Pro Lys Val Glu Lys Cys Thr Leu Leu Gly Lys Ser Ala
        835                 840                 845
Arg Thr Phe Lys Gly Phe Ala Leu Asp Ala Pro Val Asn Phe Lys Leu
    850                 855                 860
Lys
865
```

<210> 182
<211> 614
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK96369.1

<400> 182

```
Met Ser Leu Ser Phe Ser Ser Asp Val Ala Leu Asn Ala Thr Glu Ala
 1               5                  10                  15
Ala Val Phe Leu Ser Glu Arg Asp Val Ala Gly Gln Ile Pro Ile Asn
            20                  25                  30
Phe Val Thr Thr Ser Ala Val Ser Leu Arg Ala Ala Cys Phe Gly Asp
        35                  40                  45
Asn Ile Tyr Asp Arg Asp Ala Ala Gly Arg Cys Ile Ser Asn Leu Leu
    50                  55                  60
Val Val Gly Tyr Arg Arg Phe Leu Val Asp Leu Tyr Trp Ser Ser Asp
```

```
65                  70                  75                  80
Gln Arg Asp Trp Met Phe Cys Pro Leu Ser Leu Ser Pro Asp Val Pro
                85                  90                  95
Val Val Thr Val Ser Ser Ile Ser Pro Ala Ser Ser Thr Thr Thr Thr
            100                 105                 110
Ala Thr Ser Gly Ile Thr Ala Thr Thr Thr Ala Thr Thr Thr Thr Thr
        115                 120                 125
Thr Thr Ser Glu Thr Ile Lys Ala Thr Val Thr Ala Val Ala Arg Ser
    130                 135                 140
Ser Gly Ser Val Leu Tyr Glu Leu Gly Pro Tyr Arg Cys Ser Leu Asp
145                 150                 155                 160
Phe Asp Leu Ser Asp Leu Ile Asn Val Phe Arg Gly Phe Phe Gln Ala
                165                 170                 175
Tyr Ser Ser Glu Leu Thr Val Phe Thr Arg Tyr Ile Ser Leu Asn Leu
            180                 185                 190
His Ala Ala Gly Ser Ala Thr Ser Pro Asp Glu Pro Ala Ser Thr Val
        195                 200                 205
Thr Gly Ser Gln Leu Pro Thr Ser Ser Glu Phe Val Ser Tyr Gln Phe
    210                 215                 220
Asp Glu His Leu Ser Ser Tyr Ile Tyr Thr Pro Ser Ser Leu Ala Ser
225                 230                 235                 240
Glu Arg Ala Asn Leu Asn Gln Ser Trp Tyr Gln Val Glu Asp Gly Tyr
                245                 250                 255
Lys Pro Ile Thr Glu Tyr Phe Thr Ile His Glu Glu Pro Asn Gly Asp
            260                 265                 270
Gln Ser Thr Pro Asp Gly Trp Pro Cys Val Lys Tyr Leu Gln Leu Ala
        275                 280                 285
Gln Glu Lys Arg Leu Leu Ile Asp Tyr Gly Thr Ile Asp Ser Gln Leu
    290                 295                 300
Gln Asp Tyr Asn Phe Ser Tyr Met Ser Asp Val Ile Phe Pro Pro Asn
305                 310                 315                 320
Tyr Leu Thr Ser Thr Val Ser Val Ser Leu Asp Ser Asp Gly Ser Val
                325                 330                 335
Asp Thr Gly Cys Phe Tyr Asp Ser Gly Ala Thr Thr Val Ser Gln Ala
            340                 345                 350
Asn Asn Ser Trp Ala Ile Ser Asp Tyr Ile Pro Ile Pro Glu Gly Leu
        355                 360                 365
Ser Glu Asn Ser Thr Ile Ala Ala Met Ser Leu Val Ala Ser Asn Leu
    370                 375                 380
Thr Ala Cys Gly Leu Thr Pro Ala Leu Asn Asn Thr Leu Phe Asn Gln
385                 390                 395                 400
Thr Ala Asp Thr His Pro Gln Pro Tyr Thr Asp Ile Ser Leu Ser Ser
                405                 410                 415
Ser Trp Ala Trp Ser Ile Gly Gln Pro Ala Asn Ala Asp Ser Ser Ser
            420                 425                 430
Ala Ser Phe Ser Ala Thr Asp Arg Cys Ala Val Ile Asp Leu Thr Asn
        435                 440                 445
Ser Gly His Trp Arg Ala Ile Asn Cys Ser Gln Val Arg Tyr Ala Ala
    450                 455                 460
Cys Arg Val Gly Asn Asn Pro Phe Thr Trp Gln Leu Ser Pro Thr Pro
465                 470                 475                 480
Tyr Thr Phe Arg Asp Ala Tyr Asp His Gly Cys Pro Glu Asn Thr Ser
                485                 490                 495
Met Ala Val Pro Arg Thr Gly Leu Glu Asn Thr Tyr Leu Tyr Gln Tyr
```

```
            500                 505                 510
Leu Leu Thr Arg Thr Asp Val Leu Asp Pro Thr Ser Ala Ile Pro Asn
        515                 520                 525
Lys Thr Lys Val Trp Leu Asn Met Asn Cys Ile Asp Val Glu Ser Cys
    530                 535                 540
Trp Val Thr Gly Gly Pro Asp Gln Glu Cys Pro Tyr Ala Ser Asp Pro
545                 550                 555                 560
Gln Gln Leu Glu Arg Arg Thr Val Leu Val Ala Ala Ile Ala Gly Ile
                565                 570                 575
Val Ile Cys Ile Ile Ala Ala Leu Thr Leu Phe Val Lys Cys Asn Ala
            580                 585                 590
Asn Arg Arg Asn Ser Arg Arg Asn Lys Arg Val Ile Lys Gly Trp Glu
        595                 600                 605
Tyr Glu Gly Val Pro Ser
    610


<210> 183
<211> 460
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK96386.1

<400> 183
Met Ala Asp Ser Lys Pro Lys Pro Ser Ser Ile Pro Pro Trp Gln Gln
 1               5                  10                  15
Ser Asn Asn Ala Ser Asn Thr Asp Asn Ser Ser Glu Ser Thr Ser Ser
            20                  25                  30
Pro Thr Ser Asp Asp Thr Ser Arg Ser Thr Leu Ile Glu Gln Ala Ser
        35                  40                  45
Lys Phe Leu Glu Asp Glu Ser Ile Arg Asp Ala Pro Thr Asp Arg Lys
    50                  55                  60
Val Ser Phe Leu Gln Ser Lys Gly Leu Arg Glu Asp Glu Ile Asn Ser
65                  70                  75                  80
Leu Leu Gly Ile Ser Ala Thr Ser Thr Ala Ser Asp Thr Thr Glu Glu
                85                  90                  95
Glu Lys Ala Ala Ser Pro Asp Thr Thr Thr Pro Ser Ser Thr Glu Pro
            100                 105                 110
Ala Pro Ala Pro Glu Pro Thr Asp Asn Ala Ser Ala Ser Ser Asn Gln
        115                 120                 125
Ser Thr Pro Ser Ser Ser Ile Thr Thr Pro Thr Pro Ser Pro Ser Thr
    130                 135                 140
Thr Thr Pro Lys Thr Asn Asn Thr Arg Asp Val Pro Pro Ile Ile Thr
145                 150                 155                 160
Tyr Pro Glu Phe Leu Ser Thr Pro Thr Lys Pro Pro Pro Leu Val Thr
                165                 170                 175
Leu Arg Ser Val Leu Tyr Thr Leu Tyr Gly Ala Ala Gly Ile Ser Ala
            180                 185                 190
Ser Phe Tyr Gly Ala Ser Glu Tyr Leu Ile Lys Pro Met Leu Ser Asn
        195                 200                 205
Leu Thr Ser Ala Arg Gln Glu Leu Ala Ser Thr Ala Thr Ser Asn Leu
    210                 215                 220
```

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


<210> 184
<211> 537
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK47557.1

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

```
            100                 105                 110
Arg Pro Ala Thr Val Pro Gln Tyr Gln Glu Ala Ala Pro Val Val Asp
        115                 120                 125
Glu Arg Pro Leu His Pro Ser Arg Leu Pro Arg Arg Ala Tyr Asp Gly
    130                 135                 140
Lys Trp Tyr Glu Asn Phe Gly Asp Lys Ala Met Lys Ser Ala Gly Phe
145                 150                 155                 160
Asp Ser Glu Asp Ala Asp Asp Ala Ser Gln Leu Thr Ser Met Ala Gly
                165                 170                 175
Asp Asp Glu Arg Ser Asp Thr Thr Glu Asp Ala Asn Tyr Ala Arg Arg
            180                 185                 190
Tyr Arg Ser Ser Thr Glu Glu Pro Leu Ser Lys Arg Leu Gln Ser Phe
        195                 200                 205
Trp Ser Ala Ser Arg Arg Ser Tyr Lys Asn Pro Glu Pro Gln Ala Tyr
    210                 215                 220
Pro Glu Pro Ser Lys Thr Ala Ala Ser Ala Ala Pro Pro Leu Leu Arg
225                 230                 235                 240
Gln Ser Thr Ser Asp Ala Arg Leu Ser Lys Gln Ala Leu Pro Asn Arg
                245                 250                 255
Lys Val Thr Leu Pro Arg Ser Met Thr Ala Thr Pro Arg Thr Arg Phe
            260                 265                 270
Ser Pro Pro Lys Pro Ser Leu Leu Glu Gln Leu Asp Ile Thr Pro Thr
        275                 280                 285
Arg Arg Thr Ser Gly Pro Arg Pro Gln Pro Gly Lys Glu Pro Gly Ile
    290                 295                 300
Thr Ser Thr Thr Thr His Gln His His Arg His Asn Ser Asp Asp Asn
305                 310                 315                 320
His Leu Phe Asn Thr Ser Arg Asp Ser Leu Pro Pro Leu Ser Thr Phe
                325                 330                 335
Asp Met Thr Asn Ile Asp Asp Leu Asp Val Asp Asp Asp Asn Asp Pro
            340                 345                 350
Ile Asn Asp Pro Phe Ala Arg Arg Asn Ser Val Gln Arg Ile Val Ser
        355                 360                 365
Asp Pro Asp Phe Gln Pro Asn Lys Ser Thr Ile Thr Ser Ser Ser Ser
    370                 375                 380
Gln Asn Lys Arg Arg Asn Leu Glu Ser Asp Tyr Pro Pro Glu Ile Leu
385                 390                 395                 400
Arg Gln Lys Ser Phe Lys Asp Leu Gln Ser Glu Pro Phe Asp His Thr
                405                 410                 415
Pro Thr Ala Thr Ala Ser Ala Pro Val Lys Thr Thr Thr Pro Ala Pro
            420                 425                 430
Thr Pro Gly Pro Asn Ala Thr Ser Asp Glu Lys Met Asp Phe Leu Met
        435                 440                 445
Asn Ser Glu Asp Lys Asp Arg Arg Asp Phe Phe Ser Thr Leu Thr Met
    450                 455                 460
Asn Glu Trp Glu Asp Tyr Gly Asp Leu Leu Ile Asp Gln Phe Ser Asp
465                 470                 475                 480
Ala Leu Ser Lys Met Lys Asp Leu Arg His Ala Arg Arg Lys Thr Ala
                485                 490                 495
Ala Leu Phe Glu Ala Glu Ile Ala Arg Arg Asn Glu Val Val Glu Glu
            500                 505                 510
Gln Ser Ala Asp Leu Thr Arg Lys Leu Glu Glu Met Arg Ser Gly Gly
        515                 520                 525
Ala Glu Val Leu Lys Gly Arg Thr Pro
```

530 535

<210> 185
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK47704.1

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

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


<210> 186
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK44239.1

<400> 186
Met Lys Ile Phe Ile Leu Leu Ala Ile Trp Leu Leu Ala Ser Leu Gly
 1               5                  10                  15
Tyr Ala Thr Ser Phe Val Gly Asn Met Ala Glu Val Tyr His Glu Ile
            20                  25                  30
Thr Asp Val Leu Arg Gly Pro His His Ala Ala His Phe Ala Lys Leu
        35                  40                  45
Asn Gly Gly Lys Pro Lys Pro Asp Lys Pro Lys Gly Val Gly Lys Thr
    50                  55                  60
Leu Asp Asp Val Val Thr Leu Thr Val Cys Lys Thr Asp Val Ser Leu
65                  70                  75                  80
Ala Pro Thr Val Gly Thr Phe Ser Leu Pro Thr Ile Val Thr Ala Ala
                85                  90                  95
Thr Leu Ala Pro Thr Val Val Val Thr Gly Val Val Pro Thr Glu Ile
            100                 105                 110
Ser Ile Gly Leu Pro Thr Glu Phe Ala Pro Glu Ile Gln Thr Gly Val
        115                 120                 125
Leu Thr Gly Glu Ser His Ser Thr Asp Thr Thr Val Val Pro Thr Asn
    130                 135                 140
Ser Val Val Ser Gly Leu Ser Ser Phe Leu Thr Gly Ser Gln Thr Val
145                 150                 155                 160
Ser Glu Ile Thr Gly Ser Thr Glu Asn His Thr Ile Thr Thr Glu Ile
                165                 170                 175
Asn Ala Ser Ala Val Thr Ser Thr Phe Ala His Thr Thr Phe Pro Thr
            180                 185                 190
Ala Asn Ala Gly Asn Asp His Glu Gly Met Ala Ser Ser Ala Val Ala
```

```
        195                 200                 205
Leu Leu Val Ala Leu Ile Phe Ser Leu Val Arg Ile
    210                 215                 220


<210> 187
<211> 1106
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK44326.1

<400> 187
Met Arg Thr Arg Ser Gln Gln Ala Ser Pro Gly Gly Phe Val Ser Leu
 1               5                  10                  15
Asp Glu Asn Ala Pro Arg Arg Thr Arg Ser Ala Lys Asn Ala Ala Gln
            20                  25                  30
Gln Glu Pro Ala Thr Ser Glu Gln Pro Pro Thr Arg Ser Lys Ser Gln
        35                  40                  45
Arg Ala Pro Lys Lys Thr Thr Thr Thr Thr Thr Thr Lys Lys Ser Thr
    50                  55                  60
Ala Lys Ala Gln Thr Arg Lys Ala Thr Thr Thr Lys Arg Thr Thr Arg
65                  70                  75                  80
Gln Ser Thr Arg Lys Thr Asp Gln Pro Val Ser Asn Glu Asp Ala Gln
                85                  90                  95
Thr Thr His Thr Glu Glu Asp Phe Ala Thr Asp Asn Thr Thr Ala Glu
            100                 105                 110
Lys Asn Thr Pro Arg Glu Val Pro Glu Thr Val Asp Pro Thr Pro Ala
        115                 120                 125
Ser Ser Glu Asn Glu Asn Pro Asp Arg Glu Ser Leu Pro His Val Ser
    130                 135                 140
His Pro Phe Met Val Pro Gln Pro Pro Lys Glu Ser Gln Glu Ile Asp
145                 150                 155                 160
Cys Phe Asp Gly Pro Asp Pro Arg Gly Ile Gly Ala Ala Ser Cys Leu
                165                 170                 175
Lys Ser Leu Ile Asp Glu Leu Ser Ser Val Gly Ser Pro Leu Ser Glu
            180                 185                 190
Arg Ser Lys Thr Pro Ser Trp Thr Ser Glu Asp Gly Thr Glu Ala Ala
        195                 200                 205
Leu Ala Pro Arg Pro Ala Gln Glu Ser Gly Ala Thr Asn Val Glu Thr
    210                 215                 220
Ser Thr Thr Thr Glu Arg Val Ser Leu Pro Thr Pro Ala Ala Glu Glu
225                 230                 235                 240
Arg Thr Val Glu Pro Pro Ala Glu Pro Thr Val Ala Glu Pro Arg Gly
                245                 250                 255
Val Ala Ile Val Thr Ser Ser Glu Gln Phe Asn Thr Val Ser Ser Ala
            260                 265                 270
Ser Ala Ala Gly Ser Gly Gly Val Val Val Val Glu Asp Glu Arg Val
        275                 280                 285
Gly Ala Leu Ile Ala Ser Phe Ala Arg Leu Ser Leu Asp Asp Leu Ala
    290                 295                 300
Pro Arg Ser Ser Asn Glu Ala Ala Ala Thr Leu Met Glu Ser Thr Thr
305                 310                 315                 320
```

```
Ala Ser Phe Gly Glu Pro Val Glu Pro Ala His Val Thr Arg Arg Ser
                325                 330                 335
Leu Arg Ala Ser Arg Gln Glu Trp Ile Leu Gly Trp Ala Gln Gln Val
            340                 345                 350
Pro Ser Thr Gly Tyr Phe His Pro Ile Thr Gly Gln Leu Val Glu Gly
        355                 360                 365
Pro Ala Ala Ser Val Glu Leu Val Gly Asp Pro Ala Ser Asn Arg Gly
    370                 375                 380
Pro Pro Thr Arg Arg Ile Gly Val Arg Asp Tyr Ile Leu Arg Arg Arg
385                 390                 395                 400
Arg Arg Glu Val Gln Val Met Ser Pro Leu Gln Glu Glu Pro Gln Ser
                405                 410                 415
Ser Pro Gly Pro Gly Ser Arg Ala Val Ala Leu Asn Ala Val Pro Pro
            420                 425                 430
Arg Gly Ile Arg Ala Gln Arg Ala Gln Asn Thr Lys Arg Leu Thr Lys
        435                 440                 445
Pro Pro Val Thr Arg Lys Arg Ala Arg Thr Glu Ser Ser Asp Glu Glu
    450                 455                 460
Ala Pro Gly Pro Gln Thr Pro Ala Ala Asn Lys Arg Arg Asn Leu Gly
465                 470                 475                 480
Pro Pro Gly Ser Thr Pro Tyr Arg Pro Ala Thr Arg Pro Arg Ser Leu
                485                 490                 495
Thr Ala Asn Ile Thr Pro Tyr Ser Glu Arg Leu Arg Arg Arg Ala Ala
            500                 505                 510
Glu Lys Asp Gly Arg Ile His Ser Thr Ser Leu Arg Val Ser Gln Leu
        515                 520                 525
Leu Ala Gln Gln Glu Ala Asp Arg Arg Arg Gln Ala Ala Glu Ser Ser
    530                 535                 540
Ala Pro Pro Cys Ser Glu Leu Pro Arg Thr Thr Phe Asp Phe Ser Leu
545                 550                 555                 560
Asp Asp Ala His Glu Thr Ser Gln Gly Gln Glu Gln Ser Gln Ser Leu
                565                 570                 575
Gln Glu Gln Ser Ser Thr Pro Gln Pro Pro Ala Thr Pro Glu Arg Gln
            580                 585                 590
Ser Gly Trp Asn Ile Arg Gly Leu Leu Asn Ser Val Pro Arg Thr Phe
        595                 600                 605
Thr Arg Ile Leu Pro Ser Phe Arg Arg Thr Pro Glu Pro Thr Gln Val
    610                 615                 620
Gln Ala Pro Pro Glu Pro Ser Ser Glu Arg Ile Ser Arg Thr Gln Pro
625                 630                 635                 640
Pro Gln Ser Ser Ser Ile Ser Gln Ser Gln Ala Gln Asn Ser Arg Arg
                645                 650                 655
Ser Ser Glu Glu Pro Pro Gln Lys Arg Arg Arg Lys Ser Trp Ser Leu
            660                 665                 670
Phe Ala Gln Pro Phe Asp Arg Ser Leu Tyr Leu Gly Asp Ile Pro Lys
        675                 680                 685
Lys Asp Ser Ala Thr Ser Ser Ser Ala Pro Leu Glu Ser Arg Pro Val
    690                 695                 700
Ala Lys Leu Ser Ala Glu Ala Thr Thr Pro Gln Glu Ser Ala Thr Ser
705                 710                 715                 720
Asp Ala Lys Lys Asp Val Ala Ala Glu Gly Glu Asp Ser Arg Gly Arg
                725                 730                 735
Glu Ile Glu Glu Gln Lys Gln Lys Lys Arg Lys Arg Ser Pro Ser Pro
            740                 745                 750
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Asp Val Ile Pro Asn Pro Pro Gly Cys Ser Tyr Gly Leu Asp Leu Asp
        755                 760                 765
Tyr Phe Cys Tyr Ser Ser Glu Ser Glu Asp Glu Gln Glu Pro Pro Leu
    770                 775                 780
Pro Arg Thr Glu Pro Asn Lys Phe Gly Arg Leu Thr Arg Thr Ala Val
785                 790                 795                 800
Arg Gly Ala Leu Arg Ser Glu Arg His Ser Ser Lys Lys Val Arg Phe
                805                 810                 815
Asp Ala Ser Pro Glu Asp Thr Pro Ser Lys Leu Arg Leu Arg Ala Arg
            820                 825                 830
Ala Thr Asp Pro Tyr Arg Gly Arg His Phe Ile Gly Met Gly Asn Asp
        835                 840                 845
Ser Glu Ile Ala Thr Pro Asp Ser Pro Thr Pro Ala Pro His Ala Ala
    850                 855                 860
Asp Glu Ser Ser Ser Arg Arg Pro Gly Phe Val Pro Asn Val Gln Gly
865                 870                 875                 880
Thr Phe Gln Leu Asp Tyr Asp Ala Phe Ser Asp Asp Ser Asp Ser Ser
                885                 890                 895
Gly Ala Ser Ala Ser Ala Asn Val Ser Ala Ser Ala Pro Ile Pro Ala
            900                 905                 910
Pro Ser Ser Ala Thr Val Thr Gln Ala Ser Ile Ser Glu Ser Val Pro
        915                 920                 925
Ser Thr Glu Ser Arg Gln Thr Pro Arg Gln Ala Ala Pro Ala Pro Ser
    930                 935                 940
Thr Pro Ala Lys Ile Asp Glu Glu Ala Leu Ala Arg Ala Arg Ser Gln
945                 950                 955                 960
Ala Glu Lys Tyr Lys Pro Lys Thr Pro Ser Gly Leu Arg Thr Ala Ser
                965                 970                 975
Arg Tyr Ser Ser Pro Met Thr Ala Thr Pro Asp Thr Val Ser Ala Pro
            980                 985                 990
Val Ile Ala Pro Ala Ile Thr Pro Thr Pro Ser Thr Ser Gln Thr Ala
        995                 1000                1005
Pro Ala Ser Ala Pro Glu Pro Glu Gln Gln Thr Thr Glu Asp Phe Gly
    1010                1015                1020
Asp Asp Glu Phe Ala Arg Glu Ala Gln Trp Leu Tyr Glu Asn Cys Pro
1025                1030                1035                1040
Ser Gly Asp Leu Asn Asp Leu Val Trp Pro Gln Pro Ile Thr Tyr Glu
                1045                1050                1055
Glu Glu Gly Phe Ser Pro Glu Val Ile Asp Leu Val Asn Glu Ile Trp
            1060                1065                1070
Asp Pro Ser Thr Val Asp Tyr Ala Tyr Thr Asn Ile Trp Thr Pro Gly
        1075                1080                1085
Leu Asp Ala Phe Lys Arg Glu Leu Glu Thr Gly Ala Ser Glu Ala Ala
    1090                1095                1100
Gln Ala
1105
```

<210> 188
<211> 587
<212> PRT
<213> Artificial Sequence

<220>

<223> Transgucosidase CAK47737.1

<400> 188
Met Ala Lys Ser Ala Ser Gln Ile His Arg Ala Trp Trp Lys Glu Cys
 1               5                  10                  15
Ser Val Tyr Gln Ile Trp Pro Ala Ser Tyr Lys Asp Ser Asn Asp Asp
            20                  25                  30
Gly Ile Gly Asp Ile Pro Gly Ile Ile Ser Lys Leu Asp Tyr Ile Lys
        35                  40                  45
Asn Ile Gly Val Asp Ile Val Trp Leu Cys Pro Ser Tyr Lys Ser Pro
    50                  55                  60
Gln Val Asp Met Gly Tyr Asp Ile Ala Asp Tyr Tyr Ser Ile Ala Asp
65                  70                  75                  80
Glu Tyr Gly Thr Val Ala Asp Val Glu Lys Leu Ile Gln Gly Cys His
                85                  90                  95
Glu Arg Gly Met Lys Leu Leu Met Asp Leu Val Val Asn His Thr Ser
            100                 105                 110
Asp Gln Asn Glu Trp Phe Lys Gln Ser Arg Ser Ser Lys Asp Asn Lys
        115                 120                 125
Tyr Arg Asn Trp Tyr Val Trp Lys Pro Ala Arg Tyr Asp Glu Gln Gly
    130                 135                 140
Asn Arg His Pro Pro Asn Asn Trp Val Ser His Phe Gln Gly Ser Ala
145                 150                 155                 160
Trp Glu Trp Asp Glu His Thr Gly Glu Tyr Tyr Leu His Leu Tyr Ala
                165                 170                 175
Thr Glu Gln Pro Asp Leu Asn Trp Glu His Pro Pro Val Arg Lys Ala
            180                 185                 190
Val His Asp Ile Met Arg Phe Trp Leu Asp Lys Gly Ala Asp Gly Phe
        195                 200                 205
Arg Met Asp Val Ile Asn Phe Ile Ser Lys Asp Gln Arg Phe Pro Asp
    210                 215                 220
Ala Pro Val Lys Asp Pro Arg Thr Pro Trp Gln Trp Gly Asp Lys Tyr
225                 230                 235                 240
Tyr Ala Asn Gly Pro Arg Leu His Glu Tyr Leu Gln Asp Leu Gly Lys
                245                 250                 255
Ile Leu Lys Glu Tyr Asp Ala Phe Ser Val Gly Glu Met Pro Phe Val
            260                 265                 270
Arg Asp Thr Glu Glu Val Leu Arg Ala Val Arg Tyr Asp Arg Asn Glu
        275                 280                 285
Ile Asn Met Ile Phe Asn Phe Glu His Val Asp Ile Asp His Gly Thr
    290                 295                 300
Tyr Asp Lys Phe Glu Pro Gly Ser Trp Lys Leu Thr Asp Leu Lys Ala
305                 310                 315                 320
Phe Phe Glu Thr Trp Gln Lys Phe Met Tyr Asn Asn Asp Gly Trp Asn
                325                 330                 335
Ala Leu Tyr Trp Glu Asn His Asp Gln Pro Arg Ser Ile Asp Arg Tyr
            340                 345                 350
Ala Gln Ala Lys Glu Glu Phe Arg Thr Glu Ala Gly Lys Met Leu Ala
        355                 360                 365
Thr Val Leu Ala Leu Gln Ser Gly Thr Pro Phe Val Tyr Gln Gly Gln
    370                 375                 380
Glu Ile Gly Met Arg Asn Val Pro Val Glu Trp Asp Met Asn Glu Tyr
385                 390                 395                 400
Lys Asp Ile Asp Cys Leu Asn His Trp His Arg Leu Leu Lys His Arg

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                405                 410                 415
Pro Asp Asp Ile Glu Ala Gln Lys Ser Ala Arg Gln Glu Tyr Gln Lys
            420                 425                 430
Lys Ser Arg Asp Asn Gly Arg Thr Pro Val Gln Trp Ser Ser Ala Pro
        435                 440                 445
Asn Gly Gly Phe Thr Gly Pro Asn Ala Lys Pro Trp Met Ser Val Ser
    450                 455                 460
Pro Asp Tyr Val Arg Phe Asn Ala Glu Ala Gln Val Asn Asp Pro Asn
465                 470                 475                 480
Ser Ile Tyr His Tyr Trp Ala Ala Val Leu Gly Leu Arg Lys Lys Tyr
                485                 490                 495
Leu Asp Ile Phe Val Tyr Gly Asp Tyr Asp Leu Val Asp Lys Asp Ser
            500                 505                 510
Gln Glu Ile Phe Ala Tyr Ala Arg Gln Tyr Glu Asn Lys Lys Ala Leu
        515                 520                 525
Val Leu Thr Asn Trp Thr Glu Lys Thr Leu Glu Trp Asp Ala Thr Thr
    530                 535                 540
Asn Gly Val Lys Gly Val Lys Asp Val Leu Leu Asn Ser Tyr Glu Ser
545                 550                 555                 560
Ala Glu Ala Ala Lys Gly Arg Phe Ser Gly Gln Lys Trp Ser Leu Arg
                565                 570                 575
Pro Tyr Glu Ala Val Val Leu Leu Val Glu Ala
            580                 585


<210> 189
<211> 416
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK47819.1

<400> 189
Met Ala Tyr Tyr Glu Pro Gln Gly Trp Gln Ala Pro Ala Ala Arg Gln
 1               5                  10                  15
Ala Ser Trp Glu Gln Pro Ala Pro Pro Ser Arg Ser Gly Ser Ser Ser
            20                  25                  30
Val Ser Gln Arg Asp Glu Ile Pro Ala Phe Ser Ser Gln Phe Asp Glu
        35                  40                  45
Val Asp Arg Ala Ile Asp Asn Leu Val Lys Ser Gly Lys Leu Trp Ala
    50                  55                  60
Ala Pro Arg Arg Asp Ser Met Pro Met Met Met Gly Arg Pro Tyr Pro
65                  70                  75                  80
Asp Tyr Asp Pro Arg Met Val Asn Ser Met Ser Gln Arg His His Ser
                85                  90                  95
Ile Ser Glu Phe Asp Ser Arg Met His Pro Ser Pro Asn Val Gln Gly
            100                 105                 110
Phe Tyr Ala Ser Gln Arg Phe Gln Gly Arg Pro Asn Glu Val Glu Gln
        115                 120                 125
Met Met Gln Ala Lys Arg Arg Met Ala Ala Gln Arg Glu Arg Glu Leu
    130                 135                 140
Arg Asn Tyr His Gln Glu Gln Gln Tyr Asn Arg Ser Leu Leu Ala Glu
145                 150                 155                 160
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Met Ser Gly Asn Lys Ser Asp Arg Ser Leu Ser Pro Ala Ala Met Ser
                165                 170                 175
Glu Glu Ser Arg Arg Glu Leu Leu Ala Arg Gln His Arg Ala Leu Tyr
            180                 185                 190
Gly Asn Asp Ser Pro Ala Phe Phe Pro Pro Ala Gly Leu Ala Asp Asp
        195                 200                 205
Gly Thr Arg Ser Glu Ser Gln Ala Gly Gly Thr Pro Thr Ser Ser Thr
    210                 215                 220
Gly Val Arg Gly Ala Ser Pro Arg Asn Val Asp Pro Phe Gly Leu Ala
225                 230                 235                 240
Gln Thr Pro Val Gln Ala Gly Ala Asp Ser Leu Gly Gln Thr Ala Ala
                245                 250                 255
Ser Ala Ala Ser Leu Gln Ser Pro Ser Arg Ala Asn Ser Thr Ser Ser
            260                 265                 270
Pro Ser Ser Ala Ile Asn Pro Val Phe Gly Lys Tyr Asp Ser Ala Asp
        275                 280                 285
Gln Pro Val Thr Ser Thr Ser Ser Pro Gly Gly Ala Asp Ser Pro Ser
    290                 295                 300
Ser Arg Gln Ala Pro Ser Lys Ser Met Ala Gly Pro Ile Gly Ser Val
305                 310                 315                 320
Gly Pro Ile Gly Thr Arg Pro Leu Pro Gln Pro His Ala Gly Gln Val
                325                 330                 335
Ser Asn Pro Ala Leu Asn Lys Arg Ser Thr Thr Pro Leu Pro Ser Pro
            340                 345                 350
Leu Gly Phe Gly Phe Thr Pro Gly Asp Ala Ala Ser Asp Arg Ser Val
        355                 360                 365
Pro Ser Val Ser Thr Ala Pro Thr Thr Ala Ala Ala Thr Ala Ser Val
    370                 375                 380
Lys Asp Thr Ser Gly Gly Val Gly Leu Gly Trp Gly Asn Gly Ser Gly
385                 390                 395                 400
Val Trp Gly Ser Lys Asn Gly Leu Gly Val Gln Ala Ser Val Trp Gly
                405                 410                 415


<210> 190
<211> 464
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase  CAK49181.1

<400> 190
Met Leu Ser Lys Met Gln Leu Ala Gln Leu Ala Ala Phe Ala Met Thr
 1               5                  10                  15
Leu Ala Thr Ser Glu Ala Ala Tyr Gln Gly Phe Asn Tyr Gly Asn Lys
            20                  25                  30
Phe Ser Asp Glu Ser Ser Lys Phe Gln Ala Asp Phe Glu Ala Glu Phe
        35                  40                  45
Lys Ala Ala Lys Asn Leu Val Gly Thr Ser Gly Phe Thr Ser Ala Arg
    50                  55                  60
Leu Tyr Thr Met Ile Gln Ala Tyr Ser Thr Ser Asp Val Ile Glu Ala
65                  70                  75                  80
Ile Pro Ala Ala Ile Ala Gln Asp Thr Ser Leu Leu Leu Gly Leu Trp

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

<210> 191
<211> 846
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK49185.1

<400> 191
Met Pro Cys Val Gln Ala Ala Ala Glu Thr Asp Lys Ser Phe Val Gln
 1               5                  10                  15
Ile Ala Asn Ala Asp Ile Glu Glu Leu Ile Lys Gln Leu Thr Leu Asp
            20                  25                  30
Glu Lys Val Ala Leu Leu Thr Gly Asp Asp Phe Trp His Thr Val Pro
        35                  40                  45
Ile Pro Arg Leu Gly Ile Pro Ser Ile Arg Leu Ser Asp Gly Pro Asn
    50                  55                  60
Gly Val Arg Gly Thr Arg Phe Phe Gly Ser Val Pro Ala Ala Cys Leu
65                  70                  75                  80
Pro Cys Gly Thr Ala Ile Gly Ala Thr Phe Asp Arg Asn Leu Ala Val
                85                  90                  95
Gln Val Gly His Leu Leu Ala Ala Glu Ala Lys Ala Lys Gly Ala His
            100                 105                 110
Val Ile Leu Gly Pro Thr Ile Asn Ile Gln Arg Gly Pro Leu Gly Gly
        115                 120                 125
Arg Gly Phe Glu Ser Phe Ser Glu Asp Pro Leu Leu Ser Gly Ile Ile
    130                 135                 140
Ala Gly His Tyr Cys Lys Gly Leu Lys Glu Asp Asn Ile Val Ala Thr
145                 150                 155                 160
Leu Lys His Phe Val Cys Asn Asp Gln Glu His Glu Arg Met Ala Val
                165                 170                 175
Asn Ser Ile Leu Thr Asp Arg Ala Leu Arg Glu Ile Tyr Leu Leu Pro
            180                 185                 190
Phe Met Ile Ala Ile Ala Leu Gly Lys Pro Glu Ala Ile Met Thr Ala
        195                 200                 205
Tyr Asn Lys Val Asn Gly Leu His Ala Ser Glu Ser Pro Ala Leu Leu
    210                 215                 220
Gln Gly Ile Leu Arg Glu Glu Trp Gly Trp Glu Gly Leu Leu Met Ser
225                 230                 235                 240
Asp Trp Phe Gly Thr Tyr Ser Thr Ser Glu Ala Ile His Ala Gly Leu
                245                 250                 255
Asp Leu Glu Met Pro Gly Pro Thr Arg Trp Arg Gly Gly Ala Leu Thr
            260                 265                 270
His Ala Ile Thr Ala Asn Lys Ile Pro Met Ala Thr Val Asn Ala Arg
        275                 280                 285
Val Arg Ala Val Leu Arg Leu Val Gln Gln Ala Ser Arg Ser Gly Ile
    290                 295                 300
Pro Glu Arg Ala Leu Glu Leu Gln Leu Asn Arg Ala Glu Asp Arg Gln
305                 310                 315                 320
Leu Leu Arg Lys Ile Ala Ser Glu Ala Val Val Leu Leu Lys Asn Asp
                325                 330                 335
Asp Asn Ile Leu Pro Leu Asp Lys Thr Lys Lys Ile Ala Val Ile Gly
            340                 345                 350
Pro Asn Ser Lys Ile Ala Thr Tyr Cys Gly Gly Gly Ser Ala Ala Leu
        355                 360                 365
Asn Pro Tyr Glu Ala Val Thr Pro Phe Glu Gly Ile Ser Asn Ser Ala
    370                 375                 380
Ser Gly Gly Val Glu Phe Ala Gln Gly Ile Tyr Gly His Gln Asn Leu
385                 390                 395                 400

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Pro Leu Leu Gly Lys Arg Leu Arg Thr Gln Asp Gly Leu Thr Gly Phe
                405                 410                 415
Thr Leu Arg Ile Phe Asn Asp Pro Pro Thr Val Ala Asn Arg Val Pro
            420                 425                 430
Leu Glu Glu Arg His Glu Thr Asp Ser Met Val Phe Phe Leu Asp Tyr
        435                 440                 445
Asn His Pro Lys Leu Gln Pro Val Trp Phe Ala Asp Ala Glu Gly Tyr
    450                 455                 460
Phe Val Pro Glu Glu Ser Gly Met Tyr Asp Phe Gly Leu Cys Val Gln
465                 470                 475                 480
Gly Thr Gly Lys Leu Phe Val Asp Gly Lys Leu Leu Val Asn Asn Ala
                485                 490                 495
Asn Val Gln Arg Pro Gly Pro Ser Phe Leu Gly Ser Gly Thr Met Glu
            500                 505                 510
Glu Arg Gly Thr Leu Glu Leu Thr Ala Gly Arg Gln Tyr Lys Val His
        515                 520                 525
Val Gln Trp Gly Cys Ala Lys Thr Ser Thr Phe Lys Val Pro Gly Val
    530                 535                 540
Val Asp Phe Gly His Gly Gly Phe Arg Phe Gly Ala Cys Arg Gln Leu
545                 550                 555                 560
Ser Pro His Thr Gly Ile Glu Glu Ala Val Gln Leu Ala Ala Ser Val
                565                 570                 575
Asp Gln Val Val Leu Val Ala Gly Leu Ser Ala Glu Trp Glu Ser Glu
            580                 585                 590
Gly Glu Asp Arg Thr Ser Met Gly Leu Pro Pro His Thr Asp Glu Leu
        595                 600                 605
Ile Ser Arg Val Leu Glu Val Asn Pro Asp Thr Val Val Val Leu Gln
    610                 615                 620
Ser Gly Thr Pro Val Glu Met Pro Trp Ile Gln Asn Ala Lys Ala Val
625                 630                 635                 640
Leu His Ala Trp Tyr Gly Gly Asn Glu Thr Gly Asn Gly Leu Ala Asp
                645                 650                 655
Val Ile Phe Gly Asp Val Asn Pro Ser Gly Lys Leu Pro Leu Thr Phe
            660                 665                 670
Pro Arg His Val Lys Asn Asn Pro Thr Tyr Phe Asn His Arg Ser Glu
        675                 680                 685
Gly Gly Arg Val Leu Tyr Gly Glu Asp Val Tyr Val Gly Tyr Arg Phe
    690                 695                 700
Tyr Asp Glu Ile Glu Ile Asp Pro Leu Phe Pro Phe Gly His Gly Leu
705                 710                 715                 720
Ser Tyr Thr Thr Phe Glu Leu Ser Gly Leu Ser Phe Glu Arg Asp Ser
                725                 730                 735
Asn Ser Leu His Ala Ile Cys Thr Leu Arg Asn Thr Gly Ser Arg Ala
            740                 745                 750
Gly Ala Glu Val Ile Gln Leu Tyr Val Ala Pro Val Ser Pro Pro Ile
        755                 760                 765
Lys Arg Pro Gln Lys Glu Leu Lys Glu Phe Arg Lys Val Trp Leu Glu
    770                 775                 780
Pro Gly Ala Glu Asp Val Val Gln Ile Pro Leu Asp Leu Val Arg Ala
785                 790                 795                 800
Thr Ser Phe Trp Asp Glu Lys Ser Ser Ser Trp Cys Ser His Ser Gly
                805                 810                 815
Thr Tyr Arg Ile Met Leu Gly Thr Ser Ser Arg Gly Ala Phe Leu Glu
            820                 825                 830
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Ser Pro Ile Glu Leu Ser Glu Thr Thr Phe Trp Ser Gly Leu
        835                 840                 845


<210> 192
<211> 640
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK38411.1

<400> 192
Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
 1               5                  10                  15
Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
            20                  25                  30
Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
        35                  40                  45
Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
    50                  55                  60
Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
65                  70                  75                  80
Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
                85                  90                  95
Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
            100                 105                 110
Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
        115                 120                 125
Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp
    130                 135                 140
Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile
145                 150                 155                 160
Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr
                165                 170                 175
Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln
            180                 185                 190
Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser
        195                 200                 205
Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser
    210                 215                 220
Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln
225                 230                 235                 240
Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe
                245                 250                 255
Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr
            260                 265                 270
Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp
        275                 280                 285
Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu
    290                 295                 300
Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
305                 310                 315                 320
Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
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                325                 330                 335
Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
            340                 345                 350
Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
        355                 360                 365
Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr
    370                 375                 380
Gly Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala
385                 390                 395                 400
Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala
                405                 410                 415
Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu
            420                 425                 430
Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr
        435                 440                 445
Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr
    450                 455                 460
Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly
465                 470                 475                 480
Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr
                485                 490                 495
Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr
            500                 505                 510
Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser Thr
        515                 520                 525
Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp
    530                 535                 540
Leu Thr Ala Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser
545                 550                 555                 560
Ile Ser Gln Leu Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser
                565                 570                 575
Ala Asp Lys Tyr Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr
            580                 585                 590
Leu Pro Ala Gly Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser
        595                 600                 605
Asp Asp Ser Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val
    610                 615                 620
Pro Gln Ala Cys Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
625                 630                 635                 640


<210> 193
<211> 782
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK47899.1

<400> 193
Met Asp Pro Asn Thr Ser Asp Arg Leu Lys Arg Leu Gln Met Glu Asn
 1               5                  10                  15
Leu Gly Thr Ala Arg Arg Glu Tyr Ile Ser Thr Ala Asp Asp Arg Arg
            20                  25                  30
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```
His Lys Lys Ala Arg Leu Glu Asp Ile Gln Ala Ile Arg Met Thr Asn
        35                  40                  45
Val Pro Gly Ser Ala Ala Gln Arg Met Ala Thr Val Asn Gln Gly Arg
    50                  55                  60
Leu Glu Asp Trp Ala Asn Val His Lys Thr Ile Gly Asp Thr Glu Asp
65                  70                  75                  80
Leu Glu Asn Leu Asp Ser Leu Leu Asp Gly Gln Ser His Arg Leu Gln
                85                  90                  95
Leu Ser Ala Ile Ile Arg Glu Ser Gly Gly Gln Lys Tyr Ile Gly Ser
            100                 105                 110
Gln Arg Arg Ser Gly Ser Ala Pro Ala Thr Arg Ser Leu His Pro Val
        115                 120                 125
Gly Arg Gly Gly Gly Val Ile Gly Thr Arg Gly Arg Gly Thr Arg Gln
    130                 135                 140
Ser Ser Leu Pro Pro Ser Asn Pro Thr Pro Arg Gly His Val Thr Gln
145                 150                 155                 160
Pro Pro Lys Arg Ser His Gly Asp Ala Ala Leu Asp Asp Asn Asp Phe
                165                 170                 175
Tyr Arg Thr Ala Arg Glu Gly Asn Ala Ser Arg Lys Glu Glu Ala Met
            180                 185                 190
Arg Ala Gln Asn Arg Arg Ser Ser Val Arg Arg Pro Thr Ser Ser Thr
        195                 200                 205
Thr Arg Pro Arg Arg Pro Val Ser Gln Val Asp Tyr Ser Ser Met Leu
    210                 215                 220
Ser Gln Pro Gln Ser Phe Leu Ala Ala Ala Arg Ser Leu Val Ser Ala
225                 230                 235                 240
Arg Thr Thr Pro Ala Ala Pro Thr Pro Ala Ser Gln Ile Ser Arg Asp
                245                 250                 255
Gly Gly Arg Ser Glu Ala Ser Arg Lys Ser Ser Ser Pro Met Asp Thr
            260                 265                 270
Thr Asp Arg Pro Thr Val Gln Lys Thr Gln Gln Glu Pro Lys Pro Gln
        275                 280                 285
Met Ala Glu Pro Pro Lys Pro Phe Thr Arg Pro Val Val Gln Leu Pro
    290                 295                 300
Ala Ile Pro Pro Arg Cys Thr Ala Val Gln Gln Glu Ser Thr Thr Lys
305                 310                 315                 320
Ala Asp Glu Pro Leu Pro Val Leu Pro Ser Ser Ala Val Leu Asp Ala
                325                 330                 335
Thr Ser Gln Asp Gln Gly Ser Ala Ser Met Ser Leu Gly Ser Thr Glu
            340                 345                 350
Asp Gly Gln Ser Ile Ser Gly Ile Pro Glu Ser Gln Thr Gly Thr Gln
        355                 360                 365
Glu Lys Val Asn Ser Asp Leu Ser Thr Ala Ala Ala Pro Val Pro Asp
    370                 375                 380
Ile Lys Asp Thr Ser Pro Lys Ala Ala Thr Asp Val Lys Glu Ala Ile
385                 390                 395                 400
Leu Leu Asp Phe Ser Tyr Thr Pro Pro Glu Gln Ser Ile His Gly Gln
                405                 410                 415
Ser Pro Ala Pro Thr Glu Val Leu Thr Pro Ser Leu Glu Asp Leu Arg
            420                 425                 430
Gly Leu Asp Phe Lys Gln Asp Ile His Pro Lys Phe Pro Thr Arg Arg
        435                 440                 445
Arg Val Asp Phe Asp Met Ser Ser Asp Lys Arg Glu Ala Ser Thr Asn
    450                 455                 460
```

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


<210> 194
<211> 1042
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK38738.1

<400> 194
Met Pro Pro Ser Thr Val Phe Ala Tyr Trp Arg Arg Glu His Arg Arg
 1               5                  10                  15
Ser Ser Ala Ser Pro Val Ser Pro Ser Leu Gln Pro Thr Ser Lys Ala
```

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

```
    450                 455                 460
Phe Asp Met Asn Gly Val Glu Ser Ser Ala Gln Glu Lys Leu Leu Glu
465                 470                 475                 480
Glu Lys His Lys Glu Lys Glu Ala Ala Arg Arg Ala Lys Ala Arg Met
                485                 490                 495
Glu Gly Thr Ser Phe Ser Asp Gly Glu Asp Asp Phe Asp Glu Asp Leu
            500                 505                 510
Leu Asp Asp Met Asp Asp Leu Glu Glu Lys Ile Pro Gly Val Asn Val
        515                 520                 525
Asp Ala Asp Glu Asp Asp Asp Phe Ser Gly Phe Ser Gly Pro Gly Asn
    530                 535                 540
Ala Leu Asn Lys Pro Trp Leu Ala Pro Glu Leu Ser Pro Ile Ile Ala
545                 550                 555                 560
Ser Pro Leu Pro Thr Gly Ser Thr Asn Ser Gln Asn Val Gln Glu Leu
                565                 570                 575
Ala Gln Gly Pro Leu Ala Gly Ile Ser Ala Pro Leu Pro Val Ser Asp
            580                 585                 590
Pro Ala Val Ser Asp Val Thr Thr Asn Phe Gln Ala Leu Ser Val Ala
        595                 600                 605
Thr Ile Ala Pro Asn Asn Ala Pro Gln Val Ala Met Gly Ser His Pro
    610                 615                 620
Pro Ala Pro Gln Pro Ile Glu Asp Asp Asp Asp Leu Tyr Phe Asp Asp
625                 630                 635                 640
Gly Glu Phe Gly Asp Leu Ser Thr Glu Asp Met Gly Glu Lys Phe Asp
                645                 650                 655
Glu Ser Ile Phe Asp Asp Glu Thr Ser His Leu Tyr Glu Arg Lys Pro
            660                 665                 670
Val Val Gln Gln Pro Val Pro Ala Pro Val Pro Pro Pro Asp Asn Gly
        675                 680                 685
Thr Gly Ser Thr Asn Pro Leu Asp Val Thr Ala Glu His Asp Glu Phe
    690                 695                 700
Thr Pro Glu Pro Asp Tyr Asp Gly Gly Leu Arg His Val Pro Ser Met
705                 710                 715                 720
Ala Ser Asp Tyr Arg Lys Gly Ser Ile Arg Val Tyr Gly Gln Thr Arg
                725                 730                 735
Glu Ser Leu Ala Asn Leu Gly Ser Ala Lys Ala Gln Gly Gly Val Leu
            740                 745                 750
Ser Glu His Asn Leu Glu Ala Phe His Asn Ala Leu Ala Lys Ala Ala
        755                 760                 765
Ser Glu Ala Ala Ala Ser Asp Arg Phe Gly Arg Glu Ala Ser Ile Ser
    770                 775                 780
Glu Gln Ser Leu Gly Gln Glu Ser Thr Ala Gln Thr Met Asp Thr Pro
785                 790                 795                 800
Ser Gly Leu Val Ser Asp Asp Ser Arg Leu Ser Gln Thr Val Asp Met
                805                 810                 815
Ala Ala Phe Glu Glu Val Phe Glu Asp Phe Ser Tyr Asp Asp Asn Asp
            820                 825                 830
Asp Ala Leu Phe Asp Asp Pro Ile Ile Ala Ala Ala Asn Ala Glu Ala
        835                 840                 845
Leu Glu Asn Asp Asp Glu Gly Phe Tyr Gly Gln Glu Phe Gly Phe Tyr
    850                 855                 860
Ala Gln Ala His Gly Gly Cys Asn Gly Glu Leu Thr Asn Gly Gly Tyr
865                 870                 875                 880
Phe Gly Pro Arg Gly Val Glu Gly Val Asn Arg Ser Phe Ser Ser Arg
```

```
                885                 890                 895
Gly Lys Phe Arg Glu Pro Ser Leu Thr Pro Ile Thr Glu Arg Ser Glu
            900                 905                 910
Trp Ser Thr Arg Asn Ser Val Ile Ser Leu Thr Ala His Gly Ala Ala
        915                 920                 925
His Ser Asn Pro Ile Ala Ser Pro Gly Leu Ala Gln Leu Val Asp Leu
    930                 935                 940
Gly Ala Met Asp Asp Glu Met Ser Leu Ser Ala Leu Met Lys Leu Arg
945                 950                 955                 960
Arg Gly Ala Trp Gly Gly Ser Asn Gly Ser Leu Arg Ser Ser Ser Gly
                965                 970                 975
Ser Pro Pro Leu Leu His Ser Thr Ser Asn Arg Ala Ser Phe Ile Ser
            980                 985                 990
Asp Ala Ser Pro Thr Val Tyr Thr Ala Pro Pro Asp Ala Phe Gly Gly
        995                 1000                1005
Ser Ala Thr Glu Ser Pro Ile Arg Glu Ser Asp Lys Phe Arg Trp Ser
    1010                1015                1020
Leu Asn Asn Thr Glu Gln Arg Val Gly Gln Ser Ala Ala Gly Glu Arg
1025                1030                1035                1040
Glu Pro
```

<210> 195
<211> 1396
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK38790.1

<400> 195

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

```
Met Ala Ser Arg Gln Tyr Asn Val Pro Tyr Asn Pro Gln Asp Trp Gly
            180                 185                 190
Pro Val Gly Ser Gly Ser Met Asn Ala Gly Gln Ala Thr Tyr Thr Pro
        195                 200                 205
Pro Asn Ser Met Leu Arg Ile Val Ser Gln Pro Arg Ser Thr Gly Pro
    210                 215                 220
His Ser Asp Val Ser Leu Ser Pro Pro Pro Pro Pro Tyr Ser Pro Pro
225                 230                 235                 240
Ser Gln Gln His Gln Arg Glu Asn Val Ser Gln Asn Thr Ser Ser Met
                245                 250                 255
Gly Ser Thr Ser Pro Ser Ile Ser Ser Ser Tyr Asn Gly Ala Val Arg
            260                 265                 270
Ala Gly Val Asp Ala Pro Ser Glu Tyr Arg Gln Arg Arg Leu Pro Arg
        275                 280                 285
Thr Arg Pro Leu Ser Met Phe Val Gly Ser Glu Ser Ser His Asn Arg
    290                 295                 300
Arg Val Ser Leu Pro Pro Pro Pro Pro Leu Pro Pro Gly Leu Ser Ser
305                 310                 315                 320
Arg Ser Ser Ser Gln Asn Arg Ser Glu Thr Tyr Arg Glu Pro Ala Ser
                325                 330                 335
Val Met Ala Gly Pro Gly Pro His Ile Val Val Ser Pro Asp Asn Leu
            340                 345                 350
His Ser Thr Gln Leu Ser Asp Asp Ser Asn Met Leu Glu Pro Thr Gln
        355                 360                 365
Pro Phe Asp Thr Asp Arg Pro Pro Ala Ala Arg Arg Ala Val Ser Ala
    370                 375                 380
Gly Pro Ala Val Asn Ser Ala Ser Ser Ser Arg Ala His Ser Gln Ser
385                 390                 395                 400
Gly Ala Arg Ser Pro Pro Gly Thr Ser Trp Glu Pro Gly Met Pro Leu
                405                 410                 415
Pro Pro Pro Pro Pro Gly Pro Pro Pro Ala Thr Arg Ser Gln Ser Val
            420                 425                 430
Asn Gly Leu Ser Asp Ser Ser Ser Ser Arg Asn Ser Gln Gly Pro Val
        435                 440                 445
Arg Gly Gly Arg Ala Arg Pro Pro Pro Val Leu Gly Thr Ser Leu Asp
    450                 455                 460
Ser Ile Pro Pro Thr Pro Ala Gly Trp Val Asp Glu Thr Ile Asp Val
465                 470                 475                 480
Lys Pro Arg Thr Glu Arg Gln Pro Leu Thr Ile Asp Thr Ala Thr Thr
                485                 490                 495
Ser Asn Thr Asn Gly Pro Glu Ser Leu Glu Ser Ser Arg Ala Ser His
            500                 505                 510
Asn Pro Asn Ser Gly Gly Leu Phe Arg Ser Pro Ala Ile Lys Asp Pro
        515                 520                 525
Asn Ala Lys Gly Ile Arg Glu Arg Arg Ile Glu Arg Arg Asn Arg Gln
    530                 535                 540
Ser Gln Val Leu Asp Ser Leu Ser Ala Val Ser Met Ser Ser Asn Pro
545                 550                 555                 560
Trp Ala Glu Ala Leu Glu Gln Leu Lys Pro Ser Asn Leu Val Leu Gly
                565                 570                 575
Glu Ser Ser Val Asp Thr Asp Asn Gly Arg Asn Pro Ala Ser Ala Lys
            580                 585                 590
Ala Ala Pro Leu Ser Thr Arg Ser Ile Ser Ser Asp Gly Pro Gln Ile
        595                 600                 605
```

```
Thr Ser Arg Ser Arg Ala Ser Ser Gly Gly Leu Phe Ser Asn Arg Ser
    610                 615                 620
Cys Ser Thr Pro Lys Pro Glu Pro Ser Pro Gln Ala Pro Thr Ser Asn
625                 630                 635                 640
Ser Arg Phe Ala Gln Thr Pro Pro Phe Ser Pro Gly Thr Glu Arg Ser
                645                 650                 655
Ser Ala Phe Pro Lys Arg Thr Ser Pro Ala Leu Pro Pro Lys Ala Leu
            660                 665                 670
Pro Thr Pro Pro Leu Gln Ser Gly Ser Glu Thr Thr Pro Ser Arg Pro
        675                 680                 685
Gly Ser Lys Glu Glu Arg Pro Val Ser His Ile Leu His Leu Pro Asn
    690                 695                 700
Glu Pro Val Thr Thr Val Ser Pro Leu Ala Pro Arg Arg Val Ser Ala
705                 710                 715                 720
Gln Gln Asn Pro Ser Leu Asp Ser Val Ile Lys Arg Asp Asp Asp Tyr
                725                 730                 735
Val Arg Asn Ala Ile Gln Arg His Arg Glu Phe Ile Glu Lys Glu Ala
            740                 745                 750
Gly Thr Met Asp Glu Lys Glu Ala Leu Arg Leu Phe Ala Asp Phe Ile
        755                 760                 765
Ile Ser Glu Ser Gln Ile Arg Arg Glu Arg Tyr Ala Lys Val Trp Asp
    770                 775                 780
Leu Asp Ser Phe Asp Val Glu Ser Val Arg Arg Lys Leu Phe Val Ser
785                 790                 795                 800
Pro Pro Lys Thr Ala Pro Val Pro Gln Thr Ser Gln Val Val Pro Gly
                805                 810                 815
Pro Ser Ser Arg Arg Ala Ser Asn Pro Thr Ala Pro Lys Leu Asp Ile
            820                 825                 830
Pro Gln Val Arg Pro Glu Ser Ala Trp Trp Asn Asn Tyr Gln Pro Cys
        835                 840                 845
Leu Ser Pro Ile Ala Ser Leu Gly Leu Ser Asn Asp Glu Met Ser Ser
    850                 855                 860
Arg Gly Arg Ala Pro Ser Arg Trp Trp Glu Ser Lys Thr Gly Ser Ser
865                 870                 875                 880
Ser Glu Gly Gly Glu Arg Arg Val Gln Arg Ser Lys Arg Glu Thr Lys
                885                 890                 895
Tyr Met Gly Leu Ser Arg Gly Ala Leu Leu Trp Glu Glu Ser Gln Gly
            900                 905                 910
Ser Ser Asp Thr Gly Asn Ala Gly Thr Ser Asn Gly Gly Asn Gln Tyr
        915                 920                 925
Ala Ala Tyr Gly Pro Asp Glu Tyr Pro Pro Glu Lys Val Gly Trp His
    930                 935                 940
Glu Glu Pro Ala Leu Glu Asp Tyr Ser Asn Asn Val Arg Leu Gly Ser
945                 950                 955                 960
Ser Arg Arg Phe Glu Glu Val Gln Arg Met Asp Val Ser Arg Leu Ile
                965                 970                 975
Thr Leu Pro Pro Pro Tyr Pro Arg His Tyr Pro Ala Val Asn Asn Ser
            980                 985                 990
His Pro Asp Leu Val Thr Tyr Arg Thr Leu Val Arg Ser Ile Thr Asp
        995                 1000                1005
Leu Ser Glu Ile Lys Thr Ala Arg Gln Arg His Gln Thr Glu Met Asp
    1010                1015                1020
Gly Leu Phe Gln Asp His Gln Ala Arg Val Arg Glu Gly Arg Arg Gln
1025                1030                1035                1040
```

Phe Lys Ala Asn Ile Gln Ser Gln Ile Gln Gln Gly Ser Ile Thr Phe
1045 1050 1055
Ala Glu Ala Ala Glu Ala Glu Ala Ala Leu Ile Val Glu Glu Asn Arg
1060 1065 1070
Leu Glu Arg Asp Leu Ile Lys Gly Gly Leu Asp Thr Tyr Gln Glu Ser
1075 1080 1085
Val Phe Lys Pro Met Arg Ala Ile Leu Ala Asp Arg Ile Asp Arg Ala
1090 1095 1100
Thr Ala Cys Ile Asp Glu Leu Arg Gly Arg Leu Phe Asp Asp Ala Arg
1105 1110 1115 1120
Ser Glu Thr Pro Asp Gln Thr Gln Glu Glu Gly Asp Glu Lys Pro Glu
1125 1130 1135
Leu Leu Glu Lys Leu Thr Gln Leu Lys Trp Leu Phe Glu Ala Arg Glu
1140 1145 1150
Gln Leu His Arg Glu Val Phe Asp Leu Ile Ser Asp Arg Asp Glu Lys
1155 1160 1165
Tyr Arg Ala Val Val Leu Leu Pro Tyr Lys Gln Ala Ser Asn Glu Asp
1170 1175 1180
Lys Val Arg Glu Thr Asn Glu Phe Phe Val Lys Asp Ala Leu Asp Arg
1185 1190 1195 1200
Arg Val Asp Tyr Glu Ala Asn Ala Leu Ala Arg Leu Glu Ser Phe Leu
1205 1210 1215
Asp Val Ile Glu Gly Asn Val Ala Arg Gly Val Glu Ile Gln Leu Ser
1220 1225 1230
Ala Phe Trp Asp Ile Ala Pro Ser Leu Ser Glu Leu Val Gln Gln Ile
1235 1240 1245
Pro Glu Lys Leu Arg Gly Phe Thr Val Gln Ile Pro Ala Asn Glu Tyr
1250 1255 1260
Glu Glu Asn Pro Ser Tyr Arg Ala His Pro Leu Gln Tyr Leu Tyr Thr
1265 1270 1275 1280
Leu Val Ser His Ala Glu Lys Ser Ser Tyr Gln Tyr Ile Glu Ser Gln
1285 1290 1295
Ile Asn Leu Phe Cys Leu Leu His Glu Val Lys Ser Ala Val Met Arg
1300 1305 1310
Ala Ser Cys Asn Leu Met Glu Ala Glu Arg Ile Arg Leu Gly Glu Ser
1315 1320 1325
Glu Gly Lys Val Gln Gln Glu Met Gln Glu Thr Arg Thr Asp Glu Glu
1330 1335 1340
Arg Thr Leu Thr Ser Asp Leu Lys Asp Lys Val Ala Thr Val Glu Gly
1345 1350 1355 1360
Gln Trp Ala Glu Ala Leu Gly Ser Gly Ile Gln Arg Leu Arg Glu Arg
1365 1370 1375
Val Lys Glu Gln Leu Met Val Glu Asp Gly Trp Glu Asp Leu Glu Gln
1380 1385 1390
Leu Glu Gln Ala
1395

<210> 196
<211> 786
<212> PRT
<213> Artificial Sequence

<220>

<223> Transgucosidase CAK38810.1

<400> 196
Met Val Thr Gln Ser Ser Leu Leu Asp Arg Val Trp Leu Tyr Thr His
 1               5                  10                  15
Lys Arg Ser Pro Ile Leu Leu Ala Leu His Pro Pro Ser Gln Ser Ser
            20                  25                  30
Leu Ile Ser Ser Glu Gly His Leu Glu Glu Gln Thr Glu Pro Thr Val
        35                  40                  45
Gln Ser Arg Arg Tyr Ile Pro Asn Thr Ile Met Asn Thr Asn Met His
    50                  55                  60
Pro Gln Ser Leu Asp Ser Val Arg Ser Gly Glu Glu Ala Lys Ser Glu
65                  70                  75                  80
Asn Glu Asp Ser Asn Thr Arg Ser Gly Ala Ile Ser Leu Ile Arg Ala
                85                  90                  95
Arg Thr Ile Ser Arg Ser Ser Thr Pro Arg Asp Thr Gln Glu Gly Cys
            100                 105                 110
Ser Ser Glu Gln Ala Asp Asp Ser Gln Gln Ala Val Ser Ile Pro Arg
        115                 120                 125
Ile Val Val Met Glu Pro Pro Gly Asp Ser Lys Ala Lys Arg Asn Lys
    130                 135                 140
Met Lys Lys Asn Lys Tyr Lys Lys Lys Lys Leu Leu Leu Gly Asp Ser
145                 150                 155                 160
Glu Ser Glu Thr Ser Gly Ser Gln Gly Ser Gly Leu Asn Gly Lys Pro
                165                 170                 175
Thr Ala Glu Ser Asn Thr Ser Asn Asp Thr Ser Ser His Met Lys Glu
            180                 185                 190
Ile Glu Asp Leu Ser His Ser Ala Trp Met Pro Ala Lys Gly Leu Asn
        195                 200                 205
Ser Gly Gly Cys Ala Asn Lys Glu Lys Pro Met Ser Gly Ser Asn Val
    210                 215                 220
Ser Glu Arg Cys Thr Val Asp Ser Asp Lys Lys Arg Asp Leu Ile Glu
225                 230                 235                 240
Ser Leu Ser Lys Leu Asp Ile Lys Gly Lys Gln Arg Val Trp Gln Val
                245                 250                 255
Asn Ala Val Thr Gly Asn Asp Thr Leu Glu Glu Ile Asn Thr Gln Arg
            260                 265                 270
Gly Pro Gln Pro Val Asp Arg Ala Arg Arg Thr Val Leu Ala Pro Ser
        275                 280                 285
Tyr Ala Thr Val Leu Ser Gly Lys Arg Ala Ser Ile Glu Gly Pro Ser
    290                 295                 300
Ser Met Pro Asn Asn Ser Asp Ser Leu Leu Pro Thr Thr Met Glu Phe
305                 310                 315                 320
Pro Lys Leu Thr Asp Lys Thr Ser Ala Gly Gln Asp Ser Ser Pro Glu
                325                 330                 335
Ala Arg Ser Gly His Ala Lys Leu Ser Pro Ile Pro Glu Ile Ser Gly
            340                 345                 350
Glu Phe Ala Gly Asp Asn Ser Asn Asp Ile Pro Leu Ser Gln Thr Asp
        355                 360                 365
Leu Glu Thr Ala Gly Ser Ser Ser Leu Asp Asn Pro Ile Ser Thr Pro
    370                 375                 380
Val Ser Thr Val Ser Thr Gly Trp Ser Ser Thr Ala Leu Gln Ile Ser
385                 390                 395                 400
Pro Gln Thr Thr Glu Pro Ser Ser Glu Pro Ser Ser Ser Lys Ala Val

```
                405                 410                 415
Ser His Arg His Ala Thr Ser Leu His His Ala His Pro Leu Pro Pro
            420                 425                 430
Thr Pro Pro Ser Ser Thr His Ser His Ser Leu Ser Thr Ala Asn Ala
        435                 440                 445
Thr Ile Thr Asn Ala Gln Gly Thr Leu Ser Ala Gln Lys Pro Glu Gly
    450                 455                 460
Phe Phe Trp Gln Leu Asp Ser His Gly Phe Pro Cys Ala Lys Ala His
465                 470                 475                 480
Cys Glu Lys Arg Cys Asn Leu Trp Asp Gly Ala Thr Val Ile Cys Pro
                485                 490                 495
Arg Cys Gly Pro Tyr Ser Glu Val Arg Tyr Cys Ser Arg Ala His Leu
            500                 505                 510
Leu Glu Asp Ile Lys Pro His Trp Leu Tyr Cys Gly Gln Met Val Phe
        515                 520                 525
Gln His Pro Cys Arg Glu Thr Ser Ile Pro Arg Arg Val Arg Ala Gly
    530                 535                 540
Pro Pro Leu Ile Pro Cys Leu His His Tyr Asp Met Pro Glu Arg His
545                 550                 555                 560
Arg Gln Ala Val His Phe Asn Met Asn Ala Arg Glu Gly Asp Tyr Phe
                565                 570                 575
Ile Phe Thr Asp Trp Leu Asp Phe Val Thr Ala Gly Leu Pro Gly Asp
            580                 585                 590
Lys Thr Ala Ile Arg Cys Ser Asn Arg Ile Met Tyr Val Val Lys Phe
        595                 600                 605
Asp Asp Ala Ala Glu Lys Asp Arg Phe Arg Arg Val Leu Ala Ala Cys
    610                 615                 620
Leu Phe Met Thr Ile Glu Leu Pro Asp Leu Thr Asp Tyr Leu Tyr Arg
625                 630                 635                 640
Leu Ile Arg Asp Lys Leu Arg Leu Ala Asn Ala Pro Asn His Ile Glu
                645                 650                 655
Pro Ser Leu Arg Tyr Gln Phe Leu Gln Glu Phe Asn Val Thr Ile Gln
            660                 665                 670
Glu Arg Ile Thr Gly Ser Arg His Ala Cys Glu Thr Asp Trp Asp Gly
        675                 680                 685
Arg Asn Arg Arg Asn Cys Gln Asp Pro Val Cys Arg Ala Glu Tyr Arg
    690                 695                 700
Arg Leu Leu Gly Ser Val Gly Gly Arg Gly Tyr Ser Arg Met Ile Glu
705                 710                 715                 720
Thr Leu Glu Ser Thr Tyr Trp Ile Leu Arg Ala Ala Arg Thr Thr His
                725                 730                 735
Pro Ser Val Lys Asp Ala Met Lys Arg Met Met Gly Glu Gly Tyr Ala
            740                 745                 750
Glu Val Ala Glu Glu Asp Arg Arg Ala Phe Arg Arg Gly Asp Gly Trp
        755                 760                 765
Asp Gly Ala Gly Ser Gly Asp Met Glu Ile Glu Gly Phe Asn Glu Gly
    770                 775                 780
Asp Glu
785
```

<210> 197
<211> 394
<212> PRT

<213> Artificial Sequence

<220>
<223> Transgucosidase CAK38817.1

<400> 197
Met Leu Ala Thr Pro Met Thr Pro Gln Ala Ser His Pro Ser Ser Ser
 1               5                  10                  15
Asn Met Val Cys Ser Leu Ala Ser Thr Thr Thr Thr Thr Ser Ser Ser
            20                  25                  30
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ala Thr Gln Gln Thr
        35                  40                  45
Thr Ile Ser Ser Arg Pro Lys Leu Thr Leu Gln Thr Thr Ser Leu Pro
    50                  55                  60
Arg Thr Phe Gly Thr Ser Ser Thr Gly Leu Ser Leu Ser Ile Ala Ala
65                  70                  75                  80
Gly Thr Ala Ser Pro Thr Val Arg Asn Thr Phe Lys Asn Ala Tyr Glu
                85                  90                  95
Val Thr Gly Pro Ser Ser Ala Thr Ala Ser Pro Ser Ser Lys His Pro
            100                 105                 110
Ser Asn Leu Arg Phe Ser Lys Pro Ser Ser Pro Phe Thr Thr His Asn
        115                 120                 125
Pro Tyr Gln Leu Pro Leu Gly Val Lys Ser Ile Leu Arg Asn Ser Pro
    130                 135                 140
Leu Glu Pro Thr Cys Arg Arg Arg Ala Gly Ser Val Ala Thr Thr Gly
145                 150                 155                 160
Pro Asn Gly Gly Pro Ser Ala Arg Arg Val Phe Phe Pro Ala Lys Lys
                165                 170                 175
Gln Val Ser Tyr Arg Asn Pro Leu Glu Glu Glu Ile Gln Thr Val His
            180                 185                 190
Tyr Thr Ala Arg His Ser Asp Leu His Asp Asp Pro Glu Pro Ala Leu
        195                 200                 205
Glu Pro Gln Ser Gln Pro Gln Gln Pro Glu Val Thr Ser Ser Asp Glu
    210                 215                 220
Asp Ser Asp Ser Asn Ala Ser Gly Cys Pro Ser Asp Thr Ser Thr Ser
225                 230                 235                 240
Glu Asp Glu Pro Glu Thr Gly Leu Gly Lys Thr Thr Ser Ser Pro Ile
                245                 250                 255
Lys Arg Lys Lys Arg Lys His Ser Asn Ala Glu Arg Gln Val Arg Ala
            260                 265                 270
Val Ala Leu Met Asp Gly Ile Ala Gly Pro Ser Asn Pro Asp Ser Leu
        275                 280                 285
Thr Pro Gln Thr Pro Arg Arg Lys Arg Ala Lys Arg Arg Cys Glu Trp
    290                 295                 300
Arg Trp Thr Leu Gly Pro Leu Glu Asn Arg Asp Lys Leu Leu His Pro
305                 310                 315                 320
Val Gln Asp Glu Thr Gly Pro Thr Ser Ser Ala Ser Gln Pro Glu Thr
                325                 330                 335
Ile Pro His Glu Ser Glu Thr Glu Thr Pro Ser Ser Asp Pro Pro Leu
            340                 345                 350
Ser Ser Ala Ser Thr Thr Leu Tyr His Ser Ser Pro Ser Ser Ser Val
        355                 360                 365
Ser Ser Asp Val Glu Thr Glu Asn Asp Glu Trp Gln Thr His Thr Thr
    370                 375                 380

```
His Glu Leu Glu Cys Ala His Ala Asp Gln
385                 390


<210> 198
<211> 155
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK38846.1

<400> 198
Met Ala Phe Trp Gly Val Ala Glu Arg Glu Val Ile Glu Arg Ala Val
 1               5                  10                  15
Ala Leu Glu Trp Ala Asp Ala Ala Gln Val Asp Glu Arg Lys Glu Ser
            20                  25                  30
Pro Asn Ile Arg Gly Val Leu Ser Ala Gly Pro Ser Gln Pro Ser Arg
        35                  40                  45
Gly Asp Ala Ser Glu Ile Lys Pro Gly Phe Gly Phe Ser Ser Ala Leu
    50                  55                  60
Leu Trp Gly Ala Ile Phe Gly Ala Phe Gly Trp Thr Arg Val Leu Arg
65                  70                  75                  80
Pro Val Gly Arg Ile Pro Thr Arg Asp Ser Cys Ser Asp Arg Ser Asp
                85                  90                  95
Gly Thr Ser Trp Lys Arg Tyr Leu Asp Leu Thr Leu Leu Ser Leu Asp
            100                 105                 110
Glu Pro Pro Thr Lys Gly Thr Lys Glu Leu Glu Gly Gln Arg Lys Ser
        115                 120                 125
Gln Arg Ala Arg Glu Thr Lys Trp Ala Leu Gly Ser Arg Gly Glu Lys
    130                 135                 140
Trp Ala Leu Pro Glu Leu Ile Ile Leu Asp Asp
145                 150                 155


<210> 199
<211> 985
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK44692.1

<400> 199
Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
 1               5                  10                  15
Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
            20                  25                  30
Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
        35                  40                  45
Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
    50                  55                  60
Gly Tyr Lys Ala Ser Lys Val Gln His Asn Ser Arg Gly Phe Thr Ala
65                  70                  75                  80
```

```
Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
                85                  90                  95
Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
            100                 105                 110
Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
        115                 120                 125
Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
    130                 135                 140
Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
145                 150                 155                 160
Phe Asn Phe Lys Val Ile Arg Lys Ala Thr Gly Asp Ala Leu Phe Ser
                165                 170                 175
Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
            180                 185                 190
Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
        195                 200                 205
Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
    210                 215                 220
Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
225                 230                 235                 240
Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
                245                 250                 255
Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
            260                 265                 270
Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
        275                 280                 285
Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
    290                 295                 300
Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
305                 310                 315                 320
Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
                325                 330                 335
Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
            340                 345                 350
Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
        355                 360                 365
Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
    370                 375                 380
Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
385                 390                 395                 400
His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
                405                 410                 415
Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
            420                 425                 430
Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
        435                 440                 445
Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
    450                 455                 460
Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
465                 470                 475                 480
Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
                485                 490                 495
Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
            500                 505                 510
```

```
His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
        515                 520                 525
Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
    530                 535                 540
Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
545                 550                 555                 560
Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
                565                 570                 575
Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
            580                 585                 590
Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
        595                 600                 605
Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
    610                 615                 620
Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
625                 630                 635                 640
Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
                645                 650                 655
Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
            660                 665                 670
Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
        675                 680                 685
Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
    690                 695                 700
Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
705                 710                 715                 720
Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
                725                 730                 735
Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
            740                 745                 750
Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
        755                 760                 765
Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
    770                 775                 780
Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
785                 790                 795                 800
Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
                805                 810                 815
Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
            820                 825                 830
Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
        835                 840                 845
Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
    850                 855                 860
Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865                 870                 875                 880
Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
                885                 890                 895
Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
            900                 905                 910
Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
        915                 920                 925
Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
    930                 935                 940
```

```
Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945                 950                 955                 960
Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
                965                 970                 975
Trp Ala Glu Asn Trp Val Leu Glu Trp
            980                 985
```

<210> 200
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK44966.1

<400> 200

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

```
    290                 295                 300
Tyr Ile Ala Ala Tyr Lys Ser Gly Asp Ser Lys Pro Thr Ile Pro Gln
305                 310                 315                 320
Glu Gly Leu Val Tyr Trp Tyr Arg Pro Thr Pro Lys Gly Val Asn Cys
                325                 330                 335
Pro Glu Asp Asn Met Pro Ala Pro Asn Gly Phe Gln Met Leu Ser Asp
            340                 345                 350
Ser Ile Phe Val Ala Thr Met Leu Ser Ser Pro Ala Thr Leu Thr Val
        355                 360                 365
Thr Ser Gly Ser Leu Gly Pro Val Lys Val Asp Val Pro Ala Gly Ile
    370                 375                 380
Val Thr Thr Asn Val Thr Met Gly Ile Gly Ala Gln Thr Phe Gln Ile
385                 390                 395                 400
Ser Arg Asn Gly Gln Val Ile Leu Ser Gly Lys Gly Gly Leu Asp Val
                405                 410                 415
Ala Asp Arg Ser Lys Tyr Tyr Asn Phe Asn Val Phe Val Gly Ser Val
            420                 425                 430
Met Gly Ser Ser Ala Ala Gly Asn Ala Ser Arg Met Leu Leu Leu Leu
        435                 440                 445
His Thr Thr Leu Leu Lys Val Leu Leu Ser Gly Asp Lys Gln Val Asn
    450                 455                 460
Val Cys Ser Thr Thr Gly Ser Lys Gly Val Ile Cys His Leu Leu Ile
465                 470                 475                 480
Pro Asp Gln Val Thr Ser Leu Ile Ile Pro Lys Phe Leu Gln His Ile
                485                 490                 495
Val Gln Gly Lys Lys Tyr Asn
            500
```

<210> 201
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK47997.1

<400> 201

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

Val Asp Glu Asp Leu Asp Lys Leu Ala Gln Tyr Gly Phe Val Arg Ile
    130                 135                 140
Tyr Gly Val Asp Cys Asp Gln Thr Asn Lys Val Thr Lys Ala Ala Arg
145                 150                 155                 160
Gln Arg Asn Leu Lys Val Phe Ala Gly Val Phe Asp Leu Gln Asn Phe
                165                 170                 175
Pro Ser Ser Leu Asp Tyr Ile Thr Gly Ala Ala Asn Gly Asp Trp Ser
            180                 185                 190
Val Phe His Thr Ile Asn Ile Gly Asn Glu Leu Val Asn Asp Gly Lys
        195                 200                 205
Asn Ser Ala Ala Asp Val Val Asn Ala Val Asn Thr Ala Arg Ser Lys
    210                 215                 220
Leu Arg Ala Ala Gly Tyr Gln Gly Pro Val Val Thr Val Asp Ala Phe
225                 230                 235                 240
Ser Val Met Ile Gln His Pro Glu Leu Cys Gln Ala Ser Asp Tyr Cys
                245                 250                 255
Ala Ala Asn Cys His Ala Phe Phe Asp Asn Asn Asn Thr Pro Asp Lys
            260                 265                 270
Ala Gly Gln Tyr Val Lys Asp Gln Ala Asn Lys Val Ser Lys Ala Ala
        275                 280                 285
Arg Gly Lys Lys Thr Leu Ile Ser Glu Ser Gly Trp Pro His Asn Gly
    290                 295                 300
Gln Pro Asn Gly Lys Ala Val Pro Ser Ser Leu Asn Gln Gln Lys Ala
305                 310                 315                 320
Ile Ala Ser Leu Gln Gln Thr Phe Thr Gly Glu Asp Glu Leu Val Leu
                325                 330                 335
Phe Thr Ala Phe Asp Asp Leu Trp Lys Gln Asp Ser Ser Gly Thr Phe
            340                 345                 350
Gly Ala Glu Lys Phe Trp Gly Ile Gln Lys His
        355                 360


<210> 202
<211> 865
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK4847.1

<400> 202
Met Pro His Glu Glu Arg Val Ser Ser His Val Arg Gln Leu Leu Gln
 1               5                  10                  15
Ser Leu Thr Leu Glu Glu Lys Val Ala Leu Leu Ala Gly Lys Asn Met
            20                  25                  30
Trp Glu Thr Val Asn Ile Asp Arg Leu His Ile Pro Ser Leu Lys Met
        35                  40                  45
Thr Asp Gly Pro Ala Gly Val Arg Gly Ser Lys Trp Thr Tyr Gly Ser
    50                  55                  60
Leu Thr Thr Trp Ile Pro Cys Gly Ile Ser Leu Ala Ala Thr Phe Asp
65                  70                  75                  80
Pro Ala Met Val Glu Gln Val Gly Ser Val Leu Gly Gln Glu Ala Arg
                85                  90                  95
Arg Lys Gly Cys Gln Val Leu Leu Ala Pro Thr Met Asn Leu Ser Arg

```
            100                 105                 110
Ser Pro Leu Gly Gly Arg Asn Phe Glu Ser Tyr Gly Glu Asp Pro Tyr
        115                 120                 125
Leu Val Gly Val Ile Ala Thr Ala Met Ile Arg Gly Ile Gln Ala His
    130                 135                 140
Gly Val Gly Ala Cys Met Lys His Phe Ile Leu Asn Asp Thr Glu Thr
145                 150                 155                 160
Arg Arg Phe Asn Val Asp Gln Thr Ile Asp Glu Arg Thr Leu Arg Glu
                165                 170                 175
Val Tyr Met Lys Pro Phe Thr Met Val Leu Asn Asp Pro Ala Ser Thr
            180                 185                 190
Pro Trp Thr Ala Met Val Ser Tyr Pro Lys Ile Asn Gly Leu His Ala
        195                 200                 205
Asp Ile Ser Pro His Ile Leu Pro Arg Leu Leu Arg Gln Glu Leu Gln
    210                 215                 220
Phe Asp Arg Leu Val Met Ser Asp Trp Gly Gly Leu Asn Ser Thr Ala
225                 230                 235                 240
Glu Ser Leu Arg Ala Thr Thr Asp Leu Glu Met Pro Gly Pro Ala Val
                245                 250                 255
Arg Arg Gly Glu Arg Leu Leu Ala Ala Ile Arg Ala Gly Glu Val Glu
            260                 265                 270
Val Ala Ala His Val Asp Pro Ser Val Arg Arg Phe Leu Gln Leu Leu
        275                 280                 285
Glu Arg Thr Gly Leu Leu Gly Asp Ala Thr Lys Ser Ala Glu His Ser
    290                 295                 300
Glu Ala Ala Thr Asp Asp Pro Ile Phe His Arg Ile Ala Arg Asp Ala
305                 310                 315                 320
Ala Gln Ser Gly Leu Val Leu Leu Lys Asn Asp Lys Gly Ile Leu Pro
                325                 330                 335
Leu Lys Pro Thr Thr Leu Gln Arg Val Ala Ile Ile Gly Pro Asn Ala
            340                 345                 350
Cys Gln Pro Thr Ala Gly Gly Ala Gly Ser Ala Ala Val Asn Pro Phe
        355                 360                 365
Tyr Val Ser Thr Pro Glu Ser Cys Leu Arg Asp Val Leu His Ala Ala
    370                 375                 380
Asn Ser Glu Leu Gln Val Ser Tyr Glu Pro Gly Ile Pro Ser Ser Leu
385                 390                 395                 400
Arg Pro Pro Leu Leu Gly Lys Leu Leu Thr Val Pro Asp Gly Ser Arg
                405                 410                 415
Lys Gly Trp Gln Val Ser Phe Phe Glu Gly His Ala Leu Glu Gly Pro
            420                 425                 430
Val Val Ala Ser Ser Met Trp Asp Asp Ser Leu Ile Tyr Leu Phe Ser
        435                 440                 445
Asp Gly Asp Val Pro Ala Val Leu Asp Asp Arg Pro Tyr Ser Tyr Arg
    450                 455                 460
Ala Thr Gly Val Val Thr Pro Gln Glu Ser Gly Arg Tyr Thr Trp Ser
465                 470                 475                 480
Leu Ala Asn Thr Gly Lys Ala Lys Leu Phe Val Asn Asp Glu Leu Leu
                485                 490                 495
Ile Asp Asn Thr Glu Trp Thr Gly Leu Thr Gly Gly Phe Leu Gly Cys
            500                 505                 510
Ser Ser Ala Asp Lys Thr Ala Ser Val Tyr Leu Glu Ala Gly Arg Ala
        515                 520                 525
Tyr Gln Leu Arg Val Asp Asn Val Val Thr Leu Pro Val Val Glu Ala
```

```
    530                 535                 540
Phe Asp Asn Thr Leu Phe Pro Arg Ile Ser Gly Val Arg Val Gly Leu
545                 550                 555                 560
Ala Leu Glu Gln Asp Glu Pro Glu Met Leu Ala Gln Ala Val Ala Ala
                565                 570                 575
Ala Arg Gln Ala Asp Val Ala Val Val Val Val Gly His Asn Lys Asp
            580                 585                 590
Ser Glu Gly Glu Gly Gly Asp Arg Ala Thr Met Gln Leu Pro Gly Arg
        595                 600                 605
Thr Asp Glu Leu Val Ala Ala Val Cys Ala Ala Asn Pro Asn Thr Val
    610                 615                 620
Val Val Val Gln Ser Ala Ser Ala Val Ala Met Pro Trp Val Asp Ala
625                 630                 635                 640
Ala Ser Gly Leu Val Met Ala Trp Tyr Gln Gly Gln Glu Asn Gly His
                645                 650                 655
Ala Leu Ala Ala Ala Leu Leu Gly Asp Cys Asp Phe Ser Gly Arg Leu
            660                 665                 670
Pro Ile Thr Phe Pro Arg Arg Leu Lys Asp His Gly Ser His Ala Trp
        675                 680                 685
Phe Pro Gly Glu Ala Ala Gln Asp Arg Asn Thr Phe Gly Glu Gly Val
    690                 695                 700
Arg Val Gly Tyr Arg His Phe Asp Ala Gln Gly Ile Pro Ala Leu Trp
705                 710                 715                 720
Pro Phe Gly Phe Gly Leu Ser Tyr Thr Arg Phe Gln Leu Thr Asn Ile
                725                 730                 735
Arg Val Cys Gly Arg Val Glu Gly Arg Ser Pro Glu Ser Gln Pro Val
            740                 745                 750
Leu Ile Gln Ala Arg Val Cys Asn Val Gly Gly Arg Asp Gly Gln Glu
        755                 760                 765
Val Val Gln Val Tyr Val Ala Pro Ser Ala Gly Ile Arg Glu Ala Gly
    770                 775                 780
Glu Met Ser Phe Pro Lys Thr Leu Gly Gly Phe Cys Lys Ile Ser Val
785                 790                 795                 800
Pro Ala Gly Asp Ser Arg Glu Val Ser Ile Pro Ile Arg Gly Ser Glu
                805                 810                 815
Leu Ser Trp Tyr Asp Ala Arg Val Ala Gln Trp Arg Leu Asp Ala Gly
            820                 825                 830
Lys Tyr Ala Cys Trp Val Gly Arg Ser Ser Ser His Ile Asp Ala Glu
        835                 840                 845
Leu Glu Ile Glu Val Ala Glu Gly Glu Asp Thr Arg Gln Gly Thr Leu
    850                 855                 860
Glu
865
```

<210> 203
<211> 915
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK39248.1

<400> 203

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

```
Trp Glu Pro Asp Phe Ser Phe Thr Ser Ala Arg Tyr Ile Gln Val Glu
        435                 440                 445
Gly Val Ser Leu Asp Gly Ser Asp Gly Arg Pro Val Ile Arg Ser Val
    450                 455                 460
Val Gly Arg His Ile Ser Ser Ala Ala Arg Arg Leu Gly Thr Met Gln
465                 470                 475                 480
Thr Asp Lys Glu Asp Val Asn Gln Leu Leu Ser Ala Leu Ser Trp Thr
                485                 490                 495
Phe Ser Ser Asn Leu Phe Ser Tyr His Thr Asp Cys Pro Gln Ile Glu
            500                 505                 510
Lys Phe Gly Trp Leu Glu Val Thr His Leu Leu Ala Pro Ala Thr Gln
        515                 520                 525
Tyr Val Arg Asp Met Glu Ala Leu Tyr Thr Lys Ile Leu Asp Asp Ile
    530                 535                 540
Leu Asp Thr Gln Glu Pro Ser Gly Leu Val Pro Thr Met Ala Pro Glu
545                 550                 555                 560
Ile Arg Tyr Met Cys Gly Pro Leu His Asp Thr Ile Thr Trp Gly Cys
                565                 570                 575
Ala Val Cys Leu Leu Pro Asp Ile Leu Arg Glu Tyr Tyr Gly Ser Thr
            580                 585                 590
His Val Ile Ala Lys Val Phe Pro Ala Ala Val Arg Tyr Met Glu Tyr
        595                 600                 605
Met Arg Thr Lys Glu Arg Arg Gly Gly Leu Ile Glu His Gly Leu Gly
    610                 615                 620
Asp Trp Gly Arg Gly Ile Ala Phe Gly Asn Asn Gln Ala Asn Ile Glu
625                 630                 635                 640
Thr Ala Ile Tyr Tyr Arg Cys Leu Gln Cys Val Ala Met Met Ala Arg
                645                 650                 655
Glu Leu Gly Glu Met Gln Lys Ala Lys Glu Phe Glu Gln Trp Ala Ala
            660                 665                 670
Arg Ile Tyr Ala Val Tyr Asn Arg His Leu Leu Val Thr Asp Asp Ala
        675                 680                 685
Ser Arg Pro Tyr Ala Tyr Tyr Thr Ser Leu Asp Asn Tyr Pro Ala Arg
    690                 695                 700
Asp Arg Asp Ala Ile Ala Gln Ala Met Ala Leu Gln Phe Gly Leu Val
705                 710                 715                 720
Pro Glu Gln His Arg Lys Asp Val Met Ala Ala Phe Leu Asp Asp Val
                725                 730                 735
Ala Asp Gly Arg Ile Arg Ala Gly Glu Ile Gly Leu Arg Phe Leu Phe
            740                 745                 750
Asn Thr Leu Ala Asp Ala Lys Arg Pro Asp Leu Val Leu Gln Met Ala
        755                 760                 765
Arg Gln Glu Glu His Pro Ser Tyr Met Arg Phe Leu Arg Arg Gly Glu
    770                 775                 780
Thr Thr Leu Leu Glu Phe Trp Gln Asp Glu Cys Arg Ser Lys Cys His
785                 790                 795                 800
Asp Met Leu Gly Thr Ile Tyr Glu Trp Phe Tyr Ala Ala Val Leu Gly
                805                 810                 815
Leu Lys Pro Thr Gly Pro Ala Tyr Arg Thr Phe Val Val Asp Pro Pro
            820                 825                 830
Tyr Asn Ala Glu Phe Lys His Val Lys Gly Ser Val Asp Cys Pro Tyr
        835                 840                 845
Gly Thr Ile Ala Val Glu Phe Thr Arg Asn Glu Gln Gly Gln Ala Val
    850                 855                 860
```

Val Asn Val Arg Val Pro Phe Gly Thr Thr Ala Ile Val Lys Leu Pro
865 870 875 880
Arg Ser Gly Lys Ser Ser Ala Tyr Cys Arg Glu Gly Glu Glu Ser Arg
885 890 895
Ala Val Asp Gly Gly Glu Val Ser Leu Ser His Gly Val Tyr Ser Ile
900 905 910
Ile Glu Gly
915

<210> 204
<211> 768
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK39259.1

<400> 204
Met Pro Ser Thr Tyr Leu Gly Ala Leu Ala Thr Leu Ala Val Phe Pro
1 5 10 15
Cys Leu Gly Gln Ala Arg Ser Thr Trp Pro Leu Gly Ser Gly Leu Glu
20 25 30
Leu Ser Tyr Gln Ala Ser Gln His Gln Ile Ser Ile His Gln Asp Asn
35 40 45
Gln Thr Ile Phe Ser Thr Ile Pro Gly Gln Pro Phe Leu Ser Ala Ser
50 55 60
Ala Gly Lys Asp Gln Phe Val Glu Asp Ser Gly Asn Phe Asn Ile Thr
65 70 75 80
Asn Val Asn Gln Ala Arg Cys Arg Gly Gln Asn Ile Thr Gln Leu Ala
85 90 95
Gly Ile Pro Arg Ser Asp Ser Val Lys Asn Gln Val Ala Val Arg Gly
100 105 110
Tyr Leu Leu Asp Cys Gly Gly Glu Asp Ile Ala Tyr Gly Met Asn Phe
115 120 125
Trp Val Pro Arg Arg Phe Ser Asp Arg Val Ala Phe Glu Ala Ser Val
130 135 140
Asp Ser Glu Ala Asn Ala Ser Val Pro Val Asp Arg Leu Tyr Leu Thr
145 150 155 160
Phe Ala Ser His Ala Leu Glu Asp Phe Tyr Gly Leu Gly Ala Gln Ala
165 170 175
Ser Phe Ala Ser Met Lys Asn Arg Ser Ile Pro Ile Phe Ser Arg Glu
180 185 190
Gln Gly Val Gly Arg Gly Asp Gln Pro Tyr Thr Ala Ile Glu Asp Ser
195 200 205
Gln Gly Phe Phe Ser Gly Gly Asp Gln Tyr Thr Thr Tyr Thr Ala Ile
210 215 220
Pro Gln Tyr Val Ser Ser Asp Gly Arg Val Phe Tyr Leu Asp Glu Asn
225 230 235 240
Asp Thr Ala Tyr Ala Val Phe Asp Phe Gln Arg Ser Asp Ala Val Thr
245 250 255
Val Arg Tyr Asp Ser Leu Ser Val His Gly His Leu Met Gln Ala Asp
260 265 270
Thr Met Leu Asp Ala Ile Thr Met Leu Thr Glu Tyr Thr Gly Arg Met

```
        275                 280                 285
Pro Thr Leu Pro Glu Trp Val Asp His Gly Ala Leu Leu Gly Ile Gln
    290                 295                 300
Gly Gly Gln Glu Lys Val Asn Arg Ile Val Lys Gln Gly Phe Glu His
305                 310                 315                 320
Asp Cys Pro Val Ala Gly Val Trp Leu Gln Asp Trp Ser Gly Thr His
                325                 330                 335
Leu Gln Ser Ala Pro Tyr Gly Asn Met Asn Ile Ser Arg Leu Trp Trp
            340                 345                 350
Asn Trp Glu Ser Asp Thr Ser Leu Tyr Pro Thr Trp Ala Glu Phe Val
        355                 360                 365
Gln Thr Leu Arg Glu Gln His Gly Val Arg Thr Leu Ala Tyr Val Asn
    370                 375                 380
Pro Phe Leu Ala Asn Val Ser Ser Lys Ser Asp Gly Tyr Arg Arg Asn
385                 390                 395                 400
Leu Phe Leu Glu Ala Ser Gln His Arg Tyr Met Val Gln Asn Thr Thr
                405                 410                 415
Thr Asn Ser Thr Ala Ile Ile Ser Ser Gly Lys Gly Ile Asp Ala Gly
            420                 425                 430
Ile Leu Asp Leu Thr Asn Glu Asp Thr Arg Ala Trp Phe Ala Asp Val
        435                 440                 445
Leu Arg Thr Gln Val Trp Ser Ala Asn Ile Ser Gly Cys Met Trp Asp
    450                 455                 460
Phe Gly Glu Tyr Thr Pro Ile Thr Pro Asp Thr Ser Leu Ala Asn Ile
465                 470                 475                 480
Ser Thr Ser Ala Phe Phe Tyr His Asn Gln Tyr Pro Arg Asp Trp Ala
                485                 490                 495
Ala Tyr Gln Arg Ser Val Ala Ala Glu Met Pro Leu Phe His Glu Met
            500                 505                 510
Val Thr Phe His Arg Ser Ala Ser Met Gly Ala Asn Arg His Met Asn
        515                 520                 525
Leu Phe Trp Val Gly Asp Gln Ala Thr Leu Trp Thr Arg Asn Asp Gly
    530                 535                 540
Ile Lys Ser Val Val Thr Ile Gln Gly Gln Met Gly Ile Ser Gly Tyr
545                 550                 555                 560
Ala His Ser His Ser Asp Ile Gly Gly Tyr Thr Thr Val Phe Glu Pro
                565                 570                 575
Pro Thr Thr Ser Asn Ser Ser Gly Ala Ile Pro Arg Ser Ala Glu Leu
            580                 585                 590
Leu Gly Arg Trp Gly Glu Leu Gly Ala Val Ser Ser Ala Val Phe Arg
        595                 600                 605
Ser His Glu Gly Asn Val Pro Ser Val Asn Ala Gln Phe Tyr Ser Asn
    610                 615                 620
Ser Thr Thr Tyr Ala Tyr Phe Ala Tyr Asn Ala Arg Leu Phe Arg Ser
625                 630                 635                 640
Leu Gly Pro Tyr Arg Arg Arg Ile Leu Asn Thr Glu Ser Gln Arg Arg
                645                 650                 655
Gly Trp Pro Leu Leu Arg Met Pro Val Leu Tyr His Pro Glu Asp Leu
            660                 665                 670
Arg Ala Arg Gln Ile Ser Tyr Glu Ser Phe Phe Leu Gly Arg Asp Leu
        675                 680                 685
Tyr Val Ala Pro Val Leu Asp Glu Gly His Lys Ser Val Glu Val Tyr
    690                 695                 700
Phe Pro Gly His Ser Ala Asn Arg Thr Tyr Thr His Val Trp Thr Gly
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705 710 715 720
Gln Thr Tyr Arg Ala Gly Gln Thr Ala Lys Val Ser Ala Pro Phe Gly
725 730 735
Lys Pro Ala Val Phe Leu Val Asp Gly Ala Ser Ser Pro Glu Leu Asp
740 745 750
Val Phe Leu Asp Phe Val Arg Lys Glu Asn Gly Thr Val Leu Tyr Ala
755 760 765

<210> 205
<211> 662
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK39383.1

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

```
Ala Ala Val Ile Val Ala Ala Ile Val Gly Gly Ala Val Gly Gly Ile
    290                 295                 300
Leu Gly His Gln Glu His Asp Gly Asp Thr Ser Ser Ser Ser Ser Ser
305                 310                 315                 320
Ser Ser Ser Ser Gly Thr Gly Ser Gly Gly Ser Asp Lys Gly Asp Gly
                325                 330                 335
Leu Leu Asp Lys Asp Ser Asp Glu Ile Lys Ala Leu Met Asn Asn Lys
            340                 345                 350
Asn Leu His Lys Val Phe Pro Gly Val Asp Tyr Thr Pro Trp Gly Val
        355                 360                 365
Gln Tyr Pro Leu Cys Leu Gln Tyr Pro Pro Ser Gln Asn Asn Val Thr
    370                 375                 380
Arg Asp Leu Ala Val Leu Thr Gln Leu Thr Asn Thr Ile Arg Leu Tyr
385                 390                 395                 400
Gly Thr Asp Cys Asn Gln Thr Glu Met Val Leu Glu Ala Ile Asp Arg
                405                 410                 415
Leu Gln Leu Thr Asn Met Lys Leu Trp Leu Gly Val Trp Ile Asp Thr
            420                 425                 430
Asn Thr Thr Thr Thr Asp Arg Gln Ile Ser Gln Leu Tyr Lys Ile Val
        435                 440                 445
Glu Asn Ala Asn Asp Thr Ser Ile Phe Lys Gly Ala Ile Val Gly Asn
    450                 455                 460
Glu Ala Leu Tyr Arg Ala Gly Ser Asp Val Ala Ser Ala Glu Thr Asn
465                 470                 475                 480
Leu Ile Gly Tyr Ile Asn Asp Val Lys Asp His Phe Lys Asp Lys Asn
                485                 490                 495
Ile Asp Leu Pro Val Gly Thr Ser Asp Leu Gly Asp Asn Trp Asn Ala
            500                 505                 510
Gln Leu Val Ser Ala Ala Asp Phe Val Met Ser Asn Ile His Pro Phe
        515                 520                 525
Phe Gly Gly Val Glu Ile Asp Asp Ala Ala Ser Trp Thr Trp Thr Phe
    530                 535                 540
Trp Gln Thr His Asp Thr Pro Leu Thr Ala Gly Thr Asn Lys Gln Gln
545                 550                 555                 560
Ile Ile Ser Glu Val Gly Trp Pro Thr Gly Gly Gly Asn Asp Cys Gly
                565                 570                 575
Ser Asp Asn Lys Cys Gln Asn Asp Lys Gln Gly Ala Val Ala Gly Ile
            580                 585                 590
Asp Glu Leu Asn Gln Phe Leu Ser Glu Trp Val Cys Gln Ala Leu Asp
        595                 600                 605
Asn Gly Thr Glu Tyr Phe Trp Phe Glu Ala Phe Asp Glu Pro Trp Lys
    610                 615                 620
Val Gln Tyr Asn Thr Pro Gly Gln Glu Trp Glu Asp Lys Trp Gly Leu
625                 630                 635                 640
Met Asp Ser Ala Arg Asn Leu Lys Pro Gly Val Lys Ile Pro Asp Cys
                645                 650                 655
Gly Gly Lys Thr Ile Thr
            660
```

<210> 206
<211> 667
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK96650.1

<400> 206
Met Ser Arg Asn Phe His Pro Val Asn Thr Asn Phe Pro Ser Thr Thr
 1               5                  10                  15
Thr Leu Thr Ala Asp Pro Asp Ile Ile Pro Ser Pro Glu Asp Asn Arg
            20                  25                  30
Asn Asn Tyr Thr Ser Thr Gln Ser Tyr Phe Cys Arg Gln Asp Val Ser
        35                  40                  45
Thr Asn Pro Thr Phe Asn Ser Asn Asp Gln Ala Leu Leu Asp Asn Cys
    50                  55                  60
Ser Asn Ile Asp Val Ser Gln Leu Val Thr Glu Ala Asn Cys Phe Trp
65                  70                  75                  80
Gly Ser Arg Ser Ser Thr Leu Pro Lys Asn Glu Gly Tyr Pro Ser Val
                85                  90                  95
Glu Glu Tyr Pro Ser Thr Tyr Leu Met Gly Asn His Gly His Gly Tyr
            100                 105                 110
Ala Asp Glu Asn Met His Glu Thr Ser Ala Pro Tyr Gly Pro Cys Asp
        115                 120                 125
His Leu Gln Val Ala Gly Ala Gly Met Asp Met Glu Met Arg Met Thr
    130                 135                 140
Gly Asn Val Met Gly Lys Val Asp Glu Thr Tyr Glu Ala Asn Gln Ala
145                 150                 155                 160
Ala Met Leu Ala Ala Leu Gly Met Thr His Leu Asp Glu Gly Val Ser
                165                 170                 175
His Ala Ala Asp Asp Asp Ala Lys Thr Ser Ser Ser Val Thr Val Asp
            180                 185                 190
Asp Asp Pro Glu Trp Lys Glu Trp Lys Lys Trp Lys Glu Arg Glu Ala
        195                 200                 205
Asn Gly Gly Val Arg Leu Pro Pro Glu Glu Arg Met Asn Gln Ala Asp
    210                 215                 220
Val Ala Ala Trp Leu Gly Met Asp Ser Lys Glu Glu His Gly Val Phe
225                 230                 235                 240
Gln Thr Gln Glu Glu Asp Asp Tyr Asp Glu Asp Glu Thr Ile Ser Tyr
                245                 250                 255
Val Ser Asp Asp Asp Met Met Glu Met Glu Glu Gly Met Glu Asp Asp
            260                 265                 270
Glu Val Val Val Asn Val Val Glu Gly Pro Ser Arg Gln Val Leu Ile
        275                 280                 285
Ser Ser Gln Thr Gly Ala His Ala Glu Tyr Asp Thr Ala Ser Phe Gly
    290                 295                 300
Cys Asp Phe Glu Glu Gln Glu Glu Gln Glu Asp Ser Glu Glu Gln Glu
305                 310                 315                 320
Asn Glu Glu Arg Trp Gly Gly Asp Gly Gln Pro Pro Pro Ser Leu Phe
                325                 330                 335
Pro Arg Phe Tyr Ser Asp Asn Ala Glu Thr Gly Leu Ile Ile Glu Leu
            340                 345                 350
Ser Ser Ala Asp Ser Asp Ala Glu Glu Thr Met Ser Asp Pro Ser Pro
        355                 360                 365
Ser Ser Leu Ser Ser Ser Ser Ser Ser Ser Pro Ser Glu Thr Pro Leu
    370                 375                 380
Gln Pro His Leu Gln Glu Ala Tyr Ala Leu Pro Trp Thr Thr Ser Pro

385 390 395 400
Ser Asn Thr Ser Thr Ile Thr Ser Thr Thr Ser Thr Pro Thr Asp Thr
405 410 415
Ser Pro Val Pro Thr Pro Phe Gln Pro Asp Pro His Pro His Pro His
420 425 430
Pro His Pro Thr Thr Gln His Tyr Leu Pro Pro Pro Ser Ser Gln Thr
435 440 445
Thr Pro Pro Phe Thr Leu Leu Thr Asp Leu His Thr His Leu Thr His
450 455 460
Thr Pro Gln His Arg Ala Ser His Leu Arg Asn Leu Ala Ser Glu Ile
465 470 475 480
Ser Asn Thr Met Tyr Phe Val Asn Ser His Thr Ile Ser Gly Asp Phe
485 490 495
Ser Ala Glu Asp Ala Ala Pro Val Asp Arg Val Met Arg Ile Val Arg
500 505 510
Glu Gly Glu Leu Lys Met Arg Tyr Gln Glu Arg Tyr Glu Arg Gln Lys
515 520 525
Gly Lys Leu Val Lys Arg Glu Arg Arg Val Ala Glu Arg Glu Asp Arg
530 535 540
Val Ser Lys Arg Glu Glu Met Val Ser Arg Arg Glu Met Gly Val Ala
545 550 555 560
Gly Trp Trp Glu Val Trp Arg Glu Arg Gly Arg Glu Val Trp Glu Gly
565 570 575
Val Glu Gly Glu Met Met Gly Thr Met Glu Gly Asn Gly Tyr Arg Arg
580 585 590
Asn Gly Met Asp Thr Leu Gln Arg Thr Val Arg Val Thr Arg Glu Val
595 600 605
Val Arg Arg Met Asp Arg Ile Val Asp Glu Gly Glu Val Asp Gly Asp
610 615 620
Gly Asp Val Glu Gly Gly Val Glu Val Arg Gly Ala Tyr Lys Ile Asp
625 630 635 640
Tyr Asn Cys Asp Asp Asp Ile Val Gly Ser Thr Ser Tyr Arg Ile Glu
645 650 655
Ile Cys Asn Pro Pro Gln Arg Ser Ser Ala Ser
660 665

<210> 207
<211> 1335
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK40060.1

<400> 207
Met Ser Ser Thr Pro Asp Asp Lys Pro Gln Arg Ala Thr Ala Ala Gln
1 5 10 15
Leu Ala Asn Arg Lys Ile Lys Glu Val Arg Arg Arg Arg Pro Asn Ser
20 25 30
Ala Ala Pro Ser Ala Pro Ala Pro Ser Phe Gly Gly Gly Pro Phe Ala
35 40 45
Ser Ile Asp Pro Asn Thr Val Ser Ser Thr Pro Ala Ser Ser Gln Thr
50 55 60

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Ala Ser Asn Gly Phe Thr Phe Gly Gln Ser Gln Asn Gln Ser Phe Pro
65                  70                  75                  80
Gly Ala Ser Ser Ala Pro Ser Gln Asn Gly Gly Thr Pro Phe Ala Phe
                85                  90                  95
Gly Ser Gly Gly Gly Gly Ser Ser Ser Ser Ser Phe Asn Phe Ser Ser
            100                 105                 110
Ser Phe Gly Gly Thr Ser Ser Ala Ser Asn Pro Phe Ala Ser Met Asn
        115                 120                 125
Thr Thr Thr Ser Asp Gln Ser Ser Lys Pro Ala Ser Phe Ser Gly Phe
    130                 135                 140
Gln Gly Ser Leu Phe Asn Ile Pro Pro Gly Gly Asn Gln Ser Pro Ala
145                 150                 155                 160
Gln Gln Pro Leu Pro Ser Gly Ser Ile Phe Gly Thr Ser Ser Gln Ser
                165                 170                 175
Asn Ala Ser Thr Gly Gly Leu Phe Gly Ala Ser Thr Asn Asn Gly Pro
            180                 185                 190
Ser Ala Ser Gly Ala Ala Thr Pro Ala Ser Gly Ser Ile Phe Gly Gln
        195                 200                 205
Asn Asn Ala Ala Ala Ala Ala Ser Thr Pro Ser Thr Asn Leu Phe Gly
    210                 215                 220
Gln Ser Ser Val Lys Lys Pro Ser Pro Phe Gly Gln Ser Ser Ala Phe
225                 230                 235                 240
Ser Gly Asp Asp Ser Met Gln Thr Ser Pro Asp Ala Lys Gly Ser Gly
                245                 250                 255
Ser Gln Gln Lys Pro Ser Ile Phe Ser Ser Ala Pro Pro Ala Gln Pro
            260                 265                 270
Ser Phe Ala Gly Ala Gly Ser Thr Ser Leu Phe Gly Ala Ser Ala Ser
        275                 280                 285
Ser Ala Ala Glu Thr Pro Ser Lys Pro Val Phe Asp Phe Lys Ala Thr
    290                 295                 300
Thr Pro Ser Thr Ser Leu Phe Gly Gly Ala Ala Thr Pro Thr Pro Ser
305                 310                 315                 320
Ala Ser Thr Pro Ala Pro Ala Ala Val Thr Thr Ala Ala Pro Ala Ser
                325                 330                 335
Ser Ser Leu Phe Gly Ala Ala Ser Pro Ala Lys Pro Ser Thr Pro Phe
            340                 345                 350
Gln Asn Pro Phe Gln Ser Ser Asn Leu Phe Gln Thr Thr Pro Ser Thr
        355                 360                 365
Ser Gln Lys Pro Asp Glu Glu Lys Lys Glu Glu Pro Lys Pro Ala Asp
    370                 375                 380
Ser Gln Pro Lys Ser Pro Phe Gln Phe Ser Ala Ser Thr Thr Thr Pro
385                 390                 395                 400
Gly Ser Leu Phe Ala Lys Ser Asp Ala Pro Ala Ser Pro Ala Pro Ala
                405                 410                 415
Ala Pro Ser Thr Gly Leu Phe Gln Thr Ser Ser Thr Lys Asn Leu Phe
            420                 425                 430
Glu Pro Lys Pro Pro Ala Thr Ala Asp Ala Glu Gln Thr Lys Ala Pro
        435                 440                 445
Ala Asn Pro Phe Gly Gly Leu Phe Ala Lys Pro Ala Thr Pro Ser Lys
    450                 455                 460
Pro Ala Gly Glu Gln Gln Pro Leu Pro Ser Ser Ser Thr Pro Phe Gln
465                 470                 475                 480
Gly Leu Phe Ser Lys Pro Ser Thr Ser Asn Asp Ala Ala Lys Thr Ser
                485                 490                 495
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Glu Pro Glu Lys Gln Ala Thr Pro Gly Pro Met Ser Phe Ala Pro Ser
            500                 505                 510
Ser Gly Gly Phe Ser Gln Thr Ser Asn Leu Phe Ser Pro Lys Pro Ala
        515                 520                 525
Ala Ser Pro Ala Pro Ala Ala Glu Thr Gln Ala Thr Ala Ala Ser Thr
    530                 535                 540
Ser Ala Ala Pro Val Asp Ser Pro Ile Lys Val Asn Gly Ala Asn Ser
545                 550                 555                 560
Ser Pro Ser Val Phe Thr Asn Gly Asn Thr Ala Pro Ser Thr Phe Gly
                565                 570                 575
Gln Met Gln Thr Pro Lys Leu Ala Gly Lys Thr Thr Asp Pro Lys Thr
            580                 585                 590
Ser Glu Asp Ala Glu Met Leu Tyr Arg Met Arg Thr Leu Asn Glu Cys
        595                 600                 605
Phe Gln Arg Glu Leu Ala Lys Leu Asp Pro Ser Ser Gln Asn Phe Asp
    610                 615                 620
Ala Ala Val Gln Phe Tyr Met Arg Val Arg Ala Thr Leu Gly Ala Ser
625                 630                 635                 640
Val Gly Ser Lys Arg Lys Ala Ser Gly Glu Ala Glu Asp Ala Val Ala
                645                 650                 655
Thr Lys Lys Ala Arg Pro Phe Gly Ile Pro Ser Glu Lys Ala Asp Thr
            660                 665                 670
Pro Lys Glu Asn Ser Thr Thr Pro Ala Val Ser Ala Gln Ser Ser Thr
        675                 680                 685
Pro Phe Lys Gly Phe Gly Thr Ser Gln Ala Ser Pro Ala Ser Ser Lys
    690                 695                 700
Arg Lys Ser Ile Asp Glu Gly Asp Asp Asn Ser Pro Ala Lys Arg Val
705                 710                 715                 720
Asn Gly Asp Ser Ser Thr Ala Asn Ile Phe Ala Gln Ser Phe Ser Lys
                725                 730                 735
Ser Lys Thr Glu Ala Glu Lys Pro Glu Pro Ser Val Val Lys Pro Ser
            740                 745                 750
Thr Pro Glu Ser Thr Lys Pro Ala Leu Phe Ser Thr Thr Pro Thr Thr
        755                 760                 765
Ala Pro Ala Lys Pro Leu Phe Ser Leu Ser Asp Ser Ala Ser Lys Gly
    770                 775                 780
Ser Ala Ser Thr Ser Leu Phe Ser Ser Ser Met Ser Ser Ala Thr Ser
785                 790                 795                 800
Thr Ser Ala Ala Ser Gly Gly Asn Ala Pro Lys Asn Pro Phe Val Leu
                805                 810                 815
Lys Pro Thr Ser Ser Glu Gly Ser Ser Thr Gly Ser Ala Gly Gly Thr
            820                 825                 830
Asp Phe Phe Ala Gln Phe Lys Ala Arg Ser Phe Glu Asp Ala Glu Lys
        835                 840                 845
Glu Lys Glu Lys Arg Lys Ala Glu Asp Phe Asp Ser Glu Glu Glu Asp
    850                 855                 860
Glu Ala Glu Trp Glu Arg Arg Asp Ala Glu Glu Gln Arg Lys Lys Gln
865                 870                 875                 880
Glu Gln Phe Gly Thr Gln Thr Gln Lys Arg Ala Lys Phe Val Pro Gly
                885                 890                 895
Lys Gly Phe Val Phe Glu Asp Glu Ser Asn Glu Ser Pro Ala Lys Lys
            900                 905                 910
Ala Glu Asp Ser Ser Ser Thr Thr Pro Gly Ala Gly Thr Ile Phe Ser
        915                 920                 925
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Ser Gln Asn Asn Thr Ala Val Lys Ser Asn Asn Ile Phe Gly His Leu
    930                 935                 940
Ser Ala Thr Pro Ser Glu Ala Glu Asp Asn Asp Asn Asp Ala Asp Asp
945                 950                 955                 960
Thr Glu Glu Ala Ser Thr Pro Gly Asp Glu Ser Asp Asp Ala Ala Glu
                965                 970                 975
Asn Ala Val Ala Ala Asp Lys Lys Ala Glu Ser Ala Asp Ser Ser Ala
            980                 985                 990
Lys Glu Pro Glu Ala Gly Gly Arg Ser Leu Phe Asp Arg Val Gln Tyr
        995                 1000                1005
Gly Glu Asp Gly Lys Pro Lys Arg Gln Gly Glu Glu Glu Pro Lys Gly
    1010                1015                1020
Asn Val Ser Thr Leu Phe Gly Ser Ser Asn Phe Ser Ser Ser Phe Asn
1025                1030                1035                1040
Thr Pro Thr Ser Leu Thr Pro Ala Ser Ser Gly Glu Ser Asn Leu Ala
                1045                1050                1055
Ala Pro Lys Pro Ala Thr Thr Asn Leu Phe Gly Ala Pro Ser Thr Thr
            1060                1065                1070
Ser Ser Ile Phe Gly Thr Pro Leu Ser Gly Ser Gly Asn Ser Thr Pro
        1075                1080                1085
Ser Ile Phe Asn Ala Ala Gln Asn Ala Thr Lys Ser Thr Gly Asp Asn
    1090                1095                1100
Thr Trp Lys Pro Asp Ser Pro Ile Lys Phe Ala Ser Asp Ser Ala Ser
1105                1110                1115                1120
Ala Ser Ser Ser Lys Pro Asp Ser Gly Ser Ala Thr Pro Ala Leu Glu
                1125                1130                1135
Ala Pro Lys Pro Phe Ser Asn Leu Phe Gly Ala Pro Pro Ser Leu Thr
            1140                1145                1150
Lys Ser Ser Thr Ser Lys Asp Ala Gln Pro Ser Leu Gly Phe Thr Phe
        1155                1160                1165
Gly Thr Pro Gly Gln Ser Ser Pro Ser Val Phe Ala Pro Ser Thr Leu
    1170                1175                1180
Thr Ser Ala Ala Pro Ser Arg Ser Thr Thr Pro Gly Gly Ala Ser Asp
1185                1190                1195                1200
Thr Gly Ala Glu Glu Ser Gly Asp Gly Asp Gly Ala Glu Ser Leu Pro
                1205                1210                1215
Gln Leu Asp Leu Thr Arg Gly Gly Ala Gly Glu Glu Asn Glu Asp Leu
            1220                1225                1230
Val Ala Glu Ser Arg Ala Arg Ala Met Lys His Thr Thr Gly Thr Gly
        1235                1240                1245
Trp Glu Ser Gln Gly Val Gly Phe Leu Arg Val Leu Lys Asp Arg Thr
    1250                1255                1260
Thr Ser Arg Gly Arg Ile Val Val Arg Ala Asp Pro Ser Gly Lys Val
1265                1270                1275                1280
Ile Leu Asn Thr Arg Leu Met Lys Glu Ile Arg Tyr Ser Val Ala Lys
                1285                1290                1295
Asn Ser Val Gln Phe Leu Val Pro Gln Ser Glu Gly Pro Pro Gln Met
            1300                1305                1310
Trp Ala Leu Arg Val Lys Thr Asn Ala Asp Ala Glu Arg Leu Cys Lys
        1315                1320                1325
Ser Met Glu Glu Thr Lys Asn
    1330                1335
```

<210> 208
<211> 957
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK40395.1

<400> 208
Met Ser Asn Arg Trp Thr Leu Leu Leu Ser Leu Val Ile Leu Leu Gly
 1               5                  10                  15
Cys Leu Val Ile Pro Gly Val Thr Val Lys His Glu Asn Phe Lys Thr
            20                  25                  30
Cys Ser Gln Ser Gly Phe Cys Lys Arg Asn Arg Ala Phe Ala Asp Asp
        35                  40                  45
Ala Ala Ala Gln Gly Ser Ser Trp Ala Ser Pro Tyr Glu Leu Asp Ser
    50                  55                  60
Ser Ser Ile Gln Phe Lys Asp Gly Gln Leu His Gly Thr Ile Leu Lys
65                  70                  75                  80
Ser Val Ser Pro Asn Glu Lys Val Lys Leu Pro Leu Val Val Ser Phe
                85                  90                  95
Leu Glu Ser Gly Ala Ala Arg Val Val Val Asp Glu Glu Lys Arg Met
            100                 105                 110
Asn Gly Asp Ile Gln Leu Arg His Asp Ser Lys Ala Arg Lys Glu Arg
        115                 120                 125
Tyr Asn Glu Ala Glu Lys Trp Val Leu Val Gly Gly Leu Glu Leu Ser
    130                 135                 140
Lys Thr Ala Thr Leu Arg Pro Glu Thr Glu Ser Gly Phe Thr Arg Val
145                 150                 155                 160
Leu Tyr Gly Pro Asp Asn Gln Phe Glu Ala Val Ile Arg His Ala Pro
                165                 170                 175
Phe Ser Ala Asp Phe Lys Arg Asp Gly Gln Thr His Val Gln Leu Asn
            180                 185                 190
Asn Lys Gly Tyr Leu Asn Met Glu His Trp Arg Pro Lys Val Glu Val
        195                 200                 205
Glu Gly Glu Gly Glu Gln Gln Thr Gln Glu Asp Glu Ser Thr Trp Trp
    210                 215                 220
Asp Glu Ser Phe Gly Gly Asn Thr Asp Thr Lys Pro Arg Gly Pro Glu
225                 230                 235                 240
Ser Val Gly Leu Asp Ile Thr Phe Pro Gly Tyr Lys His Val Phe Gly
                245                 250                 255
Ile Pro Glu His Ala Asp Ser Leu Ser Leu Lys Glu Thr Arg Gly Gly
            260                 265                 270
Glu Gly Asn His Glu Glu Pro Tyr Arg Met Tyr Asn Ala Asp Val Phe
        275                 280                 285
Glu Tyr Glu Leu Ser Ser Pro Met Thr Leu Tyr Gly Ala Ile Pro Phe
    290                 295                 300
Met Gln Ala His Arg Lys Asp Ser Thr Val Gly Val Phe Trp Leu Asn
305                 310                 315                 320
Ala Ala Glu Thr Trp Val Asp Ile Val Lys Ser Thr Ser Ser Pro Asn
                325                 330                 335
Pro Leu Ala Leu Gly Val Gly Ala Thr Thr Asp Thr Gln Ser His Trp
            340                 345                 350
Phe Ser Glu Ser Gly Gln Leu Asp Val Phe Val Phe Leu Gly Pro Thr

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        355                 360                 365
Pro Gln Glu Ile Ser Lys Thr Tyr Gly Glu Leu Thr Gly Tyr Thr Gln
    370                 375                 380
Leu Pro Gln His Phe Ala Ile Ala Tyr His Gln Cys Arg Trp Asn Tyr
385                 390                 395                 400
Ile Thr Asp Glu Asp Val Lys Glu Val Asp Arg Asn Phe Asp Lys Tyr
                405                 410                 415
Gln Ile Pro Tyr Asp Val Ile Trp Leu Asp Ile Glu Tyr Thr Asp Asp
            420                 425                 430
Arg Lys Tyr Phe Thr Trp Asp Pro Leu Ser Phe Pro Asp Pro Ile Ser
        435                 440                 445
Met Glu Glu Gln Leu Asp Glu Ser Glu Arg Lys Leu Val Val Ile Ile
    450                 455                 460
Asp Pro His Ile Lys Asn Gln Asp Lys Tyr Ser Ile Val Gln Glu Met
465                 470                 475                 480
Lys Ser Lys Asp Leu Ala Thr Lys Asn Lys Asp Gly Glu Ile Tyr Asp
                485                 490                 495
Gly Trp Cys Trp Pro Gly Ser Ser His Trp Ile Asp Thr Phe Asn Pro
            500                 505                 510
Ala Ala Ile Lys Trp Trp Val Ser Leu Phe Lys Phe Asp Lys Phe Lys
        515                 520                 525
Gly Thr Leu Ser Asn Val Phe Ile Trp Asn Asp Met Asn Glu Pro Ser
    530                 535                 540
Val Phe Asn Gly Pro Glu Thr Thr Met Pro Lys Asp Asn Leu His His
545                 550                 555                 560
Gly Asn Trp Glu His Arg Asp Ile His Asn Val His Gly Ile Thr Leu
                565                 570                 575
Val Asn Ala Thr Tyr Asp Ala Leu Leu Glu Arg Lys Lys Gly Glu Ile
            580                 585                 590
Arg Arg Pro Phe Ile Leu Thr Arg Ser Tyr Tyr Ala Gly Ala Gln Arg
        595                 600                 605
Met Ser Ala Met Trp Thr Gly Asp Asn Gln Ala Thr Trp Glu His Leu
    610                 615                 620
Ala Ala Ser Ile Pro Met Val Leu Asn Asn Gly Ile Ala Gly Phe Pro
625                 630                 635                 640
Phe Ala Gly Ala Asp Val Gly Gly Phe Phe Gln Asn Pro Ser Lys Glu
                645                 650                 655
Leu Leu Thr Arg Trp Tyr Gln Ala Gly Ile Trp Tyr Pro Phe Phe Arg
            660                 665                 670
Ala His Ala His Ile Asp Thr Arg Arg Arg Glu Pro Tyr Leu Ile Ala
        675                 680                 685
Glu Pro His Arg Ser Ile Ile Ser Gln Ala Ile Arg Leu Arg Tyr Gln
    690                 695                 700
Leu Leu Pro Ala Trp Tyr Thr Ala Phe His Glu Ala Ser Val Asn Gly
705                 710                 715                 720
Met Pro Ile Val Arg Pro Gln Tyr Tyr Ala His Pro Trp Asp Glu Ala
                725                 730                 735
Gly Phe Ala Ile Asp Asp Gln Leu Tyr Leu Gly Ser Thr Gly Leu Leu
            740                 745                 750
Ala Lys Pro Val Val Ser Glu Glu Ala Thr Thr Ala Asp Ile Tyr Leu
        755                 760                 765
Ala Asp Asp Glu Lys Tyr Tyr Asp Tyr Phe Asp Tyr Thr Val Tyr Gln
    770                 775                 780
Gly Ala Gly Lys Arg His Thr Val Pro Ala Pro Met Glu Thr Val Pro
```

785 790 795 800
Leu Leu Met Gln Gly Gly His Val Ile Pro Arg Lys Asp Arg Pro Arg
805 810 815
Arg Ser Ser Ala Leu Met Arg Trp Asp Pro Tyr Thr Leu Val Val Val
820 825 830
Leu Asp Lys Asn Gly Gln Ala Asp Gly Ser Leu Tyr Val Asp Asp Gly
835 840 845
Glu Thr Phe Asp Tyr Glu Arg Gly Ala Tyr Ile His Arg Arg Phe Arg
850 855 860
Phe Gln Glu Ser Ala Leu Val Ser Glu Asp Val Gly Thr Lys Gly Pro
865 870 875 880
Lys Thr Ala Glu Tyr Leu Lys Thr Met Ala Asn Val Arg Val Glu Arg
885 890 895
Val Val Val Val Asp Pro Pro Lys Glu Trp Gln Gly Lys Thr Ser Val
900 905 910
Thr Val Ile Glu Asp Gly Ala Ser Ala Ala Ser Thr Ala Ser Met Gln
915 920 925
Tyr His Ser Gln Pro Asp Gly Lys Ala Ala Tyr Ala Val Val Lys Asn
930 935 940
Pro Asn Val Gly Ile Gly Lys Thr Trp Arg Ile Glu Phe
945 950 955

<210> 209
<211> 682
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK96888.1

<400> 209
Met Pro Leu Arg Pro Pro Ala Ser Pro Leu Ser Leu Glu Thr Ile Ser
1 5 10 15
Pro Ser Pro Pro Asp Leu Asp Ser Asp Pro Leu Ile Ala Ser Asp Asp
20 25 30
Asp Leu Asp Asp Asp Asp Arg Ala Ala Arg Asp Gln Arg Ile Glu Lys
35 40 45
Leu Ala Gln Ala Tyr Cys His Gly Thr Pro Leu Phe Ile Leu Ser Ala
50 55 60
Ser Leu Arg Gly Pro Phe Glu Asn Gly Trp Ala Asn Pro Trp Lys Lys
65 70 75 80
Asp Arg Arg Thr Thr Gly Gly Gly His Val Gly Ile His Ser Glu His
85 90 95
Ser Glu Arg Pro Ile Ile Pro Glu Thr Ile Pro Gln Lys Arg Pro Leu
100 105 110
Tyr Arg Glu Ser Leu Gly Ile Ser Arg Ser Lys Ser Ala Val Pro Leu
115 120 125
Ser Asp Pro Thr Tyr Ser Ser Lys Lys Arg Glu Ser Gln Gly Gly Thr
130 135 140
Ala Gly Glu Pro Ser Ser Lys Arg Pro Arg Asp Ser Arg Gly Arg Thr
145 150 155 160
Ser Ser Ser Asn Asn Thr Pro Lys Pro Ile Ala Leu His Lys Arg Thr
165 170 175

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Ile Glu Thr Ser Gly His Ser Asp Ala Leu Thr Pro Phe Gln His Thr
            180                 185                 190
Glu Gln Ser Trp Leu Lys Arg Asp Arg Ala Glu Ile Asn Phe Arg Lys
        195                 200                 205
Val Asp Pro Pro Thr Ser Pro Thr Thr Thr Val Ser Ser Arg His Arg
    210                 215                 220
Glu Gly Gly His Tyr Thr Ile Gln Val Pro Gly Thr Asp Tyr Arg Val
225                 230                 235                 240
Thr Thr Lys Asn Ile Leu Arg Ala Arg Thr Asp Ser Arg Asp Gly Thr
                245                 250                 255
Thr Phe Asp Ser His Val Pro Asp Ser Val Lys Ala Gln Leu Thr Ser
            260                 265                 270
Arg His Pro Gly Val Arg Pro Glu Thr Glu Asp His Glu Asn Ser Ile
        275                 280                 285
Cys Val Leu Ser Ser Thr Ser His Leu Ser Lys Phe Glu Phe Arg Arg
    290                 295                 300
Arg Lys Arg Ser Ala Asp Pro Glu His Gly Thr Thr Ser Pro Val Pro
305                 310                 315                 320
Met Gln Leu Glu Asn Glu Gln Val Ser His Gln Thr Thr Val Val Glu
                325                 330                 335
Asp Ser Arg Val Ser Ser Gln Pro Ala Pro Val Pro Pro Asn Thr Thr
            340                 345                 350
Ser Met Gln Ala Ile Glu Val Asp Met Gln Val Asn Glu Asp Asn Ser
        355                 360                 365
His His Pro Asn Val Ser Glu Arg Ser Gly Thr Val Asp His Gln Gly
    370                 375                 380
Asn Ser Gln Ser Arg Lys Val Ser Ser Thr Thr Thr Ala Glu Gly Val
385                 390                 395                 400
Asn Ile Ser Asp Lys Tyr Pro Ser Ala Gln Arg Val Ser Val Asn Pro
                405                 410                 415
Ala Leu Ala Glu Asn Val Thr Ser Leu Gln Thr Ile Ser Ala Val Lys
            420                 425                 430
Pro Asn Ser Glu Cys Asp Asn Asp Thr Ile Pro Asp Leu His Phe Asn
        435                 440                 445
Thr Gln Ala Ala Leu Leu His Ala Gln Lys Ser Phe Gln Asn Asp Leu
    450                 455                 460
Glu Ser Gln Val Pro Asn Pro Gly Glu Thr His Asn Gln Pro Ser Ser
465                 470                 475                 480
Pro Ala Asn Asp Ile Thr Pro Phe His Arg Met Asn Thr Ser Arg Ile
                485                 490                 495
Gly Lys Tyr Ser Arg Ala Ile His Pro Gly Thr Ala His Met Pro Met
            500                 505                 510
Ser Thr Gln Cys Ile Ile Asp Ala Val Thr Pro Phe Thr Phe Ser Thr
        515                 520                 525
Glu Lys Lys Ala Arg Ser Arg Phe Ile Ser Pro Gln Met Pro Ser Ser
    530                 535                 540
Ser Arg Ile Asp Arg Gly Thr Ala Thr Pro Asn Thr Gly Ser Pro Leu
545                 550                 555                 560
Ser Ser Glu Ser Glu Asp Glu Asp Glu Asp Glu Asp Pro Thr Ile Leu
                565                 570                 575
Pro His Lys Ser Pro Ala Ala Gln Gln Gln Thr Pro Asp Asp Thr Gln
            580                 585                 590
Glu Gly Ser Ala Leu Pro Met Ala Leu Ser His Ser His Pro Thr Thr
        595                 600                 605
```

```
Val Gln Asp Gly Gln Gly Val Ala Pro Gly Pro Asp Ser Phe Asn Leu
    610                 615                 620
Ser Gln Ala Ile Ala Asp Ala Gly Ser Trp Leu Gln Gln Ser Phe Asp
625                 630                 635                 640
Ile Asn His Glu Ile Gln Gln Cys Arg Ser Ser Ala Lys Ser Arg Pro
                645                 650                 655
Ser Ser Ser Ala Gly Ile Ser Arg Ser Ala Ser Gly Thr Ile Leu Gly
            660                 665                 670
His Ser Thr Leu Asp Ser Val Leu Leu Cys
        675                 680


<210> 210
<211> 830
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK45960.1


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

```
Leu Glu Glu Gly Gly Pro Gly Met Glu Met Arg His Arg Gly Gly Gly
            260                 265                 270
Gly Pro Pro Ala Glu Gly Leu Leu Gln Lys Glu Gly Asp Trp Asp Gly
        275                 280                 285
Ser Thr Lys Gly Ser Ser Thr Ser Ala Arg Pro Ser Phe Trp Lys Arg
    290                 295                 300
Tyr His Lys Thr Phe Ile Phe Phe Ala Ile Leu Ile Val Leu Ala Ala
305                 310                 315                 320
Ile Ala Ile Pro Val Gly Ile Ile Glu Ala Arg Arg Leu His Gly Thr
                325                 330                 335
Ser Gly Gly Asp Asn Ser Ser Asn Ser Asn Leu Lys Gly Ile Ser Arg
            340                 345                 350
Asp Ser Ile Pro Ala Tyr Ala Arg Gly Thr Tyr Leu Asp Pro Phe Thr
        355                 360                 365
Trp Tyr Asp Thr Thr Asp Phe Asn Val Thr Phe Thr Asn Ala Thr Val
    370                 375                 380
Gly Gly Leu Ser Ile Met Gly Leu Asn Ser Thr Trp Asn Asp Ser Ala
385                 390                 395                 400
Gln Ala Asn Glu Asn Val Pro Pro Leu Asn Glu Lys Phe Pro Tyr Gly
                405                 410                 415
Ser Gln Pro Ile Arg Gly Val Asn Leu Gly Gly Trp Leu Ser Ile Glu
            420                 425                 430
Pro Phe Ile Val Pro Ser Leu Phe Asp Thr Tyr Thr Ser Ser Glu Gly
        435                 440                 445
Ile Ile Asp Glu Trp Thr Leu Ser Glu Lys Leu Gly Asp Ser Ala Ala
    450                 455                 460
Ser Val Ile Glu Lys His Tyr Ala Thr Phe Ile Thr Glu Gln Asp Phe
465                 470                 475                 480
Ala Asp Ile Arg Asp Ala Gly Leu Asp His Val Arg Ile Gln Phe Ser
                485                 490                 495
Tyr Trp Ala Ile Lys Thr Tyr Asp Gly Asp Pro Tyr Val Pro Lys Ile
            500                 505                 510
Ala Trp Arg Tyr Leu Leu Arg Ala Ile Glu Tyr Cys Arg Lys Tyr Gly
        515                 520                 525
Leu Arg Val Asn Leu Asp Pro His Gly Ile Pro Gly Ser Gln Asn Gly
    530                 535                 540
Trp Asn His Ser Gly Arg Gln Gly Thr Ile Gly Trp Leu Asn Gly Thr
545                 550                 555                 560
Asp Gly Glu Leu Asn Arg Gln Arg Ser Leu Glu Met His Asp Gln Leu
                565                 570                 575
Ser Gln Phe Phe Ala Gln Asp Arg Tyr Lys Asn Val Val Thr Ile Tyr
            580                 585                 590
Gly Leu Val Asn Glu Pro Leu Met Leu Ser Leu Pro Val Glu Lys Val
        595                 600                 605
Leu Asn Trp Thr Thr Glu Ala Thr Asn Leu Val Gln Lys Asn Gly Ile
    610                 615                 620
Lys Ala Trp Val Thr Val His Asp Gly Phe Leu Asn Leu Asp Lys Trp
625                 630                 635                 640
Asp Lys Met Leu Lys Thr Arg Pro Ser Asn Met Met Leu Asp Thr His
                645                 650                 655
Gln Tyr Thr Val Phe Asn Thr Gly Glu Ile Val Leu Asn His Thr Arg
            660                 665                 670
Arg Val Glu Leu Ile Cys Glu Ser Trp Tyr Ser Met Ile Gln Gln Ile
        675                 680                 685
```

```
Asn Ile Thr Ser Thr Gly Trp Gly Pro Thr Ile Cys Gly Glu Trp Ser
    690                 695                 700
Gln Ala Asp Thr Asp Cys Ala Gln Tyr Val Asn Asn Val Gly Arg Gly
705                 710                 715                 720
Thr Arg Trp Glu Gly Thr Phe Ser Leu Thr Asp Ser Thr Gln Tyr Cys
                725                 730                 735
Pro Thr Ala Ser Glu Gly Thr Cys Ser Cys Thr Gln Ala Asn Ala Val
            740                 745                 750
Pro Gly Val Tyr Ser Glu Gly Tyr Lys Thr Phe Leu Gln Thr Tyr Ala
        755                 760                 765
Glu Ala Gln Met Ser Ala Phe Glu Ser Ala Met Gly Trp Phe Tyr Trp
    770                 775                 780
Thr Trp Ala Thr Glu Ser Ala Ala Gln Trp Ser Tyr Arg Thr Ala Trp
785                 790                 795                 800
Lys Asn Gly Tyr Met Pro Lys Lys Ala Tyr Ser Pro Ser Phe Lys Cys
                805                 810                 815
Gly Asp Thr Ile Pro Ser Phe Gly Asn Leu Pro Glu Tyr Tyr
            820                 825                 830
```

<210> 211
<211> 336
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK40856.1

<400> 211

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

```
        195                 200                 205
Pro Ser Glu Glu Pro Met His Thr Ala Thr Ser Thr Leu Arg Pro Glu
    210                 215                 220
Pro Ser Ala Ala Ala Pro Val Ser Pro Thr Glu Thr Ser Gln Ser Thr
225                 230                 235                 240
Ser Thr Gly Ser Ser Thr Lys Arg Thr Ser Leu Tyr Asn Pro Leu Pro
                245                 250                 255
Pro Pro Pro Pro Pro Arg Arg Ser Arg Gly Ser Ser Asn His Ser Ile
            260                 265                 270
Asp Ser Ser Gly Gln Ser Leu Arg Ser Gly Lys Pro Ala Asp Glu Thr
        275                 280                 285
Thr Ala Ala Pro Ala Ala Pro Ala Ala Gln Asp Glu Phe Val Pro His
    290                 295                 300
Pro Ser Asn Ala His Asp Ile Leu Ala Asp Leu Ser Arg Leu Gln Lys
305                 310                 315                 320
Glu Val Asp Asp Leu Arg Gly His Tyr Glu Ser Arg Lys Ala Ser Gln
                325                 330                 335


<210> 212
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK40944.1


<400> 212
Met Tyr Ile Ser Lys Val Leu Leu Val Thr Cys Ala Ala Phe Ala Pro
 1               5                  10                  15
Phe Ala Ser Ala Ala Val Gln Ala Lys Pro Thr Asp Thr Pro Val Pro
            20                  25                  30
Val Ser Ser Thr His Val Ala Ser Ser Pro Leu Ala Pro Thr Pro Thr
        35                  40                  45
Pro Val Ser Pro Ser Pro Leu His Thr Ala Ser Ser Ser Val Ile Ile
    50                  55                  60
Ser Ser Ser Ser Ser Ser Val Arg Phe His Pro Ser Ser Ser Ala Ser
65                  70                  75                  80
Pro Ser His Met Ala Ser Ser Ser Arg Arg Ile Ser Ser Ser Ala Ile
                85                  90                  95
Ser Ser Ser Ala Ile Ala Ser Ser Ser Ala Ser Phe Thr Arg Ser Tyr
            100                 105                 110
Ile Thr Lys Ala Ser Ala Arg Pro Thr Thr Thr Thr Ser Thr Asp Ala
        115                 120                 125
Asp Ser Lys Ser Asn Ser Asn Ser Gly Ser Asp Ser Glu Ser Ala Thr
    130                 135                 140
Ala Ala Ala Ala Ser Ala Thr His Ser Gly Ala Ala Ala Pro Ala Val
145                 150                 155                 160
Gln Leu Ser Gly Gly Met Ala Ala Gly Val Leu Ala Ala Ala Gly Phe
                165                 170                 175
Ile Met Leu
```

<210> 213
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK41060.1

<400> 213
Met Pro Arg Ser Thr Val Asp Gln Thr Ser Ser Ala Glu Ala Pro Tyr
 1               5                  10                  15
Ser Gly Pro Arg Lys Leu Val Leu Cys Leu Asp Gly Thr Gly Asn Gln
            20                  25                  30
Phe Met Gly Phe Glu Arg Asp Ser Asn Ile Val Lys Ile Tyr Gln Met
        35                  40                  45
Leu Glu Lys Asn Thr Pro Gly Gln Phe His Tyr Tyr Gln Pro Gly Ile
    50                  55                  60
Gly Thr Tyr Val Glu Gly Gln Ser Ser Ser Ser Gly Leu Leu Arg Tyr
65                  70                  75                  80
Pro Arg Lys Leu Gln Ser Asn Ile Ile Thr Thr Ile Asp Gln Gly Val
                85                  90                  95
Gly Thr Thr Phe Glu Ser His Val Leu Ala Ala Tyr Arg Phe Ile Met
            100                 105                 110
Arg Tyr Tyr Ser Pro Gly Asp His Ile Tyr Ile Phe Gly Phe Ser Arg
        115                 120                 125
Gly Ala Tyr Thr Ala Arg Phe Leu Ala Glu Met Ile His Glu Leu Gly
    130                 135                 140
Leu Leu Ser Gln Gly Asn Glu Glu Met Ile His Phe Ala Trp Glu Thr
145                 150                 155                 160
Phe Ser Asn Phe Gln Gln Ala Arg Gly Lys Thr Asp Arg Thr Ala Lys
                165                 170                 175
Asp Glu Ala Leu Ile Ser Tyr Met Lys Lys Phe Asn Thr Thr Phe Cys
            180                 185                 190
Arg Pro Gln Val Gln Ile His Phe Leu Gly Leu Phe Asp Cys Val Asn
        195                 200                 205
Ser Val Gly Gln Phe Glu Ile Pro Phe His Arg Lys Ser His Gln Tyr
    210                 215                 220
Leu Val Ser Pro Ala Ala Arg His Ile Arg His Ala Val Ser Ile His
225                 230                 235                 240
Glu Arg Arg Leu Lys Phe Lys Pro Ala Leu Val Leu Leu Asp Lys Thr
                245                 250                 255
Lys Pro Val Asp Leu Lys Glu Val Trp Phe Ala Gly Asn His Gly Asp
            260                 265                 270
Val Gly Gly Gly Trp Ser Leu Ala Pro Gly Gln Phe His Leu Leu Ser
        275                 280                 285
Asp Thr Pro Leu Asn Trp Met Leu Gln Glu Val Leu His Leu Glu Asn
    290                 295                 300
Ser Glu Ser Lys Leu Ser Phe His Thr Leu Asn Val Ala Asp Val Val
305                 310                 315                 320
Glu Arg Glu Asn Ala Phe Pro Gly Lys Glu Glu Pro Gly Thr Thr Ala
                325                 330                 335
Tyr Asp Val Arg Lys Arg Thr Asn Gln Pro His Asp Met Leu Met Phe
            340                 345                 350

```
Asn Arg Gly Ala Thr Phe Leu Met Val Ile Phe Trp Trp Ile Leu Glu
        355                 360                 365
Ile Leu Pro Leu Phe Thr Arg Leu Glu Leu Glu His Gly Lys Trp Val
    370                 375                 380
Pro Arg Gln Trp Pro Pro Asn Met Gly Ala Pro Arg Asp Ile Pro Glu
385                 390                 395                 400
Asp Ala Val Ile His Gln Ser Val His Glu Met Val Arg Ala Gly Ile
                405                 410                 415
Leu Asp Pro Lys Ser Ile Pro Pro Arg Gly Gly Asn Asn Ser His Leu
            420                 425                 430
Pro Ser Thr Ala Arg Ile Thr Gly Ala Trp Lys Ala Met Arg Lys Asn
        435                 440                 445
Gln Glu Lys Gln Ile Ser Ser Leu Leu Gln Lys Lys Pro Ala Gly Ala
    450                 455                 460
Leu Arg Lys Glu Phe Asp Gly Lys Ala Asp
465                 470


<210> 214
<211> 694
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK41144.1

<400> 214
Met Asp Pro Ala Asn Glu Tyr Cys Gly Leu Glu Asp Tyr Gly Leu Val
 1               5                  10                  15
Gly Asp Met His Thr Cys Ala Leu Val Ser Lys Asn Gly Ser Val Asp
            20                  25                  30
Ser Met Cys Trp Pro Val Phe Asp Ser Pro Ser Ile Phe Cys Arg Ile
        35                  40                  45
Leu Asp Lys Glu Lys Gly Gly His Phe Ser Ile Thr Pro Asp Arg Arg
    50                  55                  60
Leu Lys Asn Pro Leu Ser Lys Gln Arg Tyr Arg Pro Tyr Thr Asn Met
65                  70                  75                  80
Leu Glu Thr Arg Trp Ile His Glu Glu Gly Val Met Asn Ile Leu Asp
                85                  90                  95
Tyr Phe Pro Ile Ala Lys Pro Lys Pro His Val Ala Cys Arg Ser Gly
            100                 105                 110
Met Val Arg Lys Ala Glu Cys Val Arg Gly Glu Met Glu Ile Glu Ile
        115                 120                 125
Glu Leu Phe Pro Ala Phe Asn Tyr Ala Arg Asp Ser His Val Ala Gln
    130                 135                 140
Gln Ser Ser Ala Ser Asp Asp Ala Ile Gln Val Tyr His Phe Gln Ala
145                 150                 155                 160
Glu Ser Gln Asn Leu Val Val Ser Val Leu Gly Asp Arg Gly Asp Ile
                165                 170                 175
Ser Gly Asp Asp Ser Asp Leu Ser Ile Glu Phe Glu Leu Ser Asp Arg
            180                 185                 190
Pro Gly His Leu Gly Pro Gly Leu Val Gly Lys Val Thr Leu Lys Glu
        195                 200                 205
Gly Gln Ser Ile Thr Met Leu Leu His Asp Gln Glu Ser Ile Thr Cys
```

```
    210                 215                 220
Asn Val Glu Asp Leu Ala Pro Tyr Leu Gln Gln Ile Glu Arg Thr Thr
225                 230                 235                 240
Gly Asp Phe Trp Ser Asp Trp Thr Ser Lys Cys Thr Phe Arg Gly His
                245                 250                 255
Tyr Arg Glu Gln Val Glu Arg Ser Leu Leu Val Leu Lys Leu Leu Thr
            260                 265                 270
Tyr Lys Pro Thr Gly Ala Ile Val Ala Ala Pro Thr Phe Ser Leu Pro
        275                 280                 285
Glu His Ile Gly Gly Ser Arg Asn Trp Asp Tyr Arg Tyr Ser Trp Val
    290                 295                 300
Arg Asp Ala Ala Phe Thr Val Tyr Val Phe Leu Lys Asn Gly Tyr Pro
305                 310                 315                 320
Glu Glu Ala Glu Ser Tyr Ile Asn Phe Ile Phe Glu Arg Ile Phe Pro
                325                 330                 335
Pro Met Asp Lys Asn Pro Lys Pro Gly Glu Pro Phe Leu Pro Ile Met
            340                 345                 350
Ile Thr Ile His Gly Glu Arg Glu Ile Pro Glu Met Glu Leu Glu His
        355                 360                 365
Leu Glu Gly Tyr Arg Gly Ser Arg Pro Val Arg Ile Gly Asn Gly Ala
    370                 375                 380
Ala Thr His Ile Gln Leu Asp Ile Tyr Gly Glu Leu Met Asp Ser Ile
385                 390                 395                 400
Tyr Leu Tyr Asn Lys His Ala Ala Asp Ile Ser Tyr Asp Gln Trp Arg
                405                 410                 415
Ala Ile Arg Arg Met Ile Asp Phe Val Ile Gln Ile Arg His Gln Pro
            420                 425                 430
Asp Gln Ser Ile Trp Glu Val Arg Gly Pro Pro Gln Asn Phe Val Tyr
        435                 440                 445
Ser Lys Ile Met Leu Trp Val Ala Leu Asp Arg Gly Leu Arg Leu Ala
    450                 455                 460
Glu Lys Arg Ser Asn Leu Pro Cys Pro Asp Arg Ala Arg Trp Met His
465                 470                 475                 480
Glu Arg Asp Ala Leu Tyr Asp Glu Ile Met Thr Lys Gly Tyr Asn Ser
                485                 490                 495
Glu Lys Gly Phe Phe Cys Met Ser Tyr Glu Asn Gln Asp Ala Met Asp
            500                 505                 510
Ala Ala Val Leu Ile Ala Pro Leu Val Phe Phe Val Ala Pro Asn Asp
        515                 520                 525
Pro Arg Leu Leu Ser Thr Ile Gln Lys Ile Thr Glu Val Pro Ala Lys
    530                 535                 540
Gly Gly Leu Ser Val Ala Asn Met Val Ser Arg Tyr Asp Thr Gly Lys
545                 550                 555                 560
Val Asp Asp Gly Val Gly Gly Asn Glu Gly Ala Phe Leu Met Val Thr
                565                 570                 575
Phe Trp Leu Val Glu Ala Met Met Arg Gln Leu Arg Lys Thr Ala Thr
            580                 585                 590
Ser Gln Phe Asp Ser Ile Leu Ser Phe Ala Asn His Leu Gly Met Phe
        595                 600                 605
Ser Glu Glu Val Ala Thr Ser Gly Glu Gln Ile Gly Asn Met Pro Gln
    610                 615                 620
Ala Phe Ser His Leu Ala Cys Gln Tyr Met Phe Asn Val Ile Val Lys
625                 630                 635                 640
Arg Lys Ser Leu Glu Thr Cys Glu Tyr His Ile Ala Leu Asp Val Glu
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```
                645                 650                 655
Lys Arg Ile Leu Gln Ile Cys Tyr Asn Glu Asp Ile Ser Ile Phe Asn
            660                 665                 670
Lys Trp Leu Ser Ile Ser Gly Phe Thr Tyr Arg Gln Ser Phe Thr Ile
        675                 680                 685
Ser Gln Leu Val Val Val
    690


<210> 215
<211> 946
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK46428.1

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

```
Asp Arg Arg Lys Ser Ile Pro Leu Pro Gly Thr Thr Pro Leu Ala Thr
    290                 295                 300
Thr Ser His Arg Ser Leu Ala Lys Pro Arg Thr Thr Ala Asp Lys Gly
305                 310                 315                 320
Leu Arg Arg Ser Gly Val Tyr Ser Asn Arg Arg Asp Ser Val Pro Val
                325                 330                 335
Glu Asp Glu Asp Ala Lys Leu Ile Met Glu Ser Leu Tyr Ser Lys Arg
            340                 345                 350
Ser Ser Gln Val Pro Phe Met Ala Asp His Gly Ala Ser Asp Ala Glu
        355                 360                 365
Asn Asp Gly Pro Leu Phe Asp Gln Pro Gly Ala Asn Ser Ser His Pro
    370                 375                 380
Asp Arg Arg Glu Ser Ile Gln Lys Asp Ser Leu Ser Ser Pro Val Leu
385                 390                 395                 400
Ser Asp His Leu Asp Pro Ser Ile Ala Ala His Ala Arg Leu Ala Ala
                405                 410                 415
Gln Tyr Glu Lys Ala Gln Pro Val Thr Val Ser Ser Thr Asn Lys Val
            420                 425                 430
Met Thr Pro Ser Gln Phe Glu His Tyr Arg Gln Gln Gln Glu Leu Arg
        435                 440                 445
Arg Ser Asn Ser Asp Ala Ser Lys Ser Glu Asn Ser Ala Glu Ser Asp
    450                 455                 460
Tyr Asp Asp Asp Asp Glu Val Glu Lys Asp Arg Glu Ala Glu Arg Gln
465                 470                 475                 480
Arg Arg Lys Gln Glu Ala His Leu Ser Val Tyr Arg Gln Gln Met Met
                485                 490                 495
Lys Val Thr Gly Gln Glu Ser Pro Ala Pro Ala Met Arg Thr Glu Leu
            500                 505                 510
Asp Gln Ala Ser Lys Ser Ala Pro Asn Leu Leu Gln Pro Gly Thr Thr
        515                 520                 525
Leu Gly Ser Gly Lys Ser Ser Asp Gly Asp Asp Asp Glu Glu Ile Pro
    530                 535                 540
Leu Gly Ile Leu Ala Ala His Gly Phe Pro Asn Arg Asn Arg Pro Pro
545                 550                 555                 560
Ser Arg Leu Ala Pro Ser Ser Ser Ile Pro Asn Leu Arg Ala Ser Phe
                565                 570                 575
Gln Gln Pro Tyr Leu Ser Ser Pro Ser Pro Ala Ser Val Ala Glu Arg
            580                 585                 590
Asp Pro Asn Asn Arg Gly Ser Leu Pro Val Phe Ala Arg Asn Leu Pro
        595                 600                 605
Arg Asp Pro Tyr Phe Gly Ala Ser Leu Val Asn Gln Ser Asn Arg Glu
    610                 615                 620
Ser Leu Ala Leu Gly Gly Gly Ala Ser Val His Gly Gly Pro Ser Pro
625                 630                 635                 640
Ala Leu Pro Pro Gly Gly Leu Val Gly Val Ile Ala Thr Glu Glu Arg
                645                 650                 655
Ala Arg Ala Met Arg Arg Gly Ser Pro Asn Thr Gln Ala Met Tyr Asp
            660                 665                 670
Tyr Gln Gly Gly Met Pro Val Pro Pro Val His Pro Arg Gly Ile Pro
        675                 680                 685
Arg Pro Tyr Thr Met Met Ser Leu Ser Ser Pro Asn Ala Gly Gly Val
    690                 695                 700
Gln Pro Thr Ile Ser Ala Thr Glu Gln Ala Gln Ile Glu Leu Ser Gln
705                 710                 715                 720
```

Gln Met Thr Gln Met Val Gln Met Gln Met Gln Trp Met Gln Gln Met
725 730 735
Ile His Met Gln Gly Gly Gln Ser Thr Gln Leu Met Pro Pro Gly Gly
740 745 750
Pro Pro Pro Thr Leu Gly Ala Asn Leu Asn Ala Arg Pro Ser Ser Met
755 760 765
Pro Ser Ala Gly Asn Met Asn Asn Pro His Ala Gly Tyr Ser Gly Asp
770 775 780
Gln Arg Thr Leu Ser Met Leu Asp Pro Asn Val Ser Ser Arg Leu Asn
785 790 795 800
Ser Ala Ala Met Pro His Val Ser Gly Gly Leu Arg Pro Ser Thr Pro
805 810 815
Ala Gly Gln Gly Tyr Ala Pro Ser Ile Ala Pro Ser Glu Arg Ser Asn
820 825 830
Val Gly Leu Ala Pro Arg Tyr Arg Pro Val Ser Thr Ile Gln Pro Asp
835 840 845
Leu Gly Asn Val Gly Ser Pro Ser Ile Pro Lys Ser Trp Ser Asp Glu
850 855 860
Asn Arg Lys Ser Ser Leu Ser Ala Ala Val Pro Ala Ala Pro Gln Ala
865 870 875 880
Ser Gln Met Ser His Arg Pro Met Pro Ser Asn Ser Lys Pro Ile Arg
885 890 895
Ala Ser Lys Leu Asn Val Gly Ala Asp Gln Asp Asp Glu Asp Asp Asp
900 905 910
Glu Gly Trp Ala Glu Met Met Lys Lys Arg Glu Asn Lys Arg Asn Asn
915 920 925
Trp Lys Met Lys Lys Glu Thr Ser Ser Phe Gly Asp Leu Leu Asn Ala
930 935 940
Val His
945

<210> 216
<211> 1250
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK41498.1

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

```
            100                 105                 110
Gln Ser Pro Pro Pro Leu Pro Pro Arg Pro Ser Ser Thr Ala Gln Ser
        115                 120                 125
Pro Gln Ala Gln Ser Pro Val Val Ser Pro Leu Asp Pro Asn Lys Pro
    130                 135                 140
Leu Pro Ala Ala Pro Gly Trp Ala Thr Gln Ser Ala Asp Asn Thr Ser
145                 150                 155                 160
Tyr Gln Gln Trp Pro Ser Asn Pro Pro Tyr Ala Pro Gln Gln Ser Val
                165                 170                 175
Ser Ala Ser Ser Leu Gln Pro Pro Pro Pro Pro Pro Ala Ile Ser Thr
            180                 185                 190
Gly Tyr Gln Ser Ser Ser Ala Gln Gln Ser Asn Pro Trp Gln Gln Pro
        195                 200                 205
Pro Ala Val Pro Pro Pro Pro Tyr Ser Gly Val Pro Leu Gly Gln Tyr
    210                 215                 220
Gln Asp Ser Ser Val Gln Gln Pro Ala Thr Leu Pro Ser Asn Gln Gln
225                 230                 235                 240
Ile Thr Gly His Asn Ala Pro Asn Pro Ala Ile Pro Gln Ala Pro Ser
                245                 250                 255
Pro Lys Pro Ser Thr Gly Leu His Tyr Glu Ser Gln Pro Leu Pro Gly
            260                 265                 270
Pro Pro Gln Ala Pro Val Ala Ala Thr Leu Ser Pro Thr His Gly Thr
        275                 280                 285
Pro Pro Val Val Pro Pro Pro Val Pro Pro Lys Thr Ser Pro Ile Thr
    290                 295                 300
Val Pro Thr Ser Ala Ser Val Leu Ala Thr Gly Gly Pro Ser Asp Trp
305                 310                 315                 320
Glu His Leu Ser Pro Ile Pro Gly Ser Ile Asp Asp Leu Gly Ala Phe
                325                 330                 335
Gly Ser Arg Pro Gln Asp Gly Ser Ser Ser Glu Pro Leu Ser Gln Ala
            340                 345                 350
Ser Gln Ser Arg Pro Pro Asn Ile Gly Glu Pro Val Arg Lys Asp Glu
        355                 360                 365
Ser Val Ser Pro Ile Thr Pro Pro Asn Asn Ala Pro Gln Met Thr Ser
    370                 375                 380
Gln Thr Glu Gly Pro Leu Ala Ser Gln Thr Val Val Arg Gly Asn Pro
385                 390                 395                 400
His Gln Pro Val Arg Met Gly Ser Thr Gly Ser Val Ser Ser Asp Ile
                405                 410                 415
Ser Thr Ser Glu Thr Pro Glu Ser Ile Asp Gly Ile Ile Glu Ala Trp
            420                 425                 430
Asn Arg Pro Ile Ser Ser Gln Pro Ser Ala Glu Gln Asn Pro Gln Ser
        435                 440                 445
Ser Ala Ser Gly Val Arg Ala Gly Ile Leu Pro Pro Ser Arg Lys Gln
    450                 455                 460
Ser Pro Ile Gly Thr Pro Thr Pro Arg Gln Glu Ser Ile Ile Pro Arg
465                 470                 475                 480
Lys Gln Val Arg Ser Gly Ser Ser Ser Val Glu Ser Ser Ser Val Thr
                485                 490                 495
Asn Gly Pro Thr Thr Asp Lys Arg Thr Ile Leu Pro Ala Phe Val Pro
            500                 505                 510
Leu Asp Pro Tyr Asp Asp Leu Asp Pro Trp Ser Lys Ser Ser Leu Glu
        515                 520                 525
Arg Tyr Val Ala Met Leu Arg Lys Glu Ala Val Ala Asp Ser Asp Ala
```

```
    530                 535                 540
Glu Arg Tyr Asn Ile Phe Thr Ala Phe Met Ala Lys Glu Thr Lys Leu
545                 550                 555                 560
Arg Glu Ile Leu Phe Asn Ile Glu Pro Glu Ser Thr Arg Val Gly Glu
                565                 570                 575
Asn Pro Lys Val Ser Ser Arg Gln Pro Thr Pro Ile Leu Arg Ala Ser
            580                 585                 590
Thr Ser Val Ser Asn Asp Asp Thr Glu Ser Gly Leu Ile Pro Val Glu
        595                 600                 605
Thr Glu Gly Gly His Val Val Ser Thr Thr Asp Asp Ala Asp Ser Glu
    610                 615                 620
Asp Gly Ser Tyr Ser Pro Gly Gly Arg Pro Ile Leu Pro Arg Ile Gln
625                 630                 635                 640
Thr Pro Gly Ala Thr Lys Leu Gln Arg Ser Ala Ser His Thr Val Ser
                645                 650                 655
Asn Lys Tyr Asn Thr Asp His Val Ala His Ala Thr Ser Ser Arg Ala
            660                 665                 670
Thr Ser Val Pro Pro Ser Met Leu Gly Asp Ala Arg His Glu His Ala
        675                 680                 685
Leu Pro Pro Leu Thr Thr Asn Pro Pro Gln Pro Ile Tyr Ile Pro Phe
    690                 695                 700
Arg Tyr Thr Glu Gly Pro Gln Arg Gly Ser Asp Val Leu Val Phe Asp
705                 710                 715                 720
Arg Pro Ala Tyr Gln Ala Tyr Ser Asp Leu Arg Gln Ala Ser Ala Glu
                725                 730                 735
Ser Gly Arg Val Met Ser Asn Ala Pro Ala Pro Thr Pro Gly Glu Arg
            740                 745                 750
Pro Asp Ser Ala Val Pro Ser Arg Arg Asn Glu His Asp Glu Thr Phe
        755                 760                 765
Ile Gly Leu Ile Arg Glu Lys Ser Val Ala Tyr Arg Lys Arg Ala Pro
    770                 775                 780
Arg Lys Thr Ser Ser Pro Pro Pro Leu Pro Ala Ala Leu Arg His Gly
785                 790                 795                 800
Lys Pro Ala Ser Pro Val Asp Asp Leu Arg Ser Met Ala Ser Ser Pro
                805                 810                 815
Leu Ser Lys Gln Ser Glu Ser Ser Trp Asn Met Thr Thr Arg Lys Asp
            820                 825                 830
Leu Glu Asn Tyr Ser Ser Asp Phe Ser Tyr Ile Arg Glu Ala Val Lys
        835                 840                 845
Ser Trp Glu Ile Ser Ser Lys Ser Arg Arg Glu Gln Leu Asp Lys Glu
    850                 855                 860
Arg Ile His Arg Gln Glu Val Ser Glu Lys Arg Ile Asp Ala Leu Phe
865                 870                 875                 880
Asn Gly Lys Glu Ile Gly Tyr Ala Asp Ile Asn Leu Leu Glu Glu Glu
                885                 890                 895
Phe Arg Gln Lys Glu Ala Arg Ala Gln Leu Asp Glu Glu Arg Gln Glu
            900                 905                 910
Leu Asp Lys Phe Val Ala Glu Val Phe Glu Pro Leu Asp Gln Arg Leu
        915                 920                 925
Lys Glu Glu Ile Ala Ala Leu Gln Ala Leu Tyr Glu Ala Ala Leu Ala
    930                 935                 940
Gln Leu Asp His Glu Asn Gly Arg Thr Lys Ser Ala Thr Thr Asp Arg
945                 950                 955                 960
Tyr Asn Leu Ser His Thr Met Arg Thr Val Asn Glu Ile Tyr Arg Lys
```

```
                965                 970                 975
Leu Glu Leu Arg Tyr Gln Lys Arg Leu Glu Ile Ala Leu Asp Arg Glu
            980                 985                 990
Arg Arg Arg Lys Lys Ala Glu Arg Arg Pro Leu Val Phe Met Gly Asp
        995                 1000                1005
Ser Val Ala Leu Lys Gly Val Asp Gln Glu Phe Asp Gln Met Glu Lys
    1010                1015                1020
Arg Asn Ile Leu Glu Ala Ala Arg Glu Arg Asp His Arg Ala Asn Arg
1025                1030                1035                1040
Leu Met Asp Ser Phe Asp Asp Ala Ile Met His Gly Leu Gly Glu Asn
                1045                1050                1055
Gln Ser Leu Leu Asp Glu Val Ala Ala Lys Val Ala Lys Val Asp Thr
            1060                1065                1070
Ala Thr Ile Arg Ser Ser Gly Leu Pro Glu Ser Glu Val Glu Gln Leu
        1075                1080                1085
Leu Lys Ser Val Tyr Asn Leu Ile Glu Ser Leu Arg Lys Asp Ser Glu
    1090                1095                1100
Ser Ile Leu His Asn Phe Asn Met Ala Asp Ser Val Leu Asn Asp Ala
1105                1110                1115                1120
Asp Tyr Ser Val Ser Val Ala Glu Ala Arg Tyr Ser Asp Ala Asp Ala
                1125                1130                1135
Asp Val Phe Arg Arg Leu Asp Asp Glu Lys Arg Lys Glu Asp Thr Lys
            1140                1145                1150
Ile Gln Thr Asp Leu Lys Thr Lys Leu Glu Ser Ile Arg Ser Gly Pro
        1155                1160                1165
Ala Asn Ile Val Thr Ser Ile Asn Gly Leu Leu Glu Ser Leu Gly Lys
    1170                1175                1180
Pro Pro Ile Ile Asp Gln Thr Gly Pro Ser Ser Gln Met Pro Ala Asp
1185                1190                1195                1200
Thr Pro Ala Ser Val Ser Gln His Leu Pro Ala Glu Ile Ala Pro Gln
                1205                1210                1215
Lys Pro Gln Glu Asp Pro Glu His Gln Glu Arg Leu Arg Lys Ala Leu
            1220                1225                1230
Glu Asn Ala Lys Arg Arg Asn Ala Ala Arg Val Asn Thr Glu Ile Ser
        1235                1240                1245
Arg Pro
    1250


<210> 217
<211> 610
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK41767.1

<400> 217
Met Cys Asn Lys Ser Asn Tyr Ser Ser Pro Lys Trp Trp Lys Glu Ser
 1               5                  10                  15
Val Val Tyr Gln Val Tyr Pro Ala Ser Phe Asn Cys Gly Lys Ser Thr
            20                  25                  30
Thr Asn Thr Asn Gly Trp Gly Asp Val Thr Gly Ile Ile Glu Lys Val
        35                  40                  45
```

```
Pro Tyr Leu Glu Ser Leu Gly Val Asp Ile Ser Gln Thr Ser Arg Glu
    50                  55                  60
Gln Cys Leu Thr Ser Leu Ser Leu Val Tyr Thr Ser Pro Gln Val Asp
65                  70                  75                  80
Met Gly Tyr Asp Ile Ala Asp Tyr Glu Ser Ile Asp Pro Arg Tyr Gly
                85                  90                  95
Thr Leu Ala Asp Val Asp Leu Leu Ile Lys Thr Leu Lys Asp His Asp
            100                 105                 110
Met Lys Leu Met Met Asp Leu Val Val Asn His Thr Ser Asp Gln His
        115                 120                 125
Ser Trp Phe Val Glu Ser Ala Asn Ser Lys Asp Ser Pro Lys Arg Asp
    130                 135                 140
Trp Tyr Ile Trp Arg Pro Ala Lys Gly Phe Asp Glu Ala Gly Asn Pro
145                 150                 155                 160
Val Pro Pro Asn Asn Trp Ala Gln Ile Leu Gly Asp Thr Leu Ser Ala
                165                 170                 175
Trp Thr Trp His Ala Glu Thr Gln Glu Phe Tyr Leu Thr Leu His Thr
            180                 185                 190
Ser Ala Gln Ala Glu Leu Asn Trp Glu Asn Pro Asp Val Val Thr Ala
        195                 200                 205
Val Tyr Asp Val Met Glu Phe Trp Leu Arg Arg Gly Ile Cys Gly Phe
    210                 215                 220
Arg Met Asp Val Ile Asn Phe Ile Ser Lys Asp Gln Ser Phe Pro Asp
225                 230                 235                 240
Ala Pro Ile Ile Asp Pro Ala Ser Lys Tyr Gln Pro Gly Glu Gln Phe
                245                 250                 255
Tyr Thr Asn Gly Pro Arg Phe His Glu Phe Met His Gly Ile Tyr Asp
            260                 265                 270
Asn Val Leu Ser Lys Tyr Asp Thr Ile Thr Val Gly Glu Thr Pro Tyr
        275                 280                 285
Val Thr Asp Met Lys Glu Ile Ile Lys Thr Val Gly Ser Thr Ala Lys
    290                 295                 300
Glu Leu Asn Met Ala Phe Asn Phe Asp His Met Glu Ile Glu Asp Ile
305                 310                 315                 320
Lys Thr Lys Gly Glu Ser Lys Trp Ser Leu Arg Asp Trp Lys Leu Thr
                325                 330                 335
Glu Leu Lys Gly Ile Leu Ser Gly Trp Gln Lys Arg Met Arg Glu Trp
            340                 345                 350
Asp Gly Trp Asn Ala Ile Phe Leu Glu Cys His Asp Gln Ala Arg Ser
        355                 360                 365
Val Ser Arg Tyr Thr Asn Asp Ser Asp Glu Phe Arg Asp Arg Gly Ala
    370                 375                 380
Lys Leu Leu Ala Leu Leu Glu Thr Thr Leu Gly Gly Thr Ile Phe Leu
385                 390                 395                 400
Tyr Gln Gly Gln Glu Ile Gly Met Arg Asn Phe Pro Val Glu Trp Asp
                405                 410                 415
Pro Asp Thr Glu Tyr Lys Asp Ile Glu Ser Val Asn Phe Trp Lys Lys
            420                 425                 430
Ser Lys Glu Leu His Pro Val Gly Ser Glu Gly Leu Ala Gln Ala Arg
        435                 440                 445
Thr Leu Leu Gln Lys Lys Ala Arg Asp His Ala Arg Thr Pro Met Gln
    450                 455                 460
Trp Ser Ala Asp Pro His Ala Gly Phe Thr Val Pro Asp Ala Thr Pro
465                 470                 475                 480
```

```
Trp Met Arg Val Asn Asp Asp Tyr Gly Thr Val Asn Val Glu Ala Gln
                485                 490                 495
Met Ser Phe Pro Trp Glu Met Lys Gly Glu Leu Ser Val Trp Gln Tyr
            500                 505                 510
Trp Gln Gln Ala Leu Gln Arg Arg Lys Leu His Lys Gly Ala Phe Val
        515                 520                 525
Tyr Gly Asp Phe Glu Asp Leu Asp Tyr His Asn Glu Leu Val Phe Ala
    530                 535                 540
Tyr Ser Arg Thr Ser Ala Asp Gly Lys Glu Thr Trp Leu Val Ala Met
545                 550                 555                 560
Asn Trp Thr Thr Asp Ala Val Glu Trp Thr Val Pro Ser Gly Ile His
                565                 570                 575
Val Thr Arg Trp Val Ser Ser Thr Leu Gln Thr Ala Pro Leu Met Ala
            580                 585                 590
Gly Gln Ser Thr Val Thr Leu Arg Ala Leu Glu Gly Val Val Gly Cys
        595                 600                 605
Cys Ser
    610
```

<210> 218
<211> 966
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK41979.1

<400> 218

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

```
        195                 200                 205
Ser Ser Glu Ser Ala Thr Ser Phe His Ala Val Ser Thr Ser Lys His
    210                 215                 220
Thr His Thr His Thr Pro Thr Ser Ser Thr Ser Ser Ser Asn Thr Pro
225                 230                 235                 240
Thr Arg Ser Ser Ala Leu Thr Gln His Glu Thr Ser Thr Ser Ser Ser
                245                 250                 255
Thr Pro Thr Arg Ser His Thr His Thr Ala Ser Thr Pro Ala Ser Ser
            260                 265                 270
Lys Ala Asn Thr Ser Ser Ser Ile Lys Thr His Thr Thr His Ser His
        275                 280                 285
Thr Glu Asp Thr Thr Ser Ser Ser Ala Ser His Thr Pro Thr Ser Ser
    290                 295                 300
Lys Ser Ser Ser Ser Ser Ala Glu Asp Val Ser Ser Ser Pro Ala Ser
305                 310                 315                 320
His Ser Pro Thr Pro Ser Thr His Ser Ile Thr Thr Thr Thr Asn Thr
                325                 330                 335
Asp Thr Ser Gln Ser Ala Ser Ile Thr Ser Gly Pro Ser Thr Thr Pro
            340                 345                 350
Asn Ser Thr Ile Thr Thr Thr Ser Ser Thr Thr Thr Ser Ser Val Asp
        355                 360                 365
Val Tyr Ala Ile Ile Lys His Leu Tyr Lys Leu Val Lys Asp Thr Tyr
    370                 375                 380
Pro Val Ile Lys Lys Trp Lys Glu Asp Pro Lys Ser Val Lys Ala Ser
385                 390                 395                 400
Asp Leu Ile Lys Pro Leu Lys Arg Val Ile Pro Val Ala Asp Asp Val
                405                 410                 415
Leu Asp Val Leu Gly Ala Pro Ser Ser Leu Ser Ser Ser Ser Gly Asp
            420                 425                 430
Ser Glu Ser Val Leu Asp Ser Cys Ser Ser Gly Gly Gly Leu Leu Gly
        435                 440                 445
Asp Leu Ile Gly Ile Ala Ser Cys Ile Ser Ser Thr Ala Asp Glu Ala
    450                 455                 460
Val Ser Ile Leu Gly Ser Ser Ser Asp Ser Asp Ser Ser Asp Glu Ser
465                 470                 475                 480
Thr Leu Ser Ser Tyr Phe Asp Ala Phe Glu Thr Glu Gly Ser Ser Leu
                485                 490                 495
Ser Ala Val Gly Val Thr Ala Thr Gly Ser Thr Ala Ser Ser Thr Gly
            500                 505                 510
Thr Thr Thr Thr Thr Ser Ser Gly Asp Thr Ser Ser Lys Ser Thr Lys
        515                 520                 525
Thr Ala Thr Ser Thr Asn Thr Asp Ser Asp Thr Ser Thr Gln Ser Thr
    530                 535                 540
Lys Thr Lys Thr Ser Thr Lys Ser Thr Thr Thr Ser Asp Ser Ser Ser
545                 550                 555                 560
Ser Ala Gly Ser Gly Gly His Ser Ala Ser Ala Ser Ala Ser Pro Thr
                565                 570                 575
Ser Thr Lys Ser Ser Thr Ser Thr Lys Glu Ser Ser Thr Ser Thr Lys
            580                 585                 590
Thr Lys Thr Lys Ser Asn Thr Glu Ser Ser Ser Lys Ala Ala Ser Ser
        595                 600                 605
Ser Ala Ala Ala Ser Lys Thr Asp Ser Ser Ser Ser Ser Ala Lys Ser
    610                 615                 620
Thr Ser Thr Asp Ser Thr Ser Thr Lys Lys Thr Thr Ser Thr Lys Ser
```

625 630 635 640
Thr Ala Thr Ser Ser Ser Ala Pro Leu Ser Ala Ser Ser Ser Ala His
645 650 655
Thr Ser Ser Ile Ala Thr Thr Asn Thr Thr Ser Thr Ser Thr Asn Ser
660 665 670
Lys Ser Ser Thr Ser Thr Asp Thr Thr Thr Ile Ile Ile His Thr His
675 680 685
Ser Gly Thr Ala Ser Gly Thr Thr Thr His His Thr Ser Thr Val Thr
690 695 700
Pro Ser Pro Ser Arg Asn Gln Thr Ala Thr Thr Leu Val Thr Thr Thr
705 710 715 720
Ser Ser Tyr Thr Pro Pro Leu Cys Tyr Asn His Ala Asp Pro Asp Asn
725 730 735
Gly Ala Gly Asn Val Cys Ile Cys Thr Arg Ser Asn Gly Asp Tyr Thr
740 745 750
Thr Leu Ser Glu Leu Pro Ser Gly Ser Gly Cys Ser Tyr Thr Ser Ile
755 760 765
Pro Thr Pro Thr Thr Thr Ser Thr Thr Lys Thr Thr Ser Thr Lys Thr
770 775 780
Thr Ser Asp Pro Pro Phe Thr Val Thr Glu Leu Asn Ser Asp Val Ile
785 790 795 800
Val Cys Ala Thr Ser Thr Leu Ser Tyr Phe Ser Thr Phe Thr Tyr Thr
805 810 815
Gln Cys Ala Gly Ser Ser Ser Thr Ile Tyr Thr Ala Pro Thr Pro Thr
820 825 830
Pro Thr Ala Gln Val Val Ile Ala Tyr Leu Ser Asp Val Tyr Ser Phe
835 840 845
Trp Ser Phe Phe Thr Pro Asp Ile Gly Ser Ser Ile Asp Phe Cys Asn
850 855 860
Asp Ala Glu Ala Gly Glu Leu Glu Ala Ser Gly Ser Ile Lys Val Ile
865 870 875 880
Asp Pro Pro Tyr Pro Asp Gly Thr Lys Glu Leu Asp Phe Glu Ile His
885 890 895
Asp Met Lys Asp Cys Val Tyr Lys Gly Thr Ser Asp Glu Pro Gly Thr
900 905 910
Phe Thr Cys Pro Asp Leu Ala Lys Thr Val Asp Cys Glu Ser Tyr Gly
915 920 925
Glu Asn Lys Val His Asp Cys Tyr Gly Ala Leu Ser Asp Gly Gly Val
930 935 940
Val Tyr Glu Glu Gly Ile Asp Cys Ala Ser Ile Gly Ser Val Glu Val
945 950 955 960
Gln Ala Glu Asn Gly Ile
965

<210> 219
<211> 822
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAL00956.1

<400> 219

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

```
Asp Thr Asp Leu Ala Leu Glu Ile Val Lys Ser Trp Leu Ser Leu Met
        435                 440                 445
Asp Glu Asp Gly Trp Ile Ala Arg Glu Gln Ile Leu Gly Ser Glu Ala
    450                 455                 460
Arg Ser Lys Val Pro Pro Glu Phe Thr Ile Gln Tyr Pro His Tyr Ala
465                 470                 475                 480
Asn Pro Pro Thr Leu Phe Ile Ile Leu Glu Ala Phe Ile Asp Lys Leu
                485                 490                 495
Asp Ala Lys Lys Asn Ala Ser Met Gln Thr Tyr Ala Asp Ser Gly Val
            500                 505                 510
Thr Gly Asn Leu Arg Ser Ile Phe Val Asp Gln Pro Glu Leu Gly Glu
        515                 520                 525
Ala Phe Ile Arg Ser Ile Tyr Pro Leu Leu Lys Lys His Tyr Tyr Trp
    530                 535                 540
Tyr Arg Ser Thr Gln Lys Gly Asp Ile Lys Ser Tyr Asp Arg Glu Ala
545                 550                 555                 560
Tyr Ser Thr Arg Glu Ala Tyr Arg Trp Arg Gly Arg Ser Ile Gln His
                565                 570                 575
Ile Leu Thr Ser Gly Leu Asp Asp Tyr Pro Arg Pro Gln Pro Pro His
            580                 585                 590
Pro Gly Glu Leu His Val Asp Leu Met Ser Trp Met Gly Met Met Thr
        595                 600                 605
Arg Ala Leu Arg Arg Ile Ala Val Thr Ile Gly Glu Thr Glu Asp Ala
    610                 615                 620
Glu Val Phe Lys Thr Tyr Glu Thr Ala Ile Glu Arg Asn Ile Asp Asp
625                 630                 635                 640
Leu His Trp Asp Asp Asp Ala Arg Thr Tyr Cys Asp Ala Thr Ile Asp
                645                 650                 655
Glu Tyr Glu Glu His Val His Val Cys His Lys Gly Tyr Ile Ser Ile
            660                 665                 670
Phe Pro Phe Leu Thr Gly Met Leu Gly Pro Asp Ser Pro Arg Leu Lys
        675                 680                 685
Ala Ile Leu Asp Leu Ile Gly Asp Pro Glu Glu Leu Trp Ser Asp Tyr
    690                 695                 700
Gly Ile Arg Ser Leu Ser Lys Lys Asp Gln Phe Tyr Gly Thr Ala Glu
705                 710                 715                 720
Asn Tyr Trp Arg Ser Pro Ile Trp Val Asn Ile Asn Tyr Leu Val Leu
                725                 730                 735
Lys Asn Leu Tyr Asp Ile Ala Ile Val Ser Gly Pro His Lys Glu Gln
            740                 745                 750
Ala Arg Glu Leu Tyr Ser Asn Leu Arg Lys Asn Leu Val Glu Asn Val
        755                 760                 765
Phe Gln Glu Trp Lys Lys Thr Gly Phe Ala Trp Glu Gln Tyr Asn Pro
    770                 775                 780
Glu Thr Gly Ser Gly Gln Arg Thr Gln His Phe Thr Gly Trp Thr Ser
785                 790                 795                 800
Met Val Val Lys Met Met Ser Met Pro Asp Leu Pro Ala Ser Glu Gln
                805                 810                 815
Lys Gly His Asp Glu Leu
            820
```

<210> 220
<211> 1027

<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAL00976.1

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

```
    370                 375                 380
Gly Ser Ser Val Ile Gly Phe Arg Glu Arg Pro Ser Ser Ala Gly Gly
385                 390                 395                 400
Glu Lys Glu Leu Arg Met Arg Leu Pro Arg Leu Gln Thr Lys Glu Met
                405                 410                 415
Gly Ala Pro Gly Arg Lys Arg Asp Asn Ile His Ser Thr His Glu Gly
            420                 425                 430
Pro Glu Gln Leu Arg Arg Pro Asn Gly Arg Ala Arg Gly Ala Ser Val
        435                 440                 445
Gly Glu Lys Tyr Phe Val Ser Tyr Ser Lys Leu Asp Gly Met Pro Val
    450                 455                 460
His Ser Thr Arg Gln His Gln Pro Thr Ser Gln Thr Ser Cys Met Val
465                 470                 475                 480
Tyr Glu Leu Glu Gly Gly Ser Thr Gln Pro Pro Ala Glu Leu Gln Gly
                485                 490                 495
Asp Thr Thr Ser Pro Ile Asp Val Val Pro Val Arg Ile Ser Val Gly
            500                 505                 510
Val Ser Ser Val Gly Ala Met Pro Gly Thr Leu Pro Asp Arg Val Ile
        515                 520                 525
Leu Thr Val Leu Glu His Ile Thr Ser Leu Asp Asp Leu Phe Asn Val
    530                 535                 540
Ala Val Ser Arg Lys Asp Phe Tyr Arg Val Phe Lys Met His Glu Leu
545                 550                 555                 560
Lys Leu Ile Arg Ile Ala Val Phe Ala Met Ser Ala Pro Ala Trp Glu
                565                 570                 575
Leu Arg Glu Met Ser Pro Pro Trp Asp Thr Glu Trp His Phe Val Leu
            580                 585                 590
Asp Pro Asp Ala Pro Val Pro Glu Tyr Thr Pro Ser Cys Tyr Leu Lys
        595                 600                 605
Arg Tyr Ala Glu Asp Ile Tyr Thr Leu Ala His Leu Lys Ser Leu Ile
    610                 615                 620
Leu Ala Arg Cys Gly Thr Phe Leu Arg Pro Glu Thr Ile Arg Gly Leu
625                 630                 635                 640
Ser Gly Thr Asp Asp Ile Arg Ala Ala Glu Val Asp Asp Ala Phe Trp
                645                 650                 655
Arg Val Trp Thr Phe Cys Arg Leu Phe Gly Ser Gly Lys Gly Arg Glu
            660                 665                 670
Gly Asp Ile Ala Gly Gln Leu Asp Trp Leu Arg Gly Gly Glu Val Ala
        675                 680                 685
Arg Asn Arg Arg Val Ser Glu Phe Thr Ser Ile Ala Asp Pro Tyr Asp
    690                 695                 700
Ala Asn Ser Val Leu Phe Glu Pro Pro Thr Gly Phe Gly Asp Gly Asn
705                 710                 715                 720
Asn Gly Gly Leu Ser Lys Glu Gln Leu Leu Asp Met Thr Glu Ile Trp
                725                 730                 735
Thr Cys Leu Gly Val Leu Leu Gln Pro Met His Glu Glu Trp Ala Tyr
            740                 745                 750
Tyr Ile Leu Thr Leu Gly Leu Ser Ala Val Leu Val Leu Gly Ser Ile
        755                 760                 765
His Pro Tyr Asp Asn Thr Thr Ala Val Phe Gln Arg Ala His Ser Met
    770                 775                 780
Gly Leu Thr Asn Trp Glu Ala Ser Asp Thr Gly Ala Ser Arg Ser Ser
785                 790                 795                 800
Phe Leu Arg Glu Ala Val Ser Lys Ala Cys Gln Pro Arg Gly Ser Ser
```

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                805                 810                 815
Thr Ser Gln Ala Ser Met Arg Ser Ser Gly Phe Ser Ser Gln Pro Ser
            820                 825                 830
Gly Ser His Asp Val Ser Gln Thr Ser Asn Val Arg Gly Glu Arg Glu
        835                 840                 845
Pro Ser Pro Asp Phe His Arg Arg Arg Gln Ala Ala Tyr Ser Ala Gln
    850                 855                 860
Leu Arg Ile Gln Arg Gln Gln Gln Pro Ser Pro Pro Asn Pro Met Leu
865                 870                 875                 880
Ala Glu Glu Arg Pro Ile Ser His Tyr Ala Thr Ile Met Ser Arg Leu
                885                 890                 895
Glu Gly Leu Pro Pro Ala Pro Gln Pro Pro Met Ser Val Ser Arg Ile
            900                 905                 910
Glu Ile Pro Pro Thr Thr His Ser Tyr Met Thr Asn Val Ser Tyr Met
        915                 920                 925
Gln Pro Leu Gln Ser Val Thr Pro Val Tyr Tyr Pro Pro Gln Val Arg
    930                 935                 940
Asp Pro Val Asp His Ala Ile Asp Ile Met Val Arg Glu Leu Gly Phe
945                 950                 955                 960
Gly Glu Glu Asp Ala Lys Trp Ala Leu Lys Ile Thr Asp Ser Gly Glu
                965                 970                 975
Gly Ile Asn Val Asn Ala Ala Ile Ser Leu Leu Thr Arg Glu Arg Lys
            980                 985                 990
Thr His Glu Gln Ser Ser Arg Gly Phe Ser Leu Arg Lys Arg Lys Ser
        995                 1000                1005
Phe Leu Ser Ser Val Ile Asn Ser Pro Glu Ser Arg His Ser Gly Trp
    1010                1015                1020
Lys Trp Ala
1025


<210> 221
<211> 893
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK42352.1

<400> 221
Met Glu Pro Leu Arg Arg Ser Gln Ser Ser Arg Ser Met Arg Arg Ser
 1               5                  10                  15
His His Ser Ser Gln Ser Thr Glu Pro Phe Asp Pro Glu Leu Ala Arg
            20                  25                  30
Phe Gln Ala Thr Thr Ala Ala Ser Arg Ala Met Leu Arg Ser Lys Cys
        35                  40                  45
Ser Tyr Asp Val Leu Gly Gly Pro Ser Lys Met Ala Val Pro Gln Arg
    50                  55                  60
Gln His Arg Pro Ala Gly Ala Ala Leu Asn Ala Thr Asn Ala Pro Val
65                  70                  75                  80
Glu Asp Val Asp Leu Arg Arg Ser Val Leu Asp Lys Thr Ser Asp Leu
                85                  90                  95
Ser Pro Pro Ala Gly Leu Pro Ser Ile Arg Glu Phe Gly Arg Leu Asp
            100                 105                 110
```

```
Ala Gly Ile Ala Thr Leu Pro Ser Ser Tyr Arg Arg Leu Arg Lys Thr
        115                 120                 125
Arg Ser Met Phe Thr Asn Trp Gln Arg Ser Ser His Val Pro Arg Gly
    130                 135                 140
Leu Ser Ser Pro Gly Cys Pro Thr His Asn Ile Leu Thr Arg Arg Glu
145                 150                 155                 160
Pro Gln Asp Val Leu Arg Ala Pro Gly Thr Leu Arg Arg Ser Met Ser
                165                 170                 175
Phe Phe Arg Gly Asp Thr Gln Asn Ser Asp Ser Leu Arg Tyr Ala Arg
            180                 185                 190
Gly Gln Asp Val Ala Ile Glu Met Ala Arg Ser His Tyr Gln Gln Pro
        195                 200                 205
Glu Ile Tyr Pro Thr Glu Leu Arg Lys Ser Ser Leu Thr Val Pro Lys
    210                 215                 220
Ser Arg Pro Phe Lys Lys Thr Leu Arg Ser Val Val Ser Asp Ala Glu
225                 230                 235                 240
Ser Ala Ser Val Ser Pro Ala Ile Gln Arg Ser Thr Asn Val Ile Ser
                245                 250                 255
Tyr Gly Lys Ala Arg Ser Leu Ser Ser Ser Leu Lys Lys Gly Leu Lys
            260                 265                 270
Lys Val Leu Glu Leu Ser Arg Pro Ser Ser Ala Arg Ile Ser Leu Gly
        275                 280                 285
Lys Ser Ser Ser Asn Asp Gln Gln Arg Ile Gln Gly Ser Pro Ser Thr
    290                 295                 300
Ile Ser Ala Lys His Ser Asp Pro Leu Asn Ser Gly Val Glu Gly Asn
305                 310                 315                 320
Ala Leu Thr His Ser Pro Asp Thr Glu Gly Thr Val Val Tyr Thr Gly
                325                 330                 335
Val Lys Lys Ser Glu Ser Ser Glu Ser Leu Ala Thr Ser Arg Ser Arg
            340                 345                 350
Val Thr Ser Trp Ala Asp Ser Thr Ile Ala Asn Thr Val Ile Thr Tyr
        355                 360                 365
Arg Ala Asp Asp His Ser Ser Leu Ser Val Ile Asp Glu His Asp Ser
    370                 375                 380
Ser Cys Leu Lys Pro Ser Ser Ser Glu Asp Val Ser Leu Thr Thr Cys
385                 390                 395                 400
Arg Thr Pro Lys Pro Asn Cys Thr Ile Asp Ser Gln Arg Leu Tyr Ser
                405                 410                 415
Ala Leu Met Lys Arg Ile Asp Gly Asn Lys Thr Glu Asn Ala Ser Lys
            420                 425                 430
Glu Ile Val Leu Gly His Val Arg Glu His Arg Ala Ile Pro Thr Pro
        435                 440                 445
Val Ser Ser Met Tyr Thr Arg Arg Ser Arg Lys Thr Ile Arg Leu Ile
    450                 455                 460
Ala Ser Asp Glu Ser Leu Gln Ser Pro Gly Ser Tyr Thr Thr Ala Asp
465                 470                 475                 480
Val Gly Thr Val Thr Pro Cys Glu Pro Ala Gln Arg Gln Ala Gln Arg
                485                 490                 495
Thr His Gly Gln Lys His Leu Gln Asp Ile Arg Phe Gly Ser Ala Asn
            500                 505                 510
Leu Ala Ser Ser Lys His Thr Ile Lys Glu Asp Ser Arg Asp Glu Thr
        515                 520                 525
Gly Asn Met Ala Met Gly Arg Ser Gln Ser Pro Glu Glu Asp Glu Asp
    530                 535                 540
```

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Ser Pro Ser Met Tyr Ser Arg Ser Thr Gly Gly Thr Ser Pro Lys Thr
545                 550                 555                 560
Thr Asp Pro Lys Met Gly Glu Ser Asp Pro Glu Val Ala Asn Glu Pro
                565                 570                 575
Gly Val Ala Thr Ile Tyr Ala Ser Gln Arg Ala Ile Tyr Ser Ser Pro
            580                 585                 590
Lys Arg Asn Ala Asp Gln Gly Pro Glu Ala Met Gln Arg Pro Ser Ala
        595                 600                 605
Asp Trp Gln Gln Trp Val Arg Thr Gln Met Glu Arg Ile Glu Tyr Leu
    610                 615                 620
Thr Pro Thr Arg Arg His Tyr Arg Glu Asp Ala Gln Ile Gln Asp Glu
625                 630                 635                 640
Thr Ala Asp Leu Ala Tyr Arg Thr Pro Ser Arg Asp Arg Arg Gly Phe
                645                 650                 655
Trp Ser Gly Ser Pro Asp Glu Asp Leu Arg Thr Thr Cys Lys Val Thr
            660                 665                 670
Ala Arg Asn Asn Phe Ser Arg Pro Phe Ser Arg Ser Ser Ser Val Arg
        675                 680                 685
Thr Thr Val Ile Ala Pro Lys Glu Gln Ala Asp Thr Leu Val Pro Pro
    690                 695                 700
Pro Pro Pro Ser Asp Ser Thr Pro Lys Val Leu Ser Ser Ser Ser Gly
705                 710                 715                 720
Arg Ser Leu Phe Ile Asn Gln Val Glu Thr Arg Pro Asp Gly Met Ala
                725                 730                 735
Leu Ser Pro Val Pro Ala Leu Leu Asn Asn Arg Tyr Arg Ala Pro Glu
            740                 745                 750
Ser Pro Thr Pro Arg Arg Asp Ala Thr Asp Lys Ala Arg Trp Arg Ala
        755                 760                 765
Gly Gly Arg Arg Tyr Gly Arg Gln Pro Ser Arg Leu Leu Pro Glu Ala
    770                 775                 780
Gln Asp Ser Lys Ala Ser Gln Ile Arg Ser Ser Arg Val Pro Gln Glu
785                 790                 795                 800
Asn Arg Arg Leu Thr Asp Glu Asn Val Arg Leu Glu Asn Gly Tyr Gln
                805                 810                 815
Glu Val Ala Ser Lys Asp Ser Gln Leu Gln Asn Met Tyr Ser Pro Ile
            820                 825                 830
Ser Ser Lys Arg Met Val Glu Met Phe Leu Glu Ser Arg Arg Arg Arg
        835                 840                 845
Met Gly Thr Glu Met Ser Asp Gly Ala Pro Ser Lys Asp Asp Gly Thr
    850                 855                 860
Lys Leu Ser Ser Asp Ser Val Tyr Asp Arg His His Ile Glu Ser Leu
865                 870                 875                 880
Phe Tyr Ser Leu Ala Pro Met Tyr Glu Thr Pro Thr Asn
                885                 890
```

<210> 222
<211> 542
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK42453.1

<400> 222
Met Ala Asn Ile Ile Trp Leu Ala Leu Val Leu Val Ala Leu Ser Ile
 1               5                  10                  15
His Val Gln Ala Lys Asp Val Phe Ala His Phe Ile Leu Ala Asn Ala
            20                  25                  30
Glu Asn Phe Thr Gln Thr His Trp Thr Arg Asp Ile Ser Ala Ala Lys
        35                  40                  45
Ala Ala Gln Ile Asp Ala Phe Ala Leu Asn Thr Gly Tyr Gly Ala Ala
    50                  55                  60
Asn Thr Asp Gln Leu Leu Thr Asp Ala Phe Thr Val Ala Ala Ala His
65                  70                  75                  80
Asp Phe Lys Leu Phe Leu Ser Leu Asp Tyr Ser Gly Asp Gly His Trp
                85                  90                  95
Pro Pro Asp Gln Val Leu Lys Val Leu Gln Gly Tyr Ala Asn His Thr
            100                 105                 110
Ala Tyr Tyr Arg Val Asp Asn Lys His Pro Leu Val Ser Thr Phe Glu
        115                 120                 125
Gly Tyr Glu Ala Leu Ala Asp Trp Ser Thr Ile Lys Glu Lys Leu Pro
    130                 135                 140
Asn Ile Tyr Phe Met Pro Glu Trp Ser Val Arg Thr Pro Gln Glu Leu
145                 150                 155                 160
Ala Ser Glu Asp Ala Val Asp Gly Leu Leu Ser Trp Ser Ala Trp Pro
                165                 170                 175
Tyr Gly Thr Thr Pro Met Asn Thr Ser Thr Asp Glu Gln Tyr Ile Ser
            180                 185                 190
Ala Leu Lys Ala Lys Asp Lys Pro Tyr Ile Met Pro Val Ser Pro Trp
        195                 200                 205
Phe Tyr Thr Asp Met Val Arg Tyr His Lys Asn Trp Val Trp Gln Gly
    210                 215                 220
Asp Gly Leu Trp His Thr Arg Trp Lys Gln Val Leu Asp Leu Gln Pro
225                 230                 235                 240
Gln Phe Val Glu Ile Leu Thr Trp Asn Asp Phe Gly Glu Ser His Tyr
                245                 250                 255
Ile Gly Pro Leu His Glu Asn Glu Leu Gly Ile Phe Ser Phe Gly Gln
            260                 265                 270
Ala Pro Phe Asn Tyr Ala Ser Gly Met Val His Asp Ala Trp Arg Glu
        275                 280                 285
Phe Leu Pro Tyr Val Val Gly Glu Tyr Lys Asn Gly Ser Gly Lys Gly
    290                 295                 300
Val Ile Asp Lys Glu Gly Val Val Val Trp Tyr Arg Val Thr Pro Ala
305                 310                 315                 320
Trp Ala Cys Lys Ala Gly Leu Thr Thr Gly Asn Ser Val Thr Gln Gly
                325                 330                 335
Gln Gln Thr Met Pro Pro Gly Gln Val Leu Lys Asp Glu Val Phe Phe
            340                 345                 350
Gln Ala Leu Leu Glu Asp Thr Ala Asp Val Glu Val Ser Ile Gly Gly
        355                 360                 365
Gly Glu Asn Lys Ser Val Gly Trp Thr Asp Thr Pro Ser Gly Gly Ser
    370                 375                 380
Ser Gly Gly Gly Arg Gly Leu Tyr Phe Gly Ser Val Pro Met Asp Asn
385                 390                 395                 400
Arg Thr Gly Glu Val Val Val Thr Leu Ser Arg Asn Gly Lys Phe Val
                405                 410                 415
Ala Gln Met Ile Gly Glu Lys Ile Thr Thr Gln Cys Pro Asp Lys Leu

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            420                 425                 430
Thr Asn Trp Asn Ala Trp Val Gly Thr Ala Met Ser Asn Val Ser Asn
        435                 440                 445
Ala Ser Thr Ser Arg Ala Ser Leu Ser Glu Glu Asn Gly Ala Ala Ser
    450                 455                 460
Val Arg Val Gly Gly Gly Arg Gly Met Asp Met Trp Met Gly Ala Leu
465                 470                 475                 480
Trp Met Val Val Val Val Gly Ile Arg Ala Asp Arg Ser Ile Pro Thr
                485                 490                 495
Lys Trp Ala Cys Gly Ser Gln Ile Asn Glu Glu Val Leu Ile Gln Arg
            500                 505                 510
Arg Glu Arg Leu Pro Leu Val Glu Gly Asp Arg Val Tyr Leu Asp Ser
        515                 520                 525
Ser Ser Lys Ala Phe Arg Arg Arg Arg Arg Thr Cys Thr Arg
    530                 535                 540


<210> 223
<211> 819
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK42457.1

<400> 223
Met Lys Val Pro Ala Asp His Ala Leu Leu Leu Ser Ser Leu Leu Leu
 1               5                  10                  15
Ala Pro Ser Val Gly Ala Ser Thr Cys Gln Glu Pro Ile Asn His Pro
            20                  25                  30
Gly Glu Pro Phe Ser Phe Val Gln Pro Leu Asn Thr Ser Ile Leu Thr
        35                  40                  45
Pro Tyr Gly Gly Ser Pro Pro Val Phe Pro Ser Pro Glu Thr Lys Gly
    50                  55                  60
Lys Gly Gly Trp Glu Lys Ala Met Ala Gln Ala Lys Asn Trp Val Ser
65                  70                  75                  80
Gln Leu Thr Val Glu Glu Lys Ala Trp Met Ala Thr Gly Gln Pro Gly
                85                  90                  95
Pro Cys Val Gly Asn Ile Leu Pro Ile Pro Arg Leu Asn Phe Thr Gly
            100                 105                 110
Leu Cys Leu Gln Asn Gly Pro Gln Cys Ile Gln Gln Gly Asp Tyr Ser
        115                 120                 125
Ser Val Phe Val Ser Gly Val Ser Ala Ala Ala Ser Trp Asp Arg Lys
    130                 135                 140
Leu Leu Tyr Asp Arg Gly Tyr Ala Met Ala Thr Glu His Lys Gly Lys
145                 150                 155                 160
Gly Thr His Val Val Leu Gly Pro Ile Gly Gly Pro Leu Gly Arg Ser
                165                 170                 175
Pro Tyr Asp Gly Arg Thr Trp Glu Gly Phe Ala Ala Asp Pro Tyr Leu
            180                 185                 190
Thr Gly Val Cys Met Glu Glu Thr Ile Leu Gly Ile Gln Asp Ala Gly
        195                 200                 205
Val Gln Ala Asn Ala Lys His Phe Ile Ala Asn Glu Gln Glu Thr Gln
    210                 215                 220
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Arg Asn Pro Thr Tyr Ala Pro Asp Ala Asn Ala Thr Thr Tyr Ile Gln
225                 230                 235                 240
Asp Ser Val Ser Ser Asn Leu Asp Asp Arg Thr Leu His Glu Ile Tyr
                245                 250                 255
Met Trp Pro Phe Ala Asn Ala Ala Arg Ala Arg Val Ala Ser Phe Met
            260                 265                 270
Cys Ser Tyr Asn Arg Val Asn Gly Ser His Ser Cys Gln Asn Ser Tyr
        275                 280                 285
Leu Leu Asn His Leu Leu Lys Thr Glu Leu Gly Phe Gln Gly Tyr Val
    290                 295                 300
Met Ser Asp Trp Gly Ala Thr His Ser Gly Val Ala Ser Ala Glu Ser
305                 310                 315                 320
Gly Met Asp Met Thr Met Pro Gly Gly Phe Thr Val Tyr Gly Glu Leu
                325                 330                 335
Trp Thr Glu Gly Ser Tyr Phe Gly Lys Asn Leu Thr Glu Ala Ile Asn
            340                 345                 350
Asn Gly Thr Ile Thr Thr Asp Arg Ile Asp Asp Met Ile Val Arg Ile
        355                 360                 365
Met Thr Pro Tyr Phe Trp Leu Gly Gln Asp Lys Asn Tyr Pro Ser Val
    370                 375                 380
Asp Ala Ser Val Gly Pro Leu Asn Val Asp Ser Pro Pro Asp Thr Trp
385                 390                 395                 400
Leu Tyr Asp Trp Lys Phe Thr Gly Pro Ser Asn Arg Asp Val Arg Gly
                405                 410                 415
Asn Asn Ser Ala Met Ile Arg Glu His Gly Ala Ala Ser Thr Val Leu
            420                 425                 430
Leu Lys Asn Glu Arg Asn Ala Leu Pro Leu Arg Lys Pro Arg Asn Ile
        435                 440                 445
Val Ile Val Gly Asn Asp Ala Gly Ser Asp Thr Gln Gly Pro Ser Thr
    450                 455                 460
Gln Thr Asp Phe Glu Tyr Gly Val Leu Ala Asn Ala Gly Gly Ser Gly
465                 470                 475                 480
Thr Cys Arg Phe Ser Tyr Leu Ser Thr Pro Gln Asp Ala Ile Thr Thr
                485                 490                 495
Arg Ala Arg Gln Tyr Gly Gly Arg Val Gln Thr Trp Leu Asn Asn Thr
            500                 505                 510
Leu Ile Thr Glu Lys Ser Met Pro Glu Leu Trp Asn Pro Glu Gln Pro
        515                 520                 525
Asp Val Cys Leu Val Phe Leu Lys Ser Trp Ser Glu Glu Asn Val Asp
    530                 535                 540
Arg Thr Tyr Leu Thr Leu Asp Trp Asn Gly Asn Ala Val Val Glu Ala
545                 550                 555                 560
Val Ala Lys Tyr Cys Asn Asn Thr Val Val Val Thr His Ser Ala Gly
                565                 570                 575
Val Asn Val Leu Pro Phe Ala Asp His Pro Asn Val Thr Ala Ile Leu
            580                 585                 590
Ala Ala His Tyr Pro Gly Glu Glu Ala Gly Asn Ala Ile Ala Asp Leu
        595                 600                 605
Leu Tyr Gly Asp Ala Asn Pro Ser Ala Lys Leu Pro Tyr Val Ile Ala
    610                 615                 620
Tyr Asn Glu Ser Asp Tyr Asn Ala Pro Leu Thr Thr Ala Val Ala Thr
625                 630                 635                 640
Asn Gly Thr Tyr Asp Trp Gln Ser Trp Phe Asp Glu Glu Leu Glu Val
                645                 650                 655
```

Gly Tyr Arg Tyr Phe Asp Ala His Asn Ile Pro Val Arg Tyr Glu Phe
660 665 670
Gly Phe Gly Leu Ser Tyr Thr Thr Tyr Asn Leu Thr Lys Leu Val Ala
675 680 685
Ala Lys Pro Val Ala Ser Asn Leu Thr Ala Leu Pro Glu Gln Arg Ala
690 695 700
Val Gln Pro Gly Gly Asn Pro Ala Leu Trp Asp Thr Val Tyr Thr Leu
705 710 715 720
Thr Ala Gln Val Ser Asn Thr Gly Ser Val Asp Gly Tyr Ala Ile Pro
725 730 735
Gln Leu Tyr Val Gly Phe Pro Asp Thr Ala Pro Ala Gly Thr Pro Pro
740 745 750
Ser Gln Leu Arg Gly Phe Asp Lys Ile Trp Leu Glu Ala Gly Glu Thr
755 760 765
Lys Lys Val Thr Phe Glu Leu Met Arg Arg Asp Val Ser Tyr Trp Asp
770 775 780
Val Thr Ala Gln Asp Trp Arg Ile Pro Ala Gly Glu Phe Thr Phe Lys
785 790 795 800
Ala Gly Phe Ser Ser Arg Asp Phe His Ala Asn Ala Thr Ala Thr Phe
805 810 815
Phe Arg Lys

<210> 224
<211> 358
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK42741.1

<400> 224
Met His Leu Arg Arg Ile Phe Val Leu Thr Val Leu Ser Tyr Val Thr
1 5 10 15
Ala Leu Pro Ser Asp Ile Asn Leu Gly Val Ala Leu Arg Gly Cys Asp
20 25 30
Val Glu Ala Cys Asp Met Glu Cys Arg Met Ala Gly Ser Ile Gly Gly
35 40 45
Asn Cys Gly Gly Asn Pro Ala Leu Asn Leu Leu Gly Leu Pro Leu Leu
50 55 60
Ser Thr Asn Thr Pro Asn Ser Ser Ser Ala Gly Pro Val Thr Leu Ala
65 70 75 80
Ala Thr Glu Thr Leu Thr Asp Val Glu Ser Thr Thr Thr Thr Lys Thr
85 90 95
Thr Thr Asp Arg Glu Ser Val Thr Ala Thr Glu Thr Thr Thr Asp Ile
100 105 110
Glu Ser Thr Thr Ala Thr Gln Thr Val Thr Asp Thr His Leu Leu Thr
115 120 125
Val Thr Lys Ser Ile Thr Glu Lys Gln Pro Thr Thr Ala Thr Gln Thr
130 135 140
Ala Thr Asp Thr Lys Phe Leu Arg Thr Thr Gln Thr Ile Asn Asn Thr
145 150 155 160
Leu Thr Ala Thr Gln Thr Thr Thr Asp Ile Glu Ser Leu Arg Val Thr

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                165                 170                 175
Lys Thr Lys Asn Asn Thr Ile Thr Ala Thr Gln Thr Thr Thr Asp Ile
            180                 185                 190
Glu Pro Thr Thr Ala Thr Gln Thr Ile Asn Asn Thr Leu Thr Ala Thr
        195                 200                 205
Gln Thr Thr Thr Asp Thr Glu Ser Tyr Thr Ala Met Glu Ile Thr Thr
    210                 215                 220
Ala Thr Ala Ser Phe Thr Thr Thr Gln Thr Thr Thr Asp Thr Glu Ser
225                 230                 235                 240
Ile Thr Ala Thr Gln Asn Ile Thr Asp Thr Gln Thr Ile His His Thr
                245                 250                 255
Glu Ser Leu Thr Ala Thr Arg Thr Ile Thr Asp Thr Asp Ser Val Thr
            260                 265                 270
Ala Thr Ala Thr Pro Thr Thr Val Thr Asp Thr Gln Thr Ser Ile Ser
        275                 280                 285
Thr Thr Thr Ala Thr Gln Thr Ala Thr Pro Thr Pro Glu Val Gly Ala
    290                 295                 300
Cys Phe Cys Cys Thr Glu Gln Val Arg Leu Pro Tyr Glu Leu Asn Gly
305                 310                 315                 320
Asn Cys Asp Asn Ile Pro Val Ser Asn Ser Thr Asp Gly Cys Pro Ser
                325                 330                 335
Gly Asp Asp Pro Lys Arg Asn His Leu Leu Cys Cys Asp Ser Ser Gly
            340                 345                 350
Tyr Cys Thr Gln Leu Ser
        355


<210> 225
<211> 648
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK46804.1

<400> 225
Met Gly Ser Tyr Thr Phe Thr Trp Pro Tyr Asn Ala Asn Glu Val Phe
 1               5                  10                  15
Val Thr Gly Thr Phe Asp Asp Trp Gly Lys Thr Val Lys Leu Asp Arg
            20                  25                  30
Val Gly Asp Val Phe Glu Lys Glu Val Pro Leu Pro Val Thr Asp Glu
        35                  40                  45
Lys Val His Tyr Lys Phe Val Val Asp Gly Ile Trp Thr Thr Asp Asn
    50                  55                  60
Arg Ala Pro Glu Glu Asp Asp Gly Ser Ser Asn Ile Asn Asn Val Leu
65                  70                  75                  80
Tyr Pro Asp Gln Ile Leu Lys Asp Ser Thr Thr Pro Leu Leu Asn Gly
                85                  90                  95
Thr Ala Ala Met Ala Gly Val Thr Pro Gly Ser Thr Thr Ala Ala Leu
            100                 105                 110
Ala Ala Gly Val Pro Lys Glu Ser Ser Ser Lys His Gly Gln Asn Gly
        115                 120                 125
Tyr Tyr Pro Thr Ile Ser Ser Ala Ala Pro Gly Ser Thr Thr Ala Ala
    130                 135                 140
```

```
Leu Gly Gln Asp Val Pro Leu Glu Gln Arg Ala Asn Val Pro Gly Ser
145                 150                 155                 160
Phe Pro Val Thr Pro Ala Ser Glu Ala Asp Lys Phe Ser Val Asn Pro
                165                 170                 175
Ile Pro Ala Ser Ser Gly Ala Gly Asn Pro Ile Lys Leu Asn Pro Gly
            180                 185                 190
Glu Lys Val Pro Asp Ser Ser Thr Phe Asn Thr Asn Thr Ile Ser Ser
        195                 200                 205
Thr Ala Arg Thr Asp Arg Ala Gly Tyr Glu Gln Gly Thr Ser Gly Gly
    210                 215                 220
Phe Pro Gly Ser Pro Ala Tyr Asp Ala Ser Ala Phe Ala Ile Pro Pro
225                 230                 235                 240
Val Ser Lys Asn Met Ile Pro Glu Ser Ser Leu Pro Met Gly Glu Asn
                245                 250                 255
Gln Gly Ala Thr Glu Pro Thr Tyr Thr Ile Gln Ser Ala Ala Pro Thr
            260                 265                 270
Ser Thr Thr Ala Gly Leu Ala Ala Ala Val Pro Leu Glu Ser Gln Arg
        275                 280                 285
Gln Thr Ser Ser Gly Ala Pro Thr Arg Asp Val Pro Asp Val Val Arg
    290                 295                 300
Gln Ser Met Ser Glu Ala His Arg Asp Pro Glu Ala Ala Thr Asn Lys
305                 310                 315                 320
Glu Ala Val Asp Glu Lys Lys Glu Met Glu Glu Glu Leu Arg Arg Lys
                325                 330                 335
Val Pro Val Asp Asn Ser Thr Gly Ala Pro Ala Pro Thr Thr Val Ala
            340                 345                 350
Gly Leu Gly Thr Ser Ser Gly Leu Gly Phe Thr Ala Gly Ala Ala Pro
        355                 360                 365
Ser Thr Asn Leu Gly Pro Ser Thr Gly Leu Asp Val Ala Thr Gly Met
    370                 375                 380
Gly Thr Thr Thr Gly Leu Asp Ser Val Ser Gly Pro Thr Ala Ala Gln
385                 390                 395                 400
Ser Phe Gln Lys Glu Thr Thr Ser Gly Leu Pro Ala His Asp Val Pro
                405                 410                 415
Asp Val Val Lys Gln Ser Ile Ser Glu Ala His Lys Asp Pro Glu Ala
            420                 425                 430
Ala Gly Val Glu Glu Ala Val Gly Glu Lys Arg Glu Val Glu Glu Glu
        435                 440                 445
Leu Gln Gln Lys Val Pro Val Ser Asn Gln Ser Gly Thr Pro Ala Pro
    450                 455                 460
Val Ile Thr Ala Ala Thr Ser Glu Thr Ala Pro Gly Ser Gly Ala Glu
465                 470                 475                 480
Pro Ala Ser Glu Arg Ala Pro Arg Ala Thr Gly Gly Gly Pro Ala Ser
                485                 490                 495
Ala Gln Ile Ser Pro Arg Ala Thr Thr Pro Thr Asp Gly Pro Thr Val
            500                 505                 510
Thr Thr Gly Val Ala Thr Ser Lys Ala Pro Glu Glu Ser Gly Pro Gly
        515                 520                 525
Ala Ser Gly Arg Glu Glu Thr Thr Glu Ile Pro Thr Lys Pro Ala Ala
    530                 535                 540
Gly Ala Thr Gly Ala Ser Ala Thr Lys Thr Val Asp Ser Gly Val Glu
545                 550                 555                 560
Ser Gly Ile Ala Pro Glu Asp Thr Thr Ser Ala Pro Thr Ala Gly Ala
                565                 570                 575
```

```
Thr Gly Ala Ser Ala Thr Lys Thr Ala Asp Pro Thr Glu Thr Ser Gly
            580                 585                 590
Ala Pro Thr Ser Gly Ala Ser Lys Pro Ala Glu Ser Ala Pro Thr Asn
        595                 600                 605
Asn Ala Ala Ala Thr Ser Lys Pro Ala Thr Asn Asn Ala Ala Gly Ala
    610                 615                 620
Ala Thr Asn Gly Lys Glu Glu Lys Lys Lys Lys Gly Phe Phe Ser Arg
625                 630                 635                 640
Leu Lys Glu Lys Leu Lys Ser Val
                645
```

<210> 226
<211> 818
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK97412.1

<400> 226

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

```
            260                 265                 270
Glu Lys Ala Leu Asn Arg Pro Gln Asp Arg Asp Leu Leu Arg Arg Ala
        275                 280                 285
Ala Ala Glu Ser Val Val Leu Met Lys Asn Glu Asp Asn Ile Leu Pro
    290                 295                 300
Leu Arg Lys Asp Lys Pro Ile Leu Val Ile Gly Pro Asn Ala Gln Ile
305                 310                 315                 320
Ala Ala Tyr Cys Gly Gly Gly Ser Ala Ser Leu Asp Pro Tyr Tyr Thr
                325                 330                 335
Val Ser Pro Phe Glu Gly Val Thr Ala Lys Ala Thr Ser Glu Val Gln
            340                 345                 350
Phe Ser Gln Gly Val Tyr Ser His Lys Glu Leu Pro Leu Leu Gly Pro
        355                 360                 365
Leu Leu Lys Thr Gln Asp Gly Lys Pro Gly Phe Thr Phe Arg Val Tyr
    370                 375                 380
Asn Glu Pro Pro Ser His Lys Asp Arg Thr Leu Val Asp Glu Leu His
385                 390                 395                 400
Leu Leu Arg Ser Ser Gly Phe Leu Met Asp Tyr Ile Asn Pro Lys Ile
                405                 410                 415
His Ser Phe Thr Phe Phe Val Asp Met Glu Gly Tyr Phe Thr Pro Thr
            420                 425                 430
Glu Ser Gly Val Tyr Asp Phe Gly Val Thr Val Val Gly Thr Gly Arg
        435                 440                 445
Leu Leu Ile Asp Asn Glu Thr Val Val Asp Asn Thr Lys Asn Gln Arg
    450                 455                 460
Gln Gly Thr Ala Phe Phe Gly Asn Ala Thr Val Glu Glu Arg Gly Ser
465                 470                 475                 480
Lys His Leu Asn Ala Gly Gln Thr Tyr Lys Val Val Leu Glu Phe Gly
                485                 490                 495
Ser Ala Pro Thr Ser Asp Leu Asp Thr Arg Gly Ile Val Val Phe Gly
            500                 505                 510
Pro Gly Gly Phe Arg Phe Gly Ala Ala Arg Gln Val Ser Gln Glu Glu
        515                 520                 525
Leu Ile Ser Asn Ala Val Ser Gln Ala Ser Gln Ala Ser Gln Val Ile
    530                 535                 540
Ile Phe Ala Gly Leu Thr Ser Glu Trp Glu Thr Glu Gly Asn Asp Arg
545                 550                 555                 560
Glu His Met Asp Leu Pro Pro Gly Thr Asp Glu Met Ile Ser Arg Val
                565                 570                 575
Leu Asp Ala Asn Pro Asp Asn Thr Val Val Cys Leu Gln Ser Gly Thr
            580                 585                 590
Pro Val Thr Met Pro Trp Val His Lys Ala Lys Ala Leu Val His Ala
        595                 600                 605
Trp Phe Gly Gly Asn Glu Cys Gly Asn Gly Ile Ala Asp Val Leu Phe
    610                 615                 620
Gly Asp Val Asn Pro Ser Ala Lys Leu Pro Val Thr Phe Pro Val Arg
625                 630                 635                 640
Leu Gln Asp Asn Pro Ser Tyr Leu Asn Phe Arg Ser Glu Arg Gly Arg
                645                 650                 655
Val Leu Tyr Gly Glu Asp Val Tyr Val Gly Tyr Arg Tyr Tyr Glu Lys
            660                 665                 670
Thr Asn Val Lys Pro Leu Tyr Pro Phe Gly His Gly Leu Ser Tyr Thr
        675                 680                 685
Thr Phe Ser Arg Ser Asp Leu Lys Ile Thr Thr Ser Pro Glu Lys Ser
```

```
    690                 695                 700
Thr Leu Thr Asp Gly Glu Pro Ile Thr Ala Thr Val Gln Val Lys Asn
705                 710                 715                 720
Thr Gly Thr Val Ala Gly Ala Glu Ile Val Gln Leu Trp Val Leu Pro
                725                 730                 735
Pro Lys Thr Glu Val Asn Arg Pro Val Arg Glu Leu Lys Gly Phe Thr
            740                 745                 750
Lys Val Phe Leu Gln Pro Gly Glu Glu Lys Gln Val Glu Ile Val Val
        755                 760                 765
Glu Lys Lys Leu Ala Thr Ser Trp Trp Asp Glu Gln Arg Gly Lys Trp
    770                 775                 780
Ala Ser Glu Lys Gly Thr Tyr Gly Val Ser Val Thr Gly Thr Gly Glu
785                 790                 795                 800
Glu Glu Leu Ser Gly Glu Phe Gly Val Glu Arg Thr Arg Tyr Trp Val
                805                 810                 815
Gly Leu
```

<210> 227
<211> 774
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK43189.1

<400> 227

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

```
His Pro Ser Lys Val Arg Gln Ser Thr Thr Lys Gln Ala Asp Ser Gly
    210                 215                 220
Leu Ile Leu Gly Phe Lys Pro Ile Lys Lys Asp Ala Glu Gly Lys Val
225                 230                 235                 240
Ile Lys Asp Thr Leu Ala Asp Asn Thr Pro Thr Lys Ala Lys Ala Ser
                245                 250                 255
Pro Ala Pro Tyr Tyr Gly Thr Pro Ala Phe Glu Phe Lys Phe Ser Cys
            260                 265                 270
Glu Ser Gln Leu Ser Asp Glu Ala Lys Lys Leu Met Glu Thr Val Arg
        275                 280                 285
Glu Asp Ala Ala Lys Ile Lys Ala Gln Met Thr Leu Glu Pro Asp Gln
    290                 295                 300
Asn Arg Ala Glu Ala Ala Asp Arg Lys Ile Val Gln Pro Lys Gly Lys
305                 310                 315                 320
Ala Ser Arg Phe Ser Asp Val His Met Ala Glu Phe Lys Lys Met Asp
                325                 330                 335
Ser Ile Ala Gly His Ala Ser Ala Phe Arg Ala Thr Pro Gly Arg Phe
            340                 345                 350
Gln Pro Val Val Lys Thr Leu Lys Arg Thr Asn Ser Lys Ala Arg Leu
        355                 360                 365
Asp Glu Ser Asp Arg Asn Ser Pro Ser Pro Ser Lys Ile Ala Arg Pro
    370                 375                 380
Ser Pro Ala Ile Val Ala Pro Ala Ser Asn Lys Arg Val Lys His Asp
385                 390                 395                 400
Lys Ala Asp Asp Ala Ser Thr Arg Arg Pro Thr Ala Ala Ser Pro Pro
                405                 410                 415
Lys Pro Val Gln Pro Arg Pro Arg Ser Thr Val Arg Ser Ser Leu Met
            420                 425                 430
Thr Pro Thr Arg Ser Ser Ala Ala Arg Ala Ser Ser Val Thr Ala Arg
        435                 440                 445
Pro Pro Arg Thr Ser Met Ile Pro Ser Leu Val Arg Ser Pro Ala Ala
    450                 455                 460
Lys Pro Ala Asp Val Pro Arg Thr Pro Gln Thr Glu Phe Asn Pro Arg
465                 470                 475                 480
Leu Lys Ser Asn Leu Pro Thr Leu Gly Asn Leu Lys Ser Ile Leu Arg
                485                 490                 495
Arg His Gln Pro Leu Phe Ser Lys Asp Pro Ser Lys Ile Ala Ala Gly
            500                 505                 510
Thr His Val Ala Ala Pro Asp Phe Thr Ser Asn Leu Leu Phe Gly Ser
        515                 520                 525
Arg Gly Thr Thr Glu Glu Pro Ala Gln Thr Pro Ser Pro Lys Lys Arg
    530                 535                 540
Val Glu Phe Thr Pro Ser Val Lys Ala Arg His Glu Glu Val Met Phe
545                 550                 555                 560
Ser Pro Ser Pro Ser Lys Val Pro Val Ala Ser Pro Ser Arg Thr Thr
                565                 570                 575
Ser Asp Val Val Tyr Pro Thr Leu Pro Val Leu Thr Pro Glu Gln Asn
            580                 585                 590
Arg Val Ser Ala Lys Ser Pro Ala Gln Ala Thr Thr Pro Thr Ile Arg
        595                 600                 605
His Val Arg Pro Ser Asp Val His Ala Asn Pro Leu Pro Glu Val Ala
    610                 615                 620
Gly Val Pro His Gly Ile Gly His Lys Lys Arg Thr Arg Glu Ser Gly
625                 630                 635                 640
```

Glu Asp Thr Lys Thr Asn Asp Leu Pro Glu Val Ala Gly Val Pro His
645 650 655
Gly Ile Gly Gln Lys Lys Arg Asn Arg Ala Ala Leu Glu Asp Glu Thr
660 665 670
Asp Thr Glu Asn Val Pro Pro Val Asp Leu Thr Ala Asp Ala Arg Ser
675 680 685
Ala Lys Arg Met Lys Met Thr Ser Pro Ser Pro Leu Lys Ala Pro Thr
690 695 700
Leu Ser Ala Arg Lys Val Ala Ala Pro Ser Pro Thr Lys Ala Ala Thr
705 710 715 720
Pro Ser Pro Thr Lys Pro Arg Ser His Thr Pro Leu Arg Ser Ala Thr
725 730 735
Thr Ser Arg Met Ser Thr Pro Gly Ile Ser Thr Pro Ala Ser Val Arg
740 745 750
Ala Arg Asn Arg Gly Val Leu Ser Val Ser Arg Leu Asn Met Leu Ala
755 760 765
Gln Pro Lys Asn Arg Gly
770

<210> 228
<211> 757
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK43257.1

<400> 228
Met Ser Leu Arg Trp Arg Lys Lys Thr His Trp Pro Pro Ser Pro Cys
1 5 10 15
Val Glu Asp Glu Val Val Ser Leu Ser Arg Glu Leu His Gly Leu Ser
20 25 30
Gln Ile Arg Glu Met Pro Gly Leu Glu Gly Val Cys Ser Arg Gly Ser
35 40 45
Val Asp Gln Tyr Pro Val Leu Val Asp Val Phe Ser Tyr Ser Ser Tyr
50 55 60
Glu Glu Thr Thr Val Ile Tyr Glu Asp Phe Ser Arg Asp Ser Ser Ser
65 70 75 80
Glu Asp Asn Val Gly Pro Pro Thr Pro Val Asp Glu Lys Gln Asp Pro
85 90 95
Met Leu Tyr Leu Val Gly Asp Asp Gln Ala Val Ser Leu Ser Ala Pro
100 105 110
Leu Ala Thr Arg Glu Gln Ser Gln Asp Pro Ser Lys Thr Pro Ala Asp
115 120 125
Asn Glu Gln Gly Ser Thr Thr Arg Gly Arg Pro Arg Ala Asp Thr Arg
130 135 140
Ala Gln Arg Asp Ser Pro Ser Lys Lys Asp Thr Ala Gln Ser Ser Arg
145 150 155 160
Asp Ala Ser Arg Ala Ser Asn Ile Arg Thr Pro Ala Val Thr Gln Ser
165 170 175
Lys Ser Thr Pro Ser Leu Pro Arg Arg Phe Gly Ser Val Lys His Gly
180 185 190
Arg Ser Ala Asp Ala Leu Thr Thr Lys Ser Gly Tyr Gln Ser Asp Ser

```
        195                 200                 205
Ala Thr Val Lys Ser Lys Ala Lys Pro Glu Thr Val Asp Lys Ser Ala
    210                 215                 220
Ala Pro Gln Thr Asp Lys Lys Ser Pro Thr Gly Leu Thr Val Ala Glu
225                 230                 235                 240
Arg Leu Glu Glu Lys Ile Arg Gln Arg Gln Glu Leu Arg Ala Lys Glu
                245                 250                 255
Ser Ser Gly Asp Ala Pro Lys Thr Pro Ser Pro Pro Ser Thr Asp Gln
            260                 265                 270
Pro Ser Val Pro Val Gly Arg Ala Ala Glu Pro Ser Ile Thr Pro Ala
        275                 280                 285
Ala Thr Ala Ala Pro Lys Ser Thr Ala Pro Lys Thr Arg Pro Arg Ser
    290                 295                 300
Thr Ser Thr Pro Lys Glu Pro Thr Asn Asp His Arg Val Asp Gly Pro
305                 310                 315                 320
Glu Ala Ser Ser Ser Ala Ala Ala Pro Ala Leu Gln Leu Pro Pro Arg
                325                 330                 335
Pro Gly Leu Ala Ser Lys Pro Ala Gly Arg Ser Val Ser Ser Asn Asp
            340                 345                 350
Ala Lys Ser Thr Ala Gln Leu Pro Ala Arg Arg Ala Val Ser Phe Leu
        355                 360                 365
Asp Asp Val Pro Gln Arg Ser Ser Ser Leu Pro Arg Thr Pro Glu Asp
    370                 375                 380
Ile Pro Glu Pro Pro Pro Leu Pro Arg Arg Arg Ser Ser Ser Gln Asp
385                 390                 395                 400
Ala Val Arg His Arg Ser Ser Ser Gln Asp Ala Val Arg Gln Thr Ser
                405                 410                 415
Pro Lys Arg Pro Phe Phe Leu Pro Pro Cys Pro Arg Ser Thr Pro Ile
            420                 425                 430
Ala Gly Tyr Gln Asp Trp His Thr Val Lys Gly Leu Pro His Leu Asn
        435                 440                 445
Ile Cys Pro Ser Cys Met Lys Gln Met Arg Lys Ser Glu Phe Arg Asp
    450                 455                 460
His Phe Val Leu Ala Ser Pro Arg Ser Arg Gly Glu Lys Ile Arg Cys
465                 470                 475                 480
Ser Met Ser Glu Pro Trp Thr Arg Leu Ala Trp Met Gln Thr Leu Lys
                485                 490                 495
Lys Gln Leu Asp His Leu Glu Leu Leu His Gln Ile Thr Arg Pro Pro
            500                 505                 510
Leu Ser Ile Lys Pro Cys Pro Gly Arg Ile Ile Thr Glu Gln His Trp
        515                 520                 525
Tyr Arg Ile Val Asp Pro Glu Thr Asn Met Tyr Leu Pro Gln Phe Asn
    530                 535                 540
Val Cys Ser Ala Cys Val Arg Asn Leu Arg Val Leu Met Pro Gln His
545                 550                 555                 560
Arg Asp Thr Phe Lys Arg Ser Ser Thr Lys Gln Glu Arg Ala Cys Asp
                565                 570                 575
Phe Leu Thr Asp Ser Pro Arg Phe Val Arg Tyr Ile Asp Tyr Leu Asp
            580                 585                 590
Ile Ala Ala Asn Arg Ala Asp Gln Glu Asn Met Leu Arg Pro Asp Val
        595                 600                 605
Thr Glu Phe Leu Ser Tyr Ala Arg Arg Lys Val Val Leu Arg Asp Cys
    610                 615                 620
Arg Arg Asp Arg Arg Ile Leu Ser Thr Trp His Tyr Met Pro Gln Leu
```

625 630 635 640
Pro Glu Leu Thr Val Cys Glu Asp Cys Tyr Asp Asp Val Val Trp Pro
645 650 655
Leu Val Arg Ala Lys Gln Pro Ile Ala Arg Lys Phe Ser Thr Ser Met
660 665 670
Arg Leu Leu Pro Gly Asp Gly Pro Ser Arg Cys Arg Glu Ala Ser Cys
675 680 685
Gln Leu Tyr Ser Pro Arg Met Arg Ala Lys Phe Ala Glu Ala Val Gln
690 695 700
Ser Asn Asp Leu Met Tyr Leu Lys Gln Val Ala Leu Arg Arg Arg Asp
705 710 715 720
Ala Glu Gln Arg Tyr Arg Asp Arg Glu Glu Glu Leu Leu Glu Asp Ala
725 730 735
Ser Arg Gly Tyr Asp Val Glu Gly Glu Met Arg Arg Asn Val Glu Glu
740 745 750
Trp Lys Arg Asn Glu
755

<210> 229
<211> 616
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK97469.1

<400> 229
Met Ser Leu Leu Pro Val Ile Leu Val Thr Phe Phe Leu Val Phe Cys
1 5 10 15
Cys Ala Ala Gly Pro Ile Ala Pro Phe Ala Ser Lys Arg Asp Leu Glu
20 25 30
Ser Leu Ser Pro Ser Pro Ser Leu Thr Thr Pro Tyr Val His Val Ala
35 40 45
Ser Ser Ser Val Asp Asp Asp Asp Asp Asn Glu Ile Asn Ala Leu Thr
50 55 60
Val Val Pro Val Thr Pro Ser Ser Leu Pro Gln Thr Ala Ser Ser Ser
65 70 75 80
Ser Thr Thr Ile Glu Pro Ala Leu Ser Ser Ser Ala Ala Phe Ile Gln
85 90 95
Glu Ser Ser Ile Val Ala Ala Thr Thr Ser Ser Leu Ser Glu Ser Ser
100 105 110
Ser Ala Val Thr His Ser Phe Ala Pro Ser Thr Ser Ser Asp Ser Thr
115 120 125
Val Asn Thr Leu Ser Gln Thr Leu Thr Ser Thr Thr Thr Thr Thr Thr
130 135 140
Thr Thr Ser Ser Pro Thr Thr Leu Gly Glu Pro Ser Ser Ala Pro Phe
145 150 155 160
Ser Pro Leu Ser Ser Ala Val Arg Ser Ser His Thr Thr Ser Ser Ser
165 170 175
Ser His Ile Met His Ile Thr Thr Pro Ser Thr Thr Leu Ser Glu Ser
180 185 190
Ser Gln Ile Val Thr Pro Ser Ile Ile Ile Pro Gly Gly Pro Met Glu
195 200 205

```
Ala Ser Ser Ser His Ala Pro Gly Thr Ala Thr Ser Ser His Ile Thr
    210                 215                 220
His Glu Thr Ser Ser Ser Ala Val Arg Val Ser His Ser Ser Ser Ala
225                 230                 235                 240
Ala Ala Glu Met Ser Lys Ser Ser Pro Ser His Gln Gly Thr Leu Asn
                245                 250                 255
Ser Ser Ser Arg Leu Leu His Ser Ser Thr Ala Ala Leu Leu Pro Ser
            260                 265                 270
Ser Thr Ala Pro Glu Ser Ala Pro Glu Thr Ser Ser Thr Arg Thr Ser
        275                 280                 285
Glu Thr Thr Thr Ser Thr Ser Leu Thr Ile Gly Val Ile Val Pro Leu
    290                 295                 300
Pro Glu Ala Ser Thr Ser Pro Ser Thr Met Leu Glu Met Ser Ser Ser
305                 310                 315                 320
Thr Ser Gln Ser Ser Glu Ser Ile Thr Thr Thr Ala Asp Asp Thr Ser
                325                 330                 335
Ser Ala Ser Ser Thr Lys Val Leu Ser Thr Pro Thr Glu Ser Glu Thr
            340                 345                 350
Thr Thr Pro Thr Ser His Thr Ala Ser Pro Phe Ile Gly Val Thr Ile
        355                 360                 365
Pro Thr Thr Thr Lys Thr Thr Gln Pro Ala Asp Pro Ala Asp Ile Thr
    370                 375                 380
Thr Thr Thr Thr Thr Pro Thr Ser Glu Ala Glu Asp Ala Thr Thr Thr
385                 390                 395                 400
Ser Ala Pro Thr Pro Val Val Val Leu Val Thr Pro Glu Gly Ser Thr
                405                 410                 415
Thr Val Ile Gly Thr Ser Ser Phe Ile Ala Pro Asn Pro Asp Ile Thr
            420                 425                 430
Ser Thr Ser Thr Ser Thr Ser Ser Leu Thr Thr Thr Ile Glu Pro Thr
        435                 440                 445
Pro Thr Thr Ser Thr Thr Glu Pro Pro Thr Thr Leu His Ala Thr Ser
    450                 455                 460
Thr Thr Ile Gln Thr Val Tyr Val Val Ile Thr Asp Thr Pro Thr Pro
465                 470                 475                 480
Glu Pro Thr Trp Asp Ser Thr Thr Ile Ala Thr Ala Ile Ile Thr Val
                485                 490                 495
Tyr Asp Lys Ser Thr Ser Glu Thr Val Pro Thr Thr Thr Thr Thr Ser
            500                 505                 510
Arg Ala Gly Glu Glu Met Glu Ser Thr Thr Thr Thr Pro Leu Asp Thr
        515                 520                 525
Glu Gln Thr Ser Thr Gln Ser Thr Glu Asp Glu Ile Pro Thr Ser Thr
    530                 535                 540
Pro Ile Ala Asp Thr Glu Thr Ala Thr Ala Ile Ile Thr Ser Tyr Pro
545                 550                 555                 560
Ser Thr Ser Thr Leu Ser Gly Glu Thr Gly Asp Val Ile Arg Ile Val
                565                 570                 575
Pro Val Thr Pro Thr Gly Pro Ile Thr Val Thr Val Thr Val Thr Glu
            580                 585                 590
Lys Glu Arg Glu Thr Val Thr Lys Thr Glu Thr Val Thr Glu Arg Val
        595                 600                 605
Thr Glu Thr Glu Ser Val Thr Thr
    610                 615
```

<210> 230
<211> 847
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK97480.1

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

```
        355                 360                 365
Asp Pro Glu Ser Ser Lys Pro Gly Tyr Met Arg Leu Trp Ser Ala Gly
    370                 375                 380
Gly Ala Thr Gly Gly Asp Gly Cys His Ile Asp Phe Ser Ser Ala Val
385                 390                 395                 400
Ala Phe Lys Trp Trp Tyr Asp Gly Val Gln Ser Leu Lys Arg Ala Gly
                405                 410                 415
Ile Asp Ala Met Trp Asn Asp Asn Asn Glu Tyr Thr Leu Pro Asp Asp
            420                 425                 430
Asp Trp Lys Leu Ala Leu Asp Glu Pro Thr Val Ser Asp Ala Val Lys
        435                 440                 445
Lys Gly Val Glu Asn Ser Val Gly Gln Trp Gly Arg Ala Met His Thr
    450                 455                 460
Glu Leu Met Gly Lys Ala Ser His Asp Ala Leu Leu Asn Ile Glu Pro
465                 470                 475                 480
Asn His Arg Pro Phe Val Leu Thr Arg Ser Ala Thr Ala Gly Thr Met
                485                 490                 495
Arg Tyr Ala Ala Ser Thr Trp Ser Gly Asp Asn Val Thr Ser Trp Glu
            500                 505                 510
Gly Met Lys Gly Ala Asn Ala Leu Ser Leu Ser Ala Gly Ile Ser Leu
        515                 520                 525
Leu Gln Cys Cys Gly His Asp Ile Gly Gly Phe Glu Gly Pro Gln Pro
    530                 535                 540
Ser Pro Glu Leu Leu Leu Arg Trp Ile Gln Leu Gly Ile His Ser Pro
545                 550                 555                 560
Arg Phe Ala Ile Asn Cys Phe Lys Thr Ser Pro Gly Asn Ser Ser Val
                565                 570                 575
Gly Asp Val Ile Glu Pro Trp Met Tyr Pro Glu Ile Thr Pro Leu Val
            580                 585                 590
Arg Asp Thr Ile Lys Arg Arg Tyr Glu Ile Leu Pro Tyr Ile Tyr Ser
        595                 600                 605
Leu Gly Leu Glu Ser His Leu Thr Ala Ser Pro Pro Gln Arg Trp Val
    610                 615                 620
Gly Trp Gly Tyr Glu Ser Asp Pro Glu Val Trp Thr Lys Ala Leu Lys
625                 630                 635                 640
Ser Gly Asp Glu Gln Phe Trp Phe Gly Asp Thr Ile Met Val Gly Gly
                645                 650                 655
Val Tyr Glu Pro Gly Val Ser Val Ala Lys Leu Tyr Leu Pro Arg Lys
            660                 665                 670
Ala Asn Asp Gln Phe Asp Phe Gly Tyr Val Asn Met Asn Glu Pro Tyr
        675                 680                 685
Asn Tyr Leu Ala Ser Gly Gln Trp Val Glu Val Pro Ser Glu Trp Arg
    690                 695                 700
Lys Ser Ile Pro Leu Leu Ala Arg Ile Gly Gly Ala Ile Pro Val Gly
705                 710                 715                 720
Lys Pro Val His Thr Arg Val Pro Gly Asp Asp Thr Pro Ala Ser Val
                725                 730                 735
Ala Val Lys Glu Val Asp Asp Tyr Arg Gly Val Glu Ile Phe Pro Pro
            740                 745                 750
Leu Gly Ser Ser His Gly Gln Val Phe Ser Thr Thr Trp Phe Glu Asp
        755                 760                 765
Asp Gly Ile Ser Leu Glu Ala Arg Ile Ser Glu Tyr Thr Val Thr Tyr
    770                 775                 780
Ser Ser Thr Glu Glu Lys Val Ile Val Gly Phe Ser Arg Asp Glu Lys
```

785 790 795 800
Ser Gly Phe Val Pro Ala Trp Thr Asp Leu Asp Ile Ile Leu His Asn
805 810 815
Gly Asp Glu Arg Arg Val Val Ser Asp Ile Gly Lys Thr Val Glu Tyr
820 825 830
Lys Gly Lys Gly Ser Arg Gly Arg Val Val Tyr Thr Leu Lys Asn
835 840 845

<210> 231
<211> 1324
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAK47332.1

<400> 231
Met Asn Glu Gly Arg Leu Ala His Pro Gln Phe Asn Gln Tyr Ser Phe
1 5 10 15
Lys Ala Gly Ala Ser Thr Val Gln Ala Glu Ala Ala Pro Ala Leu Asn
20 25 30
Tyr Glu Asp Ala Ser Thr His Asn Ala Ala Lys Asn Ala Thr Lys Arg
35 40 45
Ser Gly Arg Lys Gly Asp Gln Thr Tyr Thr Tyr Ser Ile Pro Pro Glu
50 55 60
Leu Ala Glu Ala Ala Arg Leu Val Ala Glu Ala Ser Pro Gln Pro Val
65 70 75 80
Pro Thr Asp Tyr Gly Val Asp Ile Ser Leu Val Val Ser Lys Tyr Arg
85 90 95
Lys Tyr Asp Asn Asn Asp Thr Asn Val Pro Lys Gln Lys Tyr Val Glu
100 105 110
Pro Asn Gly Leu Asp Gly Tyr Val His Thr Gly Gln Pro Glu Asp Ser
115 120 125
Pro Glu Ile His Thr Glu Leu Lys Lys Arg Ala Thr Thr Asp Phe Trp
130 135 140
Leu Thr Gln Met Gly Asp Ser Gly Ser Ser Pro Tyr Ala Pro Asp Gly
145 150 155 160
Tyr Lys Val Trp Arg Asn Val Arg Asp Tyr Gly Ala Lys Gly Asp Gly
165 170 175
Ile Thr Asp Asp Thr Ala Ala Ile Asn Lys Ala Ile Ser Asp Gly Gly
180 185 190
Arg Cys Gly Ala Glu Cys Gly Ser Ser Thr Ile Tyr Pro Ala Phe Val
195 200 205
Tyr Phe Pro Ala Gly Lys Tyr Leu Val Ser Ser Pro Ile Ile Gln Tyr
210 215 220
Tyr Asn Thr Glu Phe Tyr Gly Asn Pro Phe Asp Tyr Pro Thr Ile Leu
225 230 235 240
Ala Ala Ser Ser Phe Val Gly Leu Gly Val Ile Thr Ser Asp Val Tyr
245 250 255
Thr Gly Asp Asp Thr Glu Trp Tyr Ile Asn Gln Asn Asn Phe Leu Arg
260 265 270
Ser Ile Arg Asn Phe Lys Met Asp Ile Thr Arg Thr Asp Pro Asn Ala
275 280 285

```
Tyr Val Cys Ala Ile His Trp Gln Val Ala Gln Gly Thr Ser Leu Glu
    290                 295                 300
Asn Ile Glu Phe Tyr Met Met Gln Asp Gly Leu Thr Thr Gln Gln Gly
305                 310                 315                 320
Ile Tyr Met Glu Asn Gly Ser Gly Gly Phe Leu Thr Asn Leu Thr Phe
                325                 330                 335
Val Gly Gly Asn Phe Gly Tyr Val Tyr Ala Phe Ser Gln Arg Cys Thr
            340                 345                 350
Pro Leu Ser Asp Leu Pro Ser Gly His Thr Leu Ala Thr Gln Phe Thr
        355                 360                 365
Ser Thr Ser Leu Thr Phe Met Asn Cys Lys Thr Ala Leu Gln Val His
    370                 375                 380
Trp Asp Trp Ala Trp Thr Met Gln Asp Val Val Val Glu Asn Cys Thr
385                 390                 395                 400
Asn Gly Ile Val Ile Val Gly Gly Ala Gly Gly Pro Lys Ser Thr Gly
                405                 410                 415
Gln Ser Val Gly Ser Leu Ile Leu Val Asp Ala Val Ile Ala His Thr
            420                 425                 430
Gln Thr Gly Ile Val Thr Thr Leu Leu Ala Glu Asn Ser Thr Ser Phe
        435                 440                 445
Leu Leu Gln Gly Val Val Phe Ile Glu Val Asp Thr Ala Ile Leu Asp
    450                 455                 460
Ser Ala Gln Gly Lys Thr Leu Met Ala Gly Gly Ser Asn Val Pro Val
465                 470                 475                 480
Phe Ser Trp Gly Phe Gly Arg Val Val Thr Thr Gly Ala Glu Ser Thr
                485                 490                 495
Phe Tyr Asn Gly Gln Asp Ile Pro Arg Thr Asn Arg Ser Val Pro Leu
            500                 505                 510
Thr Thr Ile Gly Tyr Ile Glu Pro Asn Phe Tyr Leu Arg Arg Arg Pro
        515                 520                 525
Thr Tyr Arg Asp Ile Gly Met Ser Gln Val Ile Asn Val Lys Asp Trp
    530                 535                 540
Gly Ala Ala Gly Asp Gly Lys Thr Asp Asp Thr Ala Val Leu Asn Ser
545                 550                 555                 560
Ile Leu Asp Arg Ala Ala Asn Met Ser Ser Ile Val Phe Phe Pro Tyr
                565                 570                 575
Gly Val Tyr Ile Ile Arg Asp Thr Leu Arg Val Pro Val Asn Ser Arg
            580                 585                 590
Ile Met Gly Gln Val Trp Ser Gln Ile Met Ala Thr Gly Pro Lys Phe
        595                 600                 605
Gln Asp Glu Gln Asn Pro His Ile Ala Val Gln Val Gly Gln Val Gly
    610                 615                 620
Asp Arg Gly Ile Val Glu Ile Gln Ser Leu Met Phe Thr Val Ser Gly
625                 630                 635                 640
Pro Thr Ala Gly Ala Val Leu Met Glu Trp Asn Val His Gln Val Ile
                645                 650                 655
Gln Gly Ser Ala Gly Met Trp Asp Ser His Phe Arg Val Gly Gly Ala
            660                 665                 670
Thr Gly Ser Gln Leu Gln Ala Asp Glu Cys Pro Lys Gly Ser Gly Val
        675                 680                 685
Val Leu Pro Ala Cys Lys Ala Ala Ser Leu Leu Leu His Leu Thr Ser
    690                 695                 700
Gln Ser Ser Ala Tyr Leu Glu Asn Ile Trp Leu Trp Val Ala Asp His
705                 710                 715                 720
```

```
Asp Leu Asp Leu Gln Asp Gln Ala Gln Ile Asp Val Tyr Ser Ala Arg
                725                 730                 735
Gly Leu Leu Val Glu Ser Gln Gly Pro Thr Trp Leu Tyr Gly Thr Ala
            740                 745                 750
Ser Glu His Asn Val Leu Tyr Gln Tyr Gln Val Ser Gln Ala Arg Asp
        755                 760                 765
Leu Tyr Met Gly Met Ile Gln Thr Glu Ser Pro Tyr Phe Gln Asn Val
    770                 775                 780
Pro Pro Ala Pro Ser Pro Phe Ser Pro Gly Leu Phe Pro Asn Asp Pro
785                 790                 795                 800
Thr Phe Ser Asp Cys Asp Ser Asp Ser Gln Thr Cys Pro Val Ser Trp
                805                 810                 815
Ala Leu Arg Ile Ile Asp Ser Thr Ser Val Tyr Ser Met Gly Ala Gly
            820                 825                 830
Ile Tyr Ser Trp Phe Ser Ala Tyr Ser Gln Asp Cys Leu Asp Thr Glu
        835                 840                 845
Ser Cys Gln Gln His Ala Val Gly Ile Ser Gln Ser Thr Asn Thr Trp
    850                 855                 860
Leu Tyr Asn Leu Val Thr Lys Gly Ile Ala Glu Met Val Thr Pro Thr
865                 870                 875                 880
Asn Glu His Pro Thr Leu Ser Ala Asp Asn Val Asn Gly Phe Met Ser
                885                 890                 895
Ser Ile Leu Ala Trp Val Arg Leu Ala Asn Thr Thr Ile Gly Ala Arg
            900                 905                 910
Lys Phe Pro Gly Phe Gln Leu Tyr Gln Pro Lys Trp Leu Asp Gly Leu
        915                 920                 925
Thr Asp Thr Cys Lys Thr Ala Leu Ser Gln Lys Ile Leu Cys His Pro
    930                 935                 940
Tyr Leu Glu Met Lys Phe Ser Asn Pro Gly Ile Gly Gln Tyr Ile Asp
945                 950                 955                 960
Asn Asn Thr Leu Ala Asp Glu Val Cys Asp Gln Gly Cys Gly Glu Ser
                965                 970                 975
Leu Gln Met Trp Thr Thr Asn Val Ala Asn Ser Cys Leu Asn Gln Thr
            980                 985                 990
Ile Asp Asp Thr Asp Pro Val Ala Ala Gly Gly Tyr Ile Tyr Ala Gly
        995                 1000                1005
Tyr Asn Leu Thr Cys Leu Arg Asp Pro His Thr Lys Lys Tyr Cys Pro
    1010                1015                1020
Asp Val Leu Ser His Phe Thr Ile Val Asp Ser Val Arg Ser Met Thr
1025                1030                1035                1040
Leu Ala Glu Met Cys Ser Tyr Cys Phe Thr Thr Ser Leu Glu Met Arg
                1045                1050                1055
Gln Ala Ser Pro Tyr Ala Ala Tyr Thr Asp Val Asp Lys Asp Ala Leu
            1060                1065                1070
Glu Thr Val Asn Ala Glu Cys Gly Leu Ser Gly Pro Thr Asp Leu His
        1075                1080                1085
Lys Pro Leu Tyr Thr Glu Asp Glu Val Asp Arg Pro Ile Cys Met Ser
    1090                1095                1100
Gly Ile Thr His Thr Thr Ser Glu Gly Asp Thr Cys Asp Leu Leu Ala
1105                1110                1115                1120
Tyr Lys Tyr His Val Ala Ser Ala Val Ile Gln Leu Ala Asn Pro Met
                1125                1130                1135
Leu Val Asn Asp Cys Ser Glu Leu Ile Pro Gly Arg Gln Leu Cys Met
            1140                1145                1150
```

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Pro Leu Ser Cys Asp Thr Gln Tyr Thr Leu Gln Asp Asn Asp Thr Cys
        1155                1160                1165
Leu Ser Ile Glu Trp Ala Gln Pro Ile Gly Phe Gly Glu Val Arg Arg
    1170                1175                1180
Tyr Asn Pro Trp Leu Asn Val Asp Cys Thr Asn Leu Gln Thr Thr Arg
1185                1190                1195                1200
Gln Val His Gly Ser Val Leu Cys Leu Ser Pro Gln Gly Gly Ser His
                1205                1210                1215
Asn Val Thr Gly Thr Gly Ser Pro Cys Pro Gly Ile Ser Asp Gly Tyr
            1220                1225                1230
Thr Asn Val Val Gln Tyr Ala Pro Thr Asn Ser Thr Ile Ala Lys Gly
        1235                1240                1245
Thr Thr Cys Tyr Cys Gly Lys Trp Tyr Thr Val Gln Gln Gly Asp Ser
    1250                1255                1260
Cys Ala Thr Ile Cys Ile Lys Gln Gly Ile Pro Ser Ser Leu Phe Leu
1265                1270                1275                1280
Ala Val Asn Pro Ser Leu Ser Thr Ser Asp Cys Asp Thr Ser Leu Gln
                1285                1290                1295
Val Gly Tyr Thr Tyr Cys Val Gly Pro Asp Thr His Trp Asp Asp Thr
            1300                1305                1310
Asp Asn Phe Trp Gly Glu Phe Ala Cys Glu Ala Tyr
        1315                1320


<210> 232
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase 1ACZ_A

<220>
<221> VARIANT
<222> 108
<223> Xaa = Any Amino Acid

<400> 232
Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu Thr Ala Thr
 1               5                  10                  15
Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln Leu
            20                  25                  30
Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser Ala Asp Lys Tyr
        35                  40                  45
Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr Leu Pro Ala Gly
    50                  55                  60
Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser Asp Asp Ser Val
65                  70                  75                  80
Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro Gln Ala Cys
                85                  90                  95
Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Xaa
            100                 105
```

<210> 233
<211> 957
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase ACF60497.1

<400> 233
Met Ser Asn Arg Trp Thr Leu Leu Leu Ser Leu Val Ile Leu Leu Gly
 1               5                  10                  15
Cys Leu Val Ile Pro Gly Val Thr Val Lys His Glu Asn Phe Lys Thr
            20                  25                  30
Cys Ser Gln Ser Gly Phe Cys Lys Arg Asn Arg Ala Phe Ala Asp Asp
        35                  40                  45
Ala Ala Ala Gln Gly Ser Ser Trp Ala Ser Pro Tyr Glu Leu Asp Ser
    50                  55                  60
Ser Ser Ile Gln Phe Lys Asp Gly Gln Leu His Gly Thr Ile Leu Lys
65                  70                  75                  80
Ser Val Ser Pro Asn Glu Lys Val Lys Leu Pro Leu Val Val Ser Phe
                85                  90                  95
Leu Glu Ser Gly Ala Ala Arg Val Val Val Asp Glu Glu Lys Arg Met
            100                 105                 110
Asn Gly Asp Ile Gln Leu Arg His Asp Ser Lys Ala Arg Lys Glu Arg
        115                 120                 125
Tyr Asn Glu Ala Glu Lys Trp Val Leu Val Gly Gly Leu Glu Leu Ser
    130                 135                 140
Lys Thr Ala Thr Leu Arg Pro Glu Thr Glu Ser Gly Phe Thr Arg Val
145                 150                 155                 160
Leu Tyr Gly Pro Asp Asn Gln Phe Glu Ala Val Ile Arg His Ala Pro
                165                 170                 175
Phe Ser Ala Asp Phe Lys Arg Asp Gly Gln Thr His Val Gln Leu Asn
            180                 185                 190
Asn Lys Gly Tyr Leu Asn Met Glu His Trp Arg Pro Lys Val Glu Val
        195                 200                 205
Glu Gly Glu Gly Glu Gln Gln Thr Gln Glu Asp Glu Ser Thr Trp Trp
    210                 215                 220
Asp Glu Ser Phe Gly Gly Asn Thr Asp Thr Lys Pro Arg Gly Pro Glu
225                 230                 235                 240
Ser Val Gly Leu Asp Ile Thr Phe Pro Gly Tyr Lys His Val Phe Gly
                245                 250                 255
Ile Pro Glu His Ala Asp Ser Leu Ser Leu Lys Glu Thr Arg Gly Gly
            260                 265                 270
Glu Gly Asn His Glu Glu Pro Tyr Arg Met Tyr Asn Ala Asp Val Phe
        275                 280                 285
Glu Tyr Glu Leu Ser Ser Pro Met Thr Leu Tyr Gly Ala Ile Pro Phe
    290                 295                 300
Met Gln Ala His Arg Lys Asp Ser Thr Val Gly Val Phe Trp Leu Asn
305                 310                 315                 320
Ala Ala Glu Thr Trp Val Asp Ile Val Lys Ser Thr Ser Ser Pro Asn
                325                 330                 335
Pro Leu Ala Leu Gly Val Gly Ala Thr Thr Asp Thr Gln Ser His Trp
            340                 345                 350
Phe Ser Glu Ser Gly Gln Leu Asp Val Phe Val Phe Leu Gly Pro Thr

```
        355                 360                 365
Pro Gln Glu Ile Ser Lys Thr Tyr Gly Glu Leu Thr Gly Tyr Thr Gln
    370                 375                 380
Leu Pro Gln His Phe Ala Ile Ala Tyr His Gln Cys Arg Trp Asn Tyr
385                 390                 395                 400
Ile Thr Asp Glu Asp Val Lys Glu Val Asp Arg Asn Phe Asp Lys Tyr
                405                 410                 415
Gln Ile Pro Tyr Asp Val Ile Trp Leu Asp Ile Glu Tyr Thr Asp Asp
            420                 425                 430
Arg Lys Tyr Phe Thr Trp Asp Pro Leu Ser Phe Pro Asp Pro Ile Ser
        435                 440                 445
Met Glu Glu Gln Leu Asp Glu Ser Glu Arg Lys Leu Val Val Ile Ile
    450                 455                 460
Asp Pro His Ile Lys Asn Gln Asp Lys Tyr Ser Ile Val Gln Glu Met
465                 470                 475                 480
Lys Ser Lys Asp Leu Ala Thr Lys Asn Lys Asp Gly Glu Ile Tyr Asp
                485                 490                 495
Gly Trp Cys Trp Pro Gly Ser Ser His Trp Ile Asp Thr Phe Asn Pro
            500                 505                 510
Ala Ala Ile Lys Trp Trp Val Ser Leu Phe Lys Phe Asp Lys Phe Lys
        515                 520                 525
Gly Thr Leu Ser Asn Val Phe Ile Trp Asn Asp Met Asn Glu Pro Ser
    530                 535                 540
Val Phe Asn Gly Pro Glu Thr Thr Met Pro Lys Asp Asn Leu His His
545                 550                 555                 560
Gly Asn Trp Glu His Arg Asp Ile His Asn Val His Gly Ile Thr Leu
                565                 570                 575
Val Asn Ala Thr Tyr Asp Ala Leu Leu Glu Arg Lys Lys Gly Glu Ile
            580                 585                 590
Arg Arg Pro Phe Ile Leu Thr Arg Ser Tyr Tyr Ala Gly Ala Gln Arg
        595                 600                 605
Met Ser Ala Met Trp Thr Gly Asp Asn Gln Ala Thr Trp Glu His Leu
    610                 615                 620
Ala Ala Ser Ile Pro Met Val Leu Asn Asn Gly Ile Ala Gly Phe Pro
625                 630                 635                 640
Phe Ala Gly Ala Asp Val Gly Gly Phe Phe Gln Asn Pro Ser Lys Glu
                645                 650                 655
Leu Leu Thr Arg Trp Tyr Gln Ala Gly Ile Trp Tyr Pro Phe Phe Arg
            660                 665                 670
Ala His Ala His Ile Asp Thr Arg Arg Arg Glu Pro Tyr Leu Ile Ala
        675                 680                 685
Glu Pro His Arg Ser Ile Ile Ser Gln Ala Ile Arg Leu Arg Tyr Gln
    690                 695                 700
Leu Leu Pro Ala Trp Tyr Thr Ala Phe His Glu Ala Ser Val Asn Gly
705                 710                 715                 720
Met Pro Ile Val Arg Pro Gln Tyr Tyr Ala His Pro Trp Asp Glu Ala
                725                 730                 735
Gly Phe Ala Ile Asp Asp Gln Leu Tyr Leu Gly Ser Thr Gly Leu Leu
            740                 745                 750
Ala Lys Pro Val Val Ser Glu Glu Ala Thr Thr Ala Asp Ile Tyr Leu
        755                 760                 765
Ala Asp Asp Glu Lys Tyr Tyr Asp Tyr Phe Asp Tyr Thr Val Tyr Gln
    770                 775                 780
Gly Ala Gly Lys Arg His Thr Val Pro Ala Pro Met Glu Thr Val Pro
```

785 790 795 800
Leu Leu Met Gln Gly Gly His Val Ile Pro Arg Lys Asp Arg Pro Arg
805 810 815
Arg Ser Ser Ala Leu Met Arg Trp Asp Pro Tyr Thr Leu Val Val Val
820 825 830
Leu Asp Lys Asn Gly Gln Ala Asp Gly Ser Leu Tyr Val Asp Asp Gly
835 840 845
Glu Thr Phe Asp Tyr Lys Arg Gly Ala Tyr Ile His Arg Arg Phe Arg
850 855 860
Phe Gln Glu Ser Ala Leu Val Ser Glu Asp Val Gly Thr Lys Gly Pro
865 870 875 880
Lys Thr Ala Glu Tyr Leu Lys Thr Met Ala Asn Val Arg Val Glu Arg
885 890 895
Val Val Val Val Asp Pro Pro Lys Glu Trp Gln Gly Lys Thr Ser Val
900 905 910
Thr Val Ile Glu Asp Gly Ala Ser Ala Ala Ser Thr Ala Ser Met Gln
915 920 925
Tyr His Ser Gln Pro Asp Gly Lys Ala Ala Tyr Ala Val Val Lys Asn
930 935 940
Pro Asn Val Gly Ile Gly Lys Thr Trp Arg Ile Glu Phe
945 950 955

<210> 234
<211> 640
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAY05387.1

<400> 234
Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
1 5 10 15
Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
20 25 30
Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
35 40 45
Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
50 55 60
Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
65 70 75 80
Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
85 90 95
Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
100 105 110
Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
115 120 125
Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp
130 135 140
Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile
145 150 155 160
Gly Phe Arg Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr
165 170 175

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Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln
            180                 185                 190
Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser
        195                 200                 205
Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser
    210                 215                 220
Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln
225                 230                 235                 240
Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe
                245                 250                 255
Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr
            260                 265                 270
Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp
        275                 280                 285
Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu
    290                 295                 300
Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
305                 310                 315                 320
Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
                325                 330                 335
Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
            340                 345                 350
Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
        355                 360                 365
Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr
    370                 375                 380
Gly Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala
385                 390                 395                 400
Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala
                405                 410                 415
Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu
            420                 425                 430
Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr
        435                 440                 445
Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr
    450                 455                 460
Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly
465                 470                 475                 480
Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr
                485                 490                 495
Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr
            500                 505                 510
Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser Thr
        515                 520                 525
Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp
    530                 535                 540
Leu Thr Ala Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser
545                 550                 555                 560
Ile Ser Gln Leu Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser
                565                 570                 575
Ala Asp Lys Tyr Thr Ser Gly Asp Pro Leu Trp Tyr Val Thr Val Thr
            580                 585                 590
Leu Pro Ala Gly Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser
        595                 600                 605
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Asp Asp Ser Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val
    610                 615                 620
Pro Gln Ala Cys Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
625                 630                 635                 640


<210> 235
<211> 639
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAY05391.1

<400> 235
Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
 1               5                  10                  15
Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Trp Asp Ser Trp Leu Ser
            20                  25                  30
Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
        35                  40                  45
Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
    50                  55                  60
Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
65                  70                  75                  80
Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
                85                  90                  95
Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
            100                 105                 110
Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
        115                 120                 125
Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp
    130                 135                 140
Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile
145                 150                 155                 160
Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr
                165                 170                 175
Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln
            180                 185                 190
Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Val Asn Gly Ser Ser
        195                 200                 205
Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser Ala
    210                 215                 220
Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln Ala
225                 230                 235                 240
Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe Ile
                245                 250                 255
Leu Ala Asn Phe Asp Ser Ser Arg Ser Ala Lys Asp Ala Asn Thr Leu
            260                 265                 270
Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp
        275                 280                 285
Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu
    290                 295                 300
Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
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305 310 315 320
Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
325 330 335
Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
340 345 350
Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
355 360 365
Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Thr Gly
370 375 380
Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala Val
385 390 395 400
Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala Ala
405 410 415
Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu Gln
420 425 430
Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr Ala
435 440 445
Asn Asn Arg Arg Asn Val Val Pro Ser Ala Ser Trp Gly Glu Thr Ser
450 455 460
Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly Thr
465 470 475 480
Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr Gly
485 490 495
Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr Ser
500 505 510
Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser Thr Ser
515 520 525
Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu
530 535 540
Thr Ala Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser Ile
545 550 555 560
Ser Gln Leu Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser Ala
565 570 575
Asp Lys Tyr Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr Leu
580 585 590
Pro Ala Gly Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser Asp
595 600 605
Asp Ser Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro
610 615 620
Gln Ala Cys Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
625 630 635

<210> 236
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase 1AC0_A

<400> 236
Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu Thr Ala Thr
1 5 10 15

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


<210> 237
<211> 957
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CAS97680.1

<400> 237
Met Ser Asn Arg Trp Thr Leu Leu Leu Ser Leu Val Ile Leu Leu Gly
 1               5                  10                  15
Cys Leu Val Ile Pro Gly Val Thr Val Lys His Glu Asn Phe Lys Thr
            20                  25                  30
Cys Ser Gln Ser Gly Phe Cys Lys Arg Asn Arg Ala Phe Ala Asp Asp
        35                  40                  45
Ala Ala Ala Gln Gly Ser Ser Trp Ala Ser Pro Tyr Glu Leu Asp Ser
    50                  55                  60
Ser Ser Ile Gln Phe Lys Asp Gly Gln Leu His Gly Thr Ile Leu Lys
65                  70                  75                  80
Ser Val Ser Pro Asn Glu Lys Val Lys Leu Pro Leu Val Val Ser Phe
                85                  90                  95
Leu Glu Ser Gly Ala Ala Arg Val Val Val Asp Glu Glu Lys Arg Met
            100                 105                 110
Asn Gly Asp Ile Gln Leu Arg His Asp Ser Lys Ala Arg Lys Glu Arg
        115                 120                 125
Tyr Asn Glu Ala Glu Lys Trp Val Leu Val Gly Gly Leu Glu Leu Ser
    130                 135                 140
Lys Thr Ala Thr Leu Arg Pro Glu Thr Glu Ser Gly Phe Thr Arg Val
145                 150                 155                 160
Leu Tyr Gly Pro Asp Asn Gln Phe Glu Ala Val Ile Arg His Ala Pro
                165                 170                 175
Phe Ser Ala Asp Phe Lys Arg Asp Gly Gln Thr His Val Gln Leu Asn
            180                 185                 190
Asn Lys Gly Tyr Leu Asn Met Glu His Trp Arg Pro Lys Val Glu Val
        195                 200                 205
Glu Gly Glu Gly Glu Gln Gln Thr Gln Glu Asp Glu Ser Thr Trp Trp
    210                 215                 220
Asp Glu Ser Phe Gly Gly Asn Thr Asp Thr Lys Pro Arg Gly Pro Glu
225                 230                 235                 240
Ser Val Gly Leu Asp Ile Thr Phe Pro Gly Tyr Lys His Val Phe Gly

```
                245                 250                 255
Ile Pro Glu His Ala Asp Ser Leu Ser Leu Lys Glu Thr Arg Gly Gly
            260                 265                 270
Glu Gly Asn His Glu Glu Pro Tyr Arg Met Tyr Asn Ala Asp Val Phe
        275                 280                 285
Glu Tyr Glu Leu Ser Ser Pro Met Thr Leu Tyr Gly Ala Ile Pro Phe
    290                 295                 300
Met Gln Ala His Arg Lys Asp Ser Thr Val Gly Val Phe Trp Leu Asn
305                 310                 315                 320
Ala Ala Glu Thr Trp Val Asp Ile Val Lys Ser Thr Ser Ser Pro Asn
                325                 330                 335
Pro Leu Ala Leu Gly Val Gly Ala Thr Thr Asp Thr Gln Ser His Trp
            340                 345                 350
Phe Ser Glu Ser Gly Gln Leu Asp Val Phe Val Phe Leu Gly Pro Thr
        355                 360                 365
Pro Gln Glu Ile Ser Lys Thr Tyr Gly Glu Leu Thr Gly Tyr Thr Gln
    370                 375                 380
Leu Pro Gln His Phe Ala Ile Ala Tyr His Gln Cys Arg Trp Asn Tyr
385                 390                 395                 400
Ile Thr Asp Glu Asp Val Lys Glu Val Asp Arg Asn Phe Asp Lys Tyr
                405                 410                 415
Gln Ile Pro Tyr Asp Val Ile Trp Leu Asp Ile Glu Tyr Thr Asp Asp
            420                 425                 430
Arg Lys Tyr Phe Thr Trp Asp Pro Leu Ser Phe Pro Asp Pro Ile Ser
        435                 440                 445
Met Glu Glu Gln Leu Asp Glu Ser Glu Arg Lys Leu Val Val Ile Ile
    450                 455                 460
Asp Pro His Ile Lys Asn Gln Asp Lys Tyr Ser Ile Val Gln Glu Met
465                 470                 475                 480
Lys Ser Lys Asp Leu Ala Thr Lys Asn Lys Asp Gly Glu Ile Tyr Asp
                485                 490                 495
Gly Trp Cys Trp Pro Gly Ser Ser His Trp Ile Asp Thr Phe Asn Pro
            500                 505                 510
Ala Ala Ile Lys Trp Trp Val Ser Leu Phe Lys Phe Asp Lys Phe Lys
        515                 520                 525
Gly Thr Leu Ser Asn Val Phe Ile Trp Asn Asp Met Asn Glu Pro Ser
    530                 535                 540
Val Phe Asn Gly Pro Glu Thr Thr Met Pro Lys Asp Asn Leu His His
545                 550                 555                 560
Gly Asn Trp Glu His Arg Asp Ile His Asn Val His Gly Ile Thr Leu
                565                 570                 575
Val Asn Ala Thr Tyr Asp Ala Leu Leu Glu Arg Lys Lys Gly Glu Ile
            580                 585                 590
Arg Arg Pro Phe Ile Leu Thr Arg Ser Tyr Tyr Ala Gly Ala Gln Arg
        595                 600                 605
Met Ser Ala Met Trp Thr Gly Asp Asn Gln Ala Thr Trp Glu His Leu
    610                 615                 620
Ala Ala Ser Ile Pro Met Val Leu Asn Asn Gly Ile Ala Gly Phe Pro
625                 630                 635                 640
Phe Ala Gly Ala Asp Val Gly Gly Phe Phe Gln Asn Pro Ser Lys Glu
                645                 650                 655
Leu Leu Thr Arg Trp Tyr Gln Ala Gly Ile Trp Tyr Pro Phe Phe Arg
            660                 665                 670
Ala His Ala His Ile Asp Thr Arg Arg Arg Glu Pro Tyr Leu Ile Ala
```

```
        675                 680                 685
Glu Pro His Arg Ser Ile Ile Ser Gln Ala Ile Arg Leu Arg Tyr Gln
    690                 695                 700
Leu Leu Pro Ala Trp Tyr Thr Ala Phe His Glu Ala Ser Val Asn Gly
705                 710                 715                 720
Met Pro Ile Val Arg Pro Gln Tyr Tyr Ala His Pro Trp Asp Glu Ala
                725                 730                 735
Gly Phe Ala Ile Asp Asp Gln Leu Tyr Leu Gly Ser Thr Gly Leu Leu
            740                 745                 750
Ala Lys Pro Val Val Ser Glu Glu Ala Thr Thr Ala Asp Ile Tyr Leu
        755                 760                 765
Ala Asp Asp Glu Lys Tyr Tyr Asp Tyr Phe Asp Tyr Thr Val Tyr Gln
    770                 775                 780
Gly Ala Gly Lys Arg His Thr Val Pro Ala Pro Met Glu Thr Val Pro
785                 790                 795                 800
Leu Leu Met Gln Gly Gly His Val Ile Pro Arg Lys Asp Arg Pro Arg
                805                 810                 815
Arg Ser Ser Ala Leu Met Arg Trp Asp Pro Tyr Thr Leu Val Val Val
            820                 825                 830
Leu Asp Lys Asn Gly Gln Ala Asp Gly Ser Leu Tyr Val Asp Asp Gly
        835                 840                 845
Glu Thr Phe Asp Tyr Glu Arg Gly Ala Tyr Ile His Arg Arg Phe Arg
    850                 855                 860
Phe Gln Glu Ser Ala Leu Val Ser Glu Asp Val Gly Thr Lys Gly Pro
865                 870                 875                 880
Lys Thr Ala Glu Tyr Leu Lys Thr Met Ala Asn Val Arg Val Glu Arg
                885                 890                 895
Val Val Val Val Asp Pro Pro Lys Glu Trp Gln Gly Lys Thr Ser Val
            900                 905                 910
Thr Val Ile Glu Asp Gly Ala Ser Ala Ala Ser Thr Ala Ser Met Gln
        915                 920                 925
Tyr His Ser Gln Pro Asp Gly Lys Ala Ala Tyr Ala Val Val Lys Asn
    930                 935                 940
Pro Asn Val Gly Ile Gly Lys Thr Trp Arg Ile Glu Phe
945                 950                 955


<210> 238

<400> 238
 000

<210> 239
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase 1KUL_A

<400> 239
Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu Thr Ala Thr
 1               5                  10                  15
Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln Leu
```

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


<210> 240
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase 1KUM_A

<400> 240
Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu Thr Ala Thr
 1               5                  10                  15
Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln Leu
            20                  25                  30
Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser Ala Asp Lys Tyr
        35                  40                  45
Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr Leu Pro Ala Gly
    50                  55                  60
Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser Asp Asp Ser Val
65                  70                  75                  80
Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro Gln Ala Cys
                85                  90                  95
Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
            100                 105


<210> 241
<211> 640
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase

<400> 241
Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
 1               5                  10                  15
Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
            20                  25                  30
Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Ser Asn Ile Gly Ala
        35                  40                  45
Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
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    50                  55                  60
Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
65                  70                  75                  80
Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Glu Asp Thr
                85                  90                  95
Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
            100                 105                 110
Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
        115                 120                 125
Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp
    130                 135                 140
Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile
145                 150                 155                 160
Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr
                165                 170                 175
Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln
            180                 185                 190
Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser
        195                 200                 205
Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser
    210                 215                 220
Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln
225                 230                 235                 240
Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe
                245                 250                 255
Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr
            260                 265                 270
Pro Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp
        275                 280                 285
Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu
    290                 295                 300
Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
305                 310                 315                 320
Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
                325                 330                 335
Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
            340                 345                 350
Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
        355                 360                 365
Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr
    370                 375                 380
Gly Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala
385                 390                 395                 400
Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala
                405                 410                 415
Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu
            420                 425                 430
Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr
        435                 440                 445
Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr
    450                 455                 460
Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly
465                 470                 475                 480
Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr
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                485                 490                 495
Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr
            500                 505                 510
Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser Thr
        515                 520                 525
Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp
    530                 535                 540
Leu Thr Ala Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser
545                 550                 555                 560
Ile Ser Gln Leu Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser
                565                 570                 575
Ala Asp Lys Tyr Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr
            580                 585                 590
Leu Pro Ala Gly Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser
        595                 600                 605
Asp Asp Ser Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val
    610                 615                 620
Pro Gln Ala Cys Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
625                 630                 635                 640


<210> 242
<211> 640
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase ADX86749.1

<400> 242
Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
 1               5                  10                  15
Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
            20                  25                  30
Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
        35                  40                  45
Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
    50                  55                  60
Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
65                  70                  75                  80
Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
                85                  90                  95
Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
            100                 105                 110
Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
        115                 120                 125
Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp
    130                 135                 140
Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile
145                 150                 155                 160
Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr
                165                 170                 175
Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln
            180                 185                 190
```

```
Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser
        195                 200                 205
Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser
    210                 215                 220
Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln
225                 230                 235                 240
Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe
                245                 250                 255
Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr
            260                 265                 270
Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp
        275                 280                 285
Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu
    290                 295                 300
Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
305                 310                 315                 320
Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
                325                 330                 335
Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
            340                 345                 350
Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
        355                 360                 365
Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr
    370                 375                 380
Gly Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala
385                 390                 395                 400
Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala
                405                 410                 415
Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu
            420                 425                 430
Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr
        435                 440                 445
Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr
    450                 455                 460
Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly
465                 470                 475                 480
Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr
                485                 490                 495
Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr
            500                 505                 510
Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser Thr
        515                 520                 525
Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp
    530                 535                 540
Leu Thr Ala Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser
545                 550                 555                 560
Ile Ser Gln Leu Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser
                565                 570                 575
Ala Asp Lys Tyr Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr
            580                 585                 590
Leu Pro Ala Gly Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser
        595                 600                 605
Asp Asp Ser Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val
    610                 615                 620
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Pro Gln Ala Cys Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
625                 630                 635                 640


<210> 243
<211> 640
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase AEE60909.1

<400> 243
Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
 1               5                  10                  15
Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
            20                  25                  30
Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
        35                  40                  45
Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
    50                  55                  60
Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
65                  70                  75                  80
Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
                85                  90                  95
Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
            100                 105                 110
Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
        115                 120                 125
Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp
    130                 135                 140
Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile
145                 150                 155                 160
Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr
                165                 170                 175
Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln
            180                 185                 190
Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser
        195                 200                 205
Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser
    210                 215                 220
Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln
225                 230                 235                 240
Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe
                245                 250                 255
Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr
            260                 265                 270
Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp
        275                 280                 285
Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu
    290                 295                 300
Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
305                 310                 315                 320
Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
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                325                 330                 335
Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
            340                 345                 350
Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
        355                 360                 365
Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr
    370                 375                 380
Gly Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala
385                 390                 395                 400
Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala
                405                 410                 415
Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu
            420                 425                 430
Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr
        435                 440                 445
Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr
    450                 455                 460
Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly
465                 470                 475                 480
Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr
                485                 490                 495
Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr
            500                 505                 510
Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser Thr
        515                 520                 525
Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp
    530                 535                 540
Leu Thr Ala Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser
545                 550                 555                 560
Ile Ser Gln Leu Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser
                565                 570                 575
Ala Asp Lys Tyr Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr
            580                 585                 590
Leu Pro Ala Gly Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser
        595                 600                 605
Asp Asp Ser Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val
    610                 615                 620
Pro Gln Ala Cys Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
625                 630                 635                 640


<210> 244
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase AFJ52556.1

<400> 244
Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu Thr Ala Thr
 1               5                  10                  15
Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln Leu
            20                  25                  30
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Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser Ala Asp Lys Tyr
        35                  40                  45
Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr Leu Pro Ala Gly
    50                  55                  60
Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser Asp Asp Ser Val
65                  70                  75                  80
Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro Gln Ala Cys
                85                  90                  95
Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
            100                 105


<210> 245
<211> 957
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase CCO73840.1

<400> 245
Met Ser Asn Arg Trp Thr Leu Leu Leu Ser Leu Val Ile Leu Leu Gly
 1               5                  10                  15
Cys Leu Val Ile Pro Gly Val Thr Val Lys His Glu Asn Phe Lys Thr
            20                  25                  30
Cys Ser Gln Ser Gly Phe Cys Lys Arg Asn Arg Ala Phe Ala Asp Asp
        35                  40                  45
Ala Ala Ala Gln Gly Ser Ser Trp Ala Ser Pro Tyr Glu Leu Asp Ser
    50                  55                  60
Ser Ser Ile Gln Phe Lys Asp Gly Gln Leu His Gly Thr Ile Leu Lys
65                  70                  75                  80
Ser Val Ser Pro Asn Glu Lys Val Lys Leu Pro Leu Val Val Ser Phe
                85                  90                  95
Leu Glu Ser Gly Ala Ala Arg Val Val Val Asp Glu Glu Lys Arg Met
            100                 105                 110
Asn Gly Asp Ile Gln Leu Arg His Asp Ser Lys Ala Arg Lys Glu Arg
        115                 120                 125
Tyr Asn Glu Ala Glu Lys Trp Val Leu Val Gly Gly Leu Glu Leu Ser
    130                 135                 140
Lys Thr Ala Thr Leu Arg Pro Glu Thr Glu Ser Gly Phe Thr Arg Val
145                 150                 155                 160
Leu Tyr Gly Pro Asp Asn Gln Phe Glu Ala Val Ile Arg His Ala Pro
                165                 170                 175
Phe Ser Ala Asp Phe Lys Arg Asp Gly Gln Thr His Val Gln Leu Asn
            180                 185                 190
Asn Lys Gly Tyr Leu Asn Met Glu His Trp Arg Pro Lys Val Glu Val
        195                 200                 205
Glu Gly Glu Gly Glu Gln Gln Thr Gln Glu Asp Glu Ser Thr Trp Trp
    210                 215                 220
Asp Glu Ser Phe Gly Gly Asn Thr Asp Thr Lys Pro Arg Gly Pro Glu
225                 230                 235                 240
Ser Val Gly Leu Asp Ile Thr Phe Pro Gly Tyr Lys His Val Phe Gly
                245                 250                 255
Ile Pro Glu His Ala Asp Ser Leu Ser Leu Lys Glu Thr Arg Gly Gly
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            260                 265                 270
Glu Gly Asn His Glu Glu Pro Tyr Arg Met Tyr Asn Ala Asp Val Phe
        275                 280                 285
Glu Tyr Glu Leu Ser Ser Pro Met Thr Leu Tyr Gly Ala Ile Pro Phe
    290                 295                 300
Met Gln Ala His Arg Lys Asp Ser Thr Val Gly Val Phe Trp Leu Asn
305                 310                 315                 320
Ala Ala Glu Thr Trp Val Asp Ile Val Lys Ser Thr Ser Ser Pro Asn
                325                 330                 335
Pro Leu Ala Leu Gly Val Gly Ala Thr Thr Asp Thr Gln Ser His Trp
            340                 345                 350
Phe Ser Glu Ser Gly Gln Leu Asp Val Phe Val Phe Leu Gly Pro Thr
        355                 360                 365
Pro Gln Glu Ile Ser Lys Thr Tyr Gly Glu Leu Thr Gly Tyr Thr Gln
    370                 375                 380
Leu Pro Gln His Phe Ala Ile Ala Tyr His Gln Cys Arg Trp Asn Tyr
385                 390                 395                 400
Ile Thr Asp Glu Asp Val Lys Glu Val Asp Arg Asn Phe Asp Lys Tyr
                405                 410                 415
Gln Ile Pro Tyr Asp Val Ile Trp Leu Asp Ile Glu Tyr Thr Asp Asp
            420                 425                 430
Arg Lys Tyr Phe Thr Trp Asp Pro Leu Ser Phe Pro Asp Pro Ile Ser
        435                 440                 445
Met Glu Glu Gln Leu Asp Glu Ser Glu Arg Lys Leu Val Val Ile Ile
    450                 455                 460
Asp Pro His Ile Lys Asn Gln Asp Lys Tyr Ser Ile Val Gln Glu Met
465                 470                 475                 480
Lys Ser Lys Asp Leu Ala Thr Lys Asn Lys Asp Gly Glu Ile Tyr Asp
                485                 490                 495
Gly Trp Cys Trp Pro Gly Ser Ser His Trp Ile Asp Thr Phe Asn Pro
            500                 505                 510
Ala Ala Ile Lys Trp Trp Val Ser Leu Phe Lys Phe Asp Lys Phe Lys
        515                 520                 525
Gly Thr Leu Ser Asn Val Phe Ile Trp Asn Asp Met Asn Glu Pro Ser
    530                 535                 540
Val Phe Asn Gly Pro Glu Thr Thr Met Pro Lys Asp Asn Leu His His
545                 550                 555                 560
Gly Asn Trp Glu His Arg Asp Ile His Asn Val His Gly Ile Thr Leu
                565                 570                 575
Val Asn Ala Thr Tyr Asp Ala Leu Leu Glu Arg Lys Lys Gly Glu Ile
            580                 585                 590
Arg Arg Pro Phe Ile Leu Thr Arg Ser Tyr Tyr Ala Gly Ala Gln Arg
        595                 600                 605
Met Ser Ala Met Trp Thr Gly Asp Asn Gln Ala Thr Trp Glu His Leu
    610                 615                 620
Ala Ala Ser Ile Pro Met Val Leu Asn Asn Gly Ile Ala Gly Phe Pro
625                 630                 635                 640
Phe Ala Gly Ala Asp Val Gly Gly Phe Phe Gln Asn Pro Ser Lys Glu
                645                 650                 655
Leu Leu Thr Arg Trp Tyr Gln Ala Gly Ile Trp Tyr Pro Phe Phe Arg
            660                 665                 670
Ala His Ala His Ile Asp Thr Arg Arg Arg Glu Pro Tyr Leu Ile Ala
        675                 680                 685
Glu Pro His Arg Ser Ile Ile Ser Gln Ala Ile Arg Leu Arg Tyr Gln
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```
    690                 695                 700
Leu Leu Pro Ala Trp Tyr Thr Ala Phe His Glu Ala Ser Val Asn Gly
705                 710                 715                 720
Met Pro Ile Val Arg Pro Gln Tyr Tyr Ala His Pro Trp Asp Glu Ala
                725                 730                 735
Gly Phe Ala Ile Asp Asp Gln Leu Tyr Leu Gly Ser Thr Gly Leu Leu
            740                 745                 750
Ala Lys Pro Val Val Ser Glu Glu Ala Thr Thr Ala Asp Ile Tyr Leu
        755                 760                 765
Ala Asp Asp Glu Lys Tyr Tyr Asp Tyr Phe Asp Tyr Thr Val Tyr Gln
    770                 775                 780
Gly Ala Gly Lys Arg His Thr Val Pro Ala Pro Met Glu Thr Val Pro
785                 790                 795                 800
Leu Leu Met Gln Gly Gly His Val Ile Pro Arg Lys Asp Arg Pro Arg
                805                 810                 815
Arg Ser Ser Ala Leu Met Arg Trp Asp Pro Tyr Thr Leu Val Val Val
            820                 825                 830
Leu Asp Lys Asn Gly Gln Ala Asp Gly Ser Leu Tyr Val Asp Asp Gly
        835                 840                 845
Glu Thr Phe Asp Tyr Glu Arg Gly Ala Tyr Ile His Arg Arg Phe Arg
    850                 855                 860
Phe Gln Glu Ser Ala Leu Val Ser Glu Asp Val Gly Thr Lys Gly Pro
865                 870                 875                 880
Lys Thr Ala Glu Tyr Leu Lys Thr Met Ala Asn Val Arg Val Glu Arg
                885                 890                 895
Val Val Val Val Asp Pro Pro Lys Glu Trp Gln Gly Lys Thr Ser Val
            900                 905                 910
Thr Val Ile Glu Asp Gly Ala Ser Ala Ala Ser Thr Ala Ser Met Gln
        915                 920                 925
Tyr His Ser Gln Pro Asp Gly Lys Ala Ala Tyr Ala Val Val Lys Asn
    930                 935                 940
Pro Asn Val Gly Ile Gly Lys Thr Trp Arg Ile Glu Phe
945                 950                 955


<210> 246
<211> 985
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase BAM72725.1

<400> 246
Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
 1               5                  10                  15
Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
            20                  25                  30
Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
        35                  40                  45
Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
    50                  55                  60
Gly Tyr Lys Ala Ser Lys Val Gln His Asn Ser Arg Gly Phe Thr Ala
65                  70                  75                  80
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Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
                85                  90                  95
Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
            100                 105                 110
Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
        115                 120                 125
Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
    130                 135                 140
Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
145                 150                 155                 160
Phe Asn Phe Lys Val Ile Arg Lys Ala Thr Gly Asp Ala Leu Phe Ser
                165                 170                 175
Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
            180                 185                 190
Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
        195                 200                 205
Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
    210                 215                 220
Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
225                 230                 235                 240
Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
                245                 250                 255
Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
            260                 265                 270
Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
        275                 280                 285
Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
    290                 295                 300
Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
305                 310                 315                 320
Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
                325                 330                 335
Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
            340                 345                 350
Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
        355                 360                 365
Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
    370                 375                 380
Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
385                 390                 395                 400
His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
                405                 410                 415
Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
            420                 425                 430
Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
        435                 440                 445
Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
    450                 455                 460
Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
465                 470                 475                 480
Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
                485                 490                 495
Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
            500                 505                 510
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His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
        515                 520                 525
Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
    530                 535                 540
Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
545                 550                 555                 560
Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
                565                 570                 575
Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
            580                 585                 590
Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
        595                 600                 605
Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
    610                 615                 620
Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
625                 630                 635                 640
Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
                645                 650                 655
Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
            660                 665                 670
Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
        675                 680                 685
Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
    690                 695                 700
Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
705                 710                 715                 720
Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
                725                 730                 735
Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
            740                 745                 750
Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
        755                 760                 765
Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
    770                 775                 780
Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
785                 790                 795                 800
Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
                805                 810                 815
Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
            820                 825                 830
Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
        835                 840                 845
Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
    850                 855                 860
Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865                 870                 875                 880
Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
                885                 890                 895
Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
            900                 905                 910
Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
        915                 920                 925
Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
    930                 935                 940
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Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945                 950                 955                 960
Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
                965                 970                 975
Trp Ala Glu Asn Trp Val Leu Glu Trp
            980                 985


<210> 247
<211> 655
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase AGN92963.1

<400> 247
Met Trp Ser Ser Trp Leu Leu Ser Ala Leu Leu Ala Thr Glu Ala Leu
 1               5                  10                  15
Ala Val Pro Tyr Glu Glu Tyr Ile Leu Ala Pro Ser Ser Arg Asp Leu
            20                  25                  30
Ala Pro Ala Ser Val Arg Gln Val Asn Gly Ser Val Thr Asn Ala Ala
        35                  40                  45
Ala Leu Thr Gly Ala Gly Gly Gln Ala Thr Phe Asn Gly Val Ser Ser
    50                  55                  60
Val Thr Tyr Asp Phe Gly Ile Asn Val Ala Gly Ile Val Ser Val Asp
65                  70                  75                  80
Val Ala Ser Ala Ser Ser Glu Ser Ala Phe Ile Gly Val Thr Phe Thr
                85                  90                  95
Glu Ser Ser Met Trp Ile Ser Asn Glu Ala Cys Asp Ala Thr Gln Asp
            100                 105                 110
Ala Gly Leu Asp Thr Pro Leu Trp Phe Ala Val Gly Gln Gly Ala Gly
        115                 120                 125
Val Tyr Ser Val Gly Lys Lys Tyr Thr Arg Gly Ala Phe Arg Tyr Met
    130                 135                 140
Thr Val Val Ser Asn Thr Thr Ala Thr Val Ser Leu Asn Ser Val Lys
145                 150                 155                 160
Ile Asn Tyr Thr Ala Ser Pro Ile Gln Asp Leu Arg Ala Tyr Thr Gly
                165                 170                 175
Tyr Phe His Ser Ser Asp Glu Leu Leu Asn Arg Ile Trp Tyr Ala Gly
            180                 185                 190
Ala Tyr Thr Leu Gln Leu Cys Ser Ile Asp Pro Thr Thr Gly Asp Ala
        195                 200                 205
Leu Val Gly Leu Gly Ala Ile Thr Ser Ser Glu Thr Ile Thr Leu Pro
    210                 215                 220
Gln Thr Asp Lys Trp Trp Thr Asn Tyr Thr Ile Thr Asn Gly Ser Ser
225                 230                 235                 240
Thr Leu Thr Asp Gly Ala Lys Arg Asp Arg Leu Val Trp Pro Gly Asp
                245                 250                 255
Met Ser Ile Ala Leu Glu Ser Val Ala Val Ser Thr Glu Asp Leu Tyr
            260                 265                 270
Ser Val Arg Thr Ala Leu Glu Ser Leu Tyr Ala Leu Gln Lys Ala Asp
        275                 280                 285
Gly Gln Leu Pro Tyr Ala Gly Lys Pro Phe Tyr Asp Thr Val Ser Phe
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    290                 295                 300
Thr Tyr His Leu His Ser Leu Val Gly Ala Ala Ser Tyr Tyr Gln Tyr
305                 310                 315                 320
Thr Gly Asp Arg Ala Trp Leu Thr Arg Tyr Trp Gly Gln Tyr Lys Lys
                325                 330                 335
Gly Val Gln Trp Ala Leu Ser Gly Val Asp Ser Thr Gly Leu Ala Asn
            340                 345                 350
Ile Thr Ala Ser Ala Asp Trp Leu Arg Phe Gly Met Gly Ala His Asn
        355                 360                 365
Ile Glu Ala Asn Ala Ile Leu Tyr Tyr Val Leu Asn Asp Ala Ile Ser
    370                 375                 380
Leu Ala Gln Ser Leu Asn Asp Asn Ala Pro Ile Arg Asn Trp Thr Ala
385                 390                 395                 400
Thr Ala Ala Arg Ile Lys Thr Val Ala Asn Glu Leu Leu Trp Asp Asp
                405                 410                 415
Lys Asn Gly Leu Tyr Thr Asp Asn Glu Thr Thr Thr Leu His Pro Gln
            420                 425                 430
Asp Gly Asn Ser Trp Ala Val Lys Ala Asn Leu Thr Leu Ser Ala Asn
        435                 440                 445
Gln Ser Ala Ile Ile Ser Glu Ser Leu Ala Ala Arg Trp Gly Pro Tyr
    450                 455                 460
Gly Ala Pro Ala Pro Glu Ala Gly Ala Thr Val Ser Pro Phe Ile Gly
465                 470                 475                 480
Gly Phe Glu Leu Gln Ala His Tyr Gln Ala Gly Gln Pro Asp Arg Ala
                485                 490                 495
Leu Asp Leu Leu Arg Leu Gln Trp Gly Phe Met Leu Asp Asp Pro Arg
            500                 505                 510
Met Thr Asn Ser Thr Phe Ile Glu Gly Tyr Ser Thr Asp Gly Ser Leu
        515                 520                 525
Val Tyr Ala Pro Tyr Thr Asn Arg Pro Arg Val Ser His Ala His Gly
    530                 535                 540
Trp Ser Thr Gly Pro Thr Ser Ala Leu Thr Ile Tyr Thr Ala Gly Leu
545                 550                 555                 560
Arg Val Thr Gly Pro Ala Gly Ala Thr Trp Leu Tyr Lys Pro Gln Pro
                565                 570                 575
Gly Asn Leu Thr Gln Val Glu Ala Gly Phe Ser Thr Arg Leu Gly Ser
            580                 585                 590
Phe Ala Ser Ser Phe Ser Arg Ser Gly Gly Arg Tyr Gln Glu Leu Ser
        595                 600                 605
Phe Thr Thr Pro Asn Gly Thr Thr Gly Ser Val Glu Leu Gly Asp Val
    610                 615                 620
Ser Gly Gln Leu Val Ser Glu Gly Gly Val Lys Val Gln Leu Val Gly
625                 630                 635                 640
Gly Lys Ala Ser Gly Leu Gln Gly Gly Lys Trp Arg Leu Asn Val
                645                 650                 655
```

<210> 248
<211> 985
<212> PRT
<213> Artificial Sequence

<220>
<223> TransgucosidaseAIY23066.1

<400> 248
Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
 1               5                  10                  15
Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
            20                  25                  30
Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
        35                  40                  45
Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Tyr Pro
    50                  55                  60
Gly Tyr Lys Ala Ser Lys Val Gln His Asn Ser Arg Gly Phe Thr Ala
65                  70                  75                  80
Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
                85                  90                  95
Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
            100                 105                 110
Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
        115                 120                 125
Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
    130                 135                 140
Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
145                 150                 155                 160
Phe Asn Phe Lys Val Ile Arg Lys Ala Thr Gly Asp Ala Leu Phe Ser
                165                 170                 175
Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
            180                 185                 190
Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
        195                 200                 205
Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
    210                 215                 220
Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
225                 230                 235                 240
Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
                245                 250                 255
Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
            260                 265                 270
Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
        275                 280                 285
Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
    290                 295                 300
Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
305                 310                 315                 320
Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
                325                 330                 335
Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
            340                 345                 350
Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
        355                 360                 365
Trp Thr Asp Ile Asp Tyr Met His Gly Tyr His Asn Phe Asp Asn Asp
    370                 375                 380
Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
385                 390                 395                 400
His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
                405                 410                 415

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Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
            420                 425                 430
Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
        435                 440                 445
Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
    450                 455                 460
Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
465                 470                 475                 480
Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
                485                 490                 495
Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
            500                 505                 510
His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
        515                 520                 525
Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
    530                 535                 540
Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
545                 550                 555                 560
Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
                565                 570                 575
Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
            580                 585                 590
Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
        595                 600                 605
Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
    610                 615                 620
Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
625                 630                 635                 640
Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
                645                 650                 655
Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
            660                 665                 670
Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
        675                 680                 685
Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
    690                 695                 700
Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
705                 710                 715                 720
Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
                725                 730                 735
Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
            740                 745                 750
Tyr Thr Leu Phe Asp Leu Ala His Thr Ser Gly Ser Thr Val Met Arg
        755                 760                 765
Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
    770                 775                 780
Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
785                 790                 795                 800
Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
                805                 810                 815
Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
            820                 825                 830
Gly Val Thr Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
        835                 840                 845
```

Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
    850                 855                 860
Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865                 870                 875                 880
Asn Gly Ala Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
                885                 890                 895
Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
            900                 905                 910
Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
        915                 920                 925
Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
    930                 935                 940
Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945                 950                 955                 960
Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
                965                 970                 975
Trp Ala Glu Asn Trp Val Leu Glu Trp
            980                 985

<210> 249
<211> 640
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase AIY23067.1

<400> 249
Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
 1               5                  10                  15
Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
            20                  25                  30
Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
        35                  40                  45
Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
    50                  55                  60
Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
65                  70                  75                  80
Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
                85                  90                  95
Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
            100                 105                 110
Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
        115                 120                 125
Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp
    130                 135                 140
Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile
145                 150                 155                 160
Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr
                165                 170                 175
Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln
            180                 185                 190
Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser

```
        195                 200                 205
Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser
    210                 215                 220
Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln
225                 230                 235                 240
Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe
                245                 250                 255
Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr
            260                 265                 270
Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp
        275                 280                 285
Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu
    290                 295                 300
Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
305                 310                 315                 320
Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
                325                 330                 335
Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
            340                 345                 350
Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
        355                 360                 365
Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr
    370                 375                 380
Gly Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala
385                 390                 395                 400
Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala
                405                 410                 415
Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu
            420                 425                 430
Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr
        435                 440                 445
Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr
    450                 455                 460
Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Ser Ser Ala Ile Gly
465                 470                 475                 480
Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr
                485                 490                 495
Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr
            500                 505                 510
Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser Thr
        515                 520                 525
Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp
    530                 535                 540
Leu Thr Ala Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser
545                 550                 555                 560
Ile Ser Gln Leu Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser
                565                 570                 575
Ala Asp Lys Tyr Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr
            580                 585                 590
Leu Pro Ala Gly Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser
        595                 600                 605
Asp Asp Ser Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val
    610                 615                 620
Pro Gln Ala Cys Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
```

625 630 635 640

<210> 250
<211> 680
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase GAQ47522.1

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

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Lys Asn Gly Tyr Pro Glu Glu Ala Glu Ser Tyr Ile Asn Phe Ile Phe
            340                 345                 350
Glu Arg Ile Phe Pro Pro Met Asp Lys Asn Pro Lys Pro Gly Glu Pro
        355                 360                 365
Phe Leu Pro Ile Met Ile Thr Ile His Gly Glu Arg Glu Ile Pro Glu
    370                 375                 380
Met Glu Leu Asp His Leu Glu Gly Tyr Arg Gly Ser Arg Pro Val Arg
385                 390                 395                 400
Ile Gly Asn Gly Ala Ala Thr His Ile Gln Leu Asp Ile Tyr Gly Glu
                405                 410                 415
Leu Met Asp Ser Ile Tyr Leu Tyr Asn Lys His Ala Ala Asp Ile Ser
            420                 425                 430
Tyr Asp Gln Trp Arg Ala Ile Arg Arg Met Ile Asp Phe Val Ile Gln
        435                 440                 445
Ile Arg His Gln Pro Asp Gln Ser Ile Trp Glu Val Arg Gly Pro Pro
    450                 455                 460
Gln Asn Phe Val Tyr Ser Lys Ile Met Leu Trp Val Ala Leu Asp Arg
465                 470                 475                 480
Gly Val Arg Leu Ala Glu Lys Arg Ser Asn Leu Pro Cys Pro Asp Arg
                485                 490                 495
Ala Arg Trp Met His Glu Arg Asp Ala Leu Tyr Asp Glu Ile Met Thr
            500                 505                 510
Lys Gly Tyr Asn Ala Glu Lys Gly Phe Phe Cys Met Ser Tyr Glu Asn
        515                 520                 525
Gln Asp Ala Met Asp Ala Ala Val Leu Ile Ala Pro Leu Val Phe Phe
    530                 535                 540
Val Ala Pro Asn Asp Pro Arg Leu Leu Ser Thr Ile Gln Lys Ile Thr
545                 550                 555                 560
Asp Val Pro Ala Lys Gly Gly Leu Ser Val Ala Asn Met Val Ser Arg
                565                 570                 575
Tyr Asp Thr Gly Lys Val Asp Asp Gly Val Gly Gly Asn Glu Gly Ala
            580                 585                 590
Phe Leu Met Val Thr Phe Trp Leu Val Glu Ala Met Met Arg Ala Ala
        595                 600                 605
Lys Ser Lys Ala Tyr Leu Pro His Asp Pro Phe Phe Gln Gln Leu Arg
    610                 615                 620
Lys Thr Ala Thr Ser Gln Phe Asp Ser Ile Leu Ser Phe Ala Asn His
625                 630                 635                 640
Leu Gly Met Phe Ser Glu Glu Val Ala Thr Ser Gly Glu Gln Ile Gly
                645                 650                 655
Asn Met Pro Gln Ala Phe Ser His Leu Ala Cys Val Ser Ala Ala Met
            660                 665                 670
Asn Leu Gly Gly Gly Gly Asp Arg
        675                 680


<210> 251
<211> 643
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase GAQ47133.1
```

<400> 251
Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Ser Gly
 1               5                  10                  15
Leu Ala Ser Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
            20                  25                  30
Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
        35                  40                  45
Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
    50                  55                  60
Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
65                  70                  75                  80
Gly Leu Val Ile Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
                85                  90                  95
Asp Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ser Gln Ala Ile Val
            100                 105                 110
Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Gly Leu Gly
        115                 120                 125
Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp Gly
    130                 135                 140
Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile Gly
145                 150                 155                 160
Phe Gly Gln Trp Leu Leu Leu Thr Gly Gln Asp Asn Gly Tyr Thr Ser
                165                 170                 175
Ala Ala Thr Glu Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr
            180                 185                 190
Val Ala Gln Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val
        195                 200                 205
Asn Gly Ser Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val
    210                 215                 220
Glu Gly Ser Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys
225                 230                 235                 240
Asp Ser Gln Ala Pro Gln Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr
                245                 250                 255
Gly Glu Tyr Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp
            260                 265                 270
Thr Asn Thr Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Gly
        275                 280                 285
Cys Asp Asp Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn
    290                 295                 300
His Lys Glu Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp
305                 310                 315                 320
Gly Leu Ser Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp
                325                 330                 335
Ser Tyr Tyr Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala
            340                 345                 350
Glu Gln Leu Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu
        355                 360                 365
Glu Ile Thr Asp Val Ser Leu Asp Phe Phe Gln Ala Leu Tyr Ser Asp
    370                 375                 380
Ala Ala Thr Gly Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile
385                 390                 395                 400
Val Asp Ala Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu
                405                 410                 415
Thr His Ala Ala Ser Asn Gly Ser Leu Ser Glu Gln Tyr Asp Lys Ser

```
            420                 425                 430
Asp Gly Asp Glu Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala
        435                 440                 445
Leu Leu Thr Ala Asn Asn Arg Arg Asn Ser Val Val Pro Pro Ser Trp
    450                 455                 460
Gly Glu Thr Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser
465                 470                 475                 480
Ala Ser Gly Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile
                485                 490                 495
Val Ala Thr Gly Gly Thr Thr Thr Thr Ala Thr Thr Thr Gly Ser Gly
            500                 505                 510
Ser Val Thr Ser Thr Ser Lys Thr Thr Thr Thr Ala Ser Lys Thr Ser
        515                 520                 525
Thr Thr Thr Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val
    530                 535                 540
Thr Phe Asp Leu Thr Ala Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu
545                 550                 555                 560
Val Gly Ser Ile Ser Gln Leu Gly Asp Trp Asp Thr Ser Asp Gly Ile
                565                 570                 575
Ala Leu Ser Ala Asp Lys Tyr Thr Ser Ser Asn Pro Leu Trp Tyr Val
            580                 585                 590
Thr Val Thr Leu Pro Ala Gly Glu Ser Phe Glu Tyr Lys Phe Ile Arg
        595                 600                 605
Ile Glu Ser Asp Asp Ser Val Glu Trp Glu Ser Asp Pro Asn Arg Glu
    610                 615                 620
Tyr Thr Val Pro Gln Ala Cys Gly Glu Ser Thr Ala Thr Val Thr Asp
625                 630                 635                 640
Thr Trp Arg
```

<210> 252
<211> 587
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase GAQ46031.1

```
<400> 252
Met Ala Lys Ser Ala Ser Gln Ile His Arg Ala Trp Trp Lys Glu Cys
 1               5                  10                  15
Ser Val Tyr Gln Ile Trp Pro Ala Ser Tyr Lys Asp Ser Asn Asp Asp
            20                  25                  30
Gly Ile Gly Asp Ile Pro Gly Ile Ile Ser Lys Leu Asp Tyr Ile Lys
        35                  40                  45
Asn Ile Gly Val Asp Ile Val Trp Leu Cys Pro Ser Tyr Lys Ser Pro
    50                  55                  60
Gln Val Asp Met Gly Tyr Asp Ile Ala Asp Tyr Tyr Ser Ile Ala Asp
65                  70                  75                  80
Glu Tyr Gly Thr Val Ala Asp Val Glu Lys Leu Ile Gln Gly Cys His
                85                  90                  95
Glu Arg Gly Met Lys Leu Leu Met Asp Leu Val Val Asn His Thr Ser
            100                 105                 110
```

```
Asp Gln Asn Glu Trp Phe Lys Gln Ser Arg Ser Ser Lys Asp Asn Glu
        115                 120                 125
Tyr Arg Asn Trp Tyr Val Trp Lys Pro Ala Arg Tyr Asp Glu Gln Gly
    130                 135                 140
Asn Arg His Pro Pro Asn Asn Trp Val Ser His Phe Gln Gly Ser Ala
145                 150                 155                 160
Trp Glu Trp Asp Glu His Thr Gln Glu Tyr Tyr Leu His Leu Tyr Ala
                165                 170                 175
Val Glu Gln Pro Asp Leu Asn Trp Glu His Pro Pro Val Arg Lys Ala
            180                 185                 190
Val His Asp Ile Met Arg Phe Trp Leu Asp Lys Gly Ala Asp Gly Phe
        195                 200                 205
Arg Met Asp Val Ile Asn Phe Val Ser Lys Asp Gln Arg Phe Pro Asp
    210                 215                 220
Ala Pro Val Lys Asp Pro Arg Thr Pro Trp Gln Trp Gly Asp Lys Tyr
225                 230                 235                 240
Tyr Ala Asn Gly Pro Arg Leu His Glu Tyr Leu Ala Asp Leu Gly Lys
                245                 250                 255
Ile Leu Lys Glu Tyr Asp Ala Phe Ser Val Gly Glu Met Pro Phe Val
            260                 265                 270
Arg Asp Thr Glu Glu Val Leu Arg Ala Val Arg Tyr Asp Arg Asn Glu
        275                 280                 285
Ile Asn Met Ile Phe Asn Phe Glu His Val Asp Ile Asp His Gly Thr
    290                 295                 300
Tyr Asp Lys Phe Glu Pro Gly Ser Trp Lys Leu Thr Asp Leu Lys Ala
305                 310                 315                 320
Phe Phe Glu Thr Trp Gln Lys Phe Met Tyr Asn Asn Asp Gly Trp Asn
                325                 330                 335
Ala Leu Tyr Trp Glu Asn His Asp Gln Pro Arg Ser Ile Asp Arg Tyr
            340                 345                 350
Ala Gln Ala Lys Glu Glu Phe Arg Thr Glu Ala Gly Lys Met Leu Ala
        355                 360                 365
Thr Val Leu Ala Leu Gln Ser Gly Thr Pro Phe Val Tyr Gln Gly Gln
    370                 375                 380
Glu Ile Gly Met Arg Asn Val Pro Ile Glu Trp Asp Met Asn Glu Tyr
385                 390                 395                 400
Lys Asp Ile Asp Cys Leu Asn His Trp His Arg Leu Leu Lys His Arg
                405                 410                 415
Pro Asp Asp Ile Glu Ala Gln Lys Ser Ala Arg Gln Glu Tyr Gln Lys
            420                 425                 430
Lys Ser Arg Asp Asn Gly Arg Thr Pro Val Gln Trp Ser Ser Ala Pro
        435                 440                 445
Asn Gly Gly Phe Thr Gly Pro Asn Ala Lys Pro Trp Met Ser Val Asn
    450                 455                 460
Pro Asp Tyr Val Arg Phe Asn Ala Glu Ala Gln Val Asn Asp Pro Asn
465                 470                 475                 480
Ser Ile Tyr His Tyr Trp Ala Ala Val Leu Gly Leu Arg Lys Lys Tyr
                485                 490                 495
Leu Asp Ile Phe Val Tyr Gly Asp Tyr Asp Leu Val Asp Lys Asp Ser
            500                 505                 510
Gln Glu Ile Phe Ala Tyr Ser Arg Gln Tyr Glu Asp Gln Lys Ala Leu
        515                 520                 525
Val Leu Thr Asn Trp Thr Glu Asn Thr Leu Glu Trp Asp Ala Thr Ala
    530                 535                 540
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Asn Gly Val Lys Gly Val Lys Asp Val Val Leu Asn Ser Tyr Glu Ser
545                 550                 555                 560
Ala Glu Ala Ala Lys Gly Arg Phe Ser Gly Gln Lys Trp Ser Leu Arg
                565                 570                 575
Pro Tyr Glu Ala Val Val Leu Leu Val Glu Ala
            580                 585


<210> 253
<211> 676
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase GAQ44395.1

<400> 253
Met Arg Cys His Arg Leu Leu Ser Gly Val Leu Ala Phe Leu Pro Leu
 1               5                  10                  15
Ser Val Ala Gln Ser Cys Trp Arg Asn Thr Thr Cys Ser Gly Pro Thr
            20                  25                  30
Asp Ser Ala Phe Ser Gly Pro Trp Glu Lys Asn Ile Phe Ala Pro Ser
        35                  40                  45
Ser Arg Thr Leu Asn Pro Glu Lys Leu Phe Leu Ile Thr Gln Pro Asp
    50                  55                  60
Lys Thr Glu Asp Tyr Ile Pro Phe Ala Leu His Gly Asn Gly Ser Leu
65                  70                  75                  80
Val Val Tyr Asp Phe Gly Lys Glu Val Gly Gly Ile Val Ser Val Asn
                85                  90                  95
Phe Ser Ser Thr Gly Ser Gly Ala Leu Gly Val Ala Phe Thr Glu Ala
            100                 105                 110
Lys Asn Tyr Ile Gly Glu Trp Ser Asp Ser Ser Asn Gly Gly Phe Lys
        115                 120                 125
Gly Pro Asp Gly Ala Leu Tyr Gly Asn Phe Thr Glu Ala Gly Ser His
    130                 135                 140
Tyr Tyr Val Met Pro Asp Lys Ser Leu Arg Gly Gly Phe Arg Tyr Leu
145                 150                 155                 160
Thr Leu Phe Leu Ile Thr Ser Asp Asn Ser Thr Ile His Ile Glu Asp
                165                 170                 175
Val Ser Leu Glu Ile Gly Phe Gln Pro Thr Trp Ser Asn Leu Lys Ala
            180                 185                 190
Tyr Gln Gly Tyr Phe His Ser Asn Asp Asp Leu Leu Asn Lys Ile Trp
        195                 200                 205
Tyr Thr Gly Ala Tyr Thr Leu Gln Thr Asn Glu Val Pro Thr Asp Thr
    210                 215                 220
Gly Arg Gln Ile Pro Ala Met Ala Glu Gly Trp Ala Asn Asn Cys Thr
225                 230                 235                 240
Leu Gly Pro Gly Asp Thr Ile Ile Val Asp Gly Ala Lys Arg Asp Arg
                245                 250                 255
Ala Val Trp Pro Gly Asp Met Gly Ile Ala Val Pro Ser Ala Phe Val
            260                 265                 270
Ser Leu Gly Asp Leu Asp Ser Val Lys Asn Ala Leu Gln Val Met Tyr
        275                 280                 285
Asp Thr Gln Asp Asn Ser Thr Gly Ala Phe Asp Glu Ser Gly Pro Pro
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    290                 295                 300
Leu Ser Gln Lys Asp Ser Asp Thr Tyr His Met Trp Thr Met Val Gly
305                 310                 315                 320
Thr Tyr Asn Tyr Met Leu Tyr Thr Asn Asp Ser Asp Phe Leu Glu Gln
                325                 330                 335
Asn Trp Glu Gly Tyr Gln Lys Ala Met Asp Tyr Ile Tyr Gly Lys Val
            340                 345                 350
Thr Tyr Pro Ser Gly Leu Leu Asn Val Thr Gly Thr Arg Asp Trp Ala
        355                 360                 365
Arg Trp Gln Gln Gly Tyr Asn Asn Ser Glu Ala Gln Met Ile Leu Tyr
    370                 375                 380
His Thr Leu Asn Thr Gly Ala Glu Leu Ala Thr Trp Ala Gly Asp Ser
385                 390                 395                 400
Gly Asp Leu Ser Ser Thr Trp Thr Ser Arg Ala Glu Lys Leu Arg Gln
                405                 410                 415
Ala Ile Asn Glu Tyr Cys Trp Asp Glu Ser Tyr Gly Ala Phe Lys Asp
            420                 425                 430
Asn Ala Thr Asp Thr Thr Leu His Pro Gln Asp Ala Asn Ser Met Ala
        435                 440                 445
Leu Leu Phe Gly Val Val Asp Ala Asp Arg Ala Ala Ser Ile Ser Glu
    450                 455                 460
Arg Leu Thr Asp Asn Trp Thr Pro Ile Gly Ala Val Ala Pro Glu Leu
465                 470                 475                 480
Pro Glu Asn Ile Ser Pro Phe Ile Ser Ser Phe Glu Ile Gln Gly His
                485                 490                 495
Leu Thr Val Gly Gln Pro Gln Arg Ala Leu Glu Leu Ile Arg Arg Ser
            500                 505                 510
Trp Gly Trp Tyr Tyr Asn Asn Ala Asn Gly Thr Gln Ser Thr Val Ile
        515                 520                 525
Glu Gly Tyr Leu Gln Asn Gly Thr Phe Gly Tyr Arg Gly Ser Arg Gly
    530                 535                 540
Tyr Tyr Tyr Asp Thr Ala Tyr Val Ser His Ser His Gly Trp Ser Ser
545                 550                 555                 560
Gly Pro Thr Ser Ala Leu Thr Asn Tyr Ile Val Gly Ile Thr Val Thr
                565                 570                 575
Ser Pro Leu Gly Ala Thr Trp Arg Ile Ala Pro Gln Phe Val Asp Leu
            580                 585                 590
Gln Ser Ala Glu Gly Gly Phe Thr Thr Ser Leu Gly Lys Phe Gln Ala
        595                 600                 605
Gly Trp Ser Lys Thr Asp Lys Gly Tyr Thr Leu Asp Phe Thr Val Pro
    610                 615                 620
His Gly Thr Gln Gly Asn Leu Thr Leu Pro Phe Val Gly Thr Ala Lys
625                 630                 635                 640
Pro Ser Ile Lys Ile Asp Gly Thr Glu Ile Thr Arg Gly Val Gln Tyr
                645                 650                 655
Ala Asn Ser Thr Ala Thr Val Thr Val Ser Gly Gly Gly Thr Tyr Lys
            660                 665                 670
Val Val Val Gln
        675
```

<210> 254
<211> 779
<212> PRT

<213> Artificial Sequence

<220>
<223> Transgucosidase GAQ43928.1

<400> 254
Met Arg Phe Arg Asp Gly Met Trp Leu Val Asp Pro Ser Lys Ser Leu
 1               5                  10                  15
Gln Tyr Ala Glu Asp Ile Tyr Ser Ile Asn Ala Ser Pro Asp Asn Arg
            20                  25                  30
Ser Leu Asn Leu Leu Cys Pro Thr Arg His Ile Phe Ser Arg Gly Asn
        35                  40                  45
Thr Leu Asn Leu Ser Thr Leu His Ile Asn Leu Glu Ser His Phe Asp
    50                  55                  60
Gly Val Ile Ser Leu Glu Val Gln His Trp Leu Gly Ala Arg Lys Gly
65                  70                  75                  80
Thr Pro Asp Phe Glu Leu Phe Pro Asp Gly Glu Gly Pro Lys Leu Ser
                85                  90                  95
Glu Glu Arg Ile Gly Ile Ser Lys Ser Glu Arg Gly Thr Thr Leu Lys
            100                 105                 110
Ser Gly Ala Leu Ser Val Thr Val Ser Pro Asp Gln His Asp Phe Ser
        115                 120                 125
Ile Arg Phe His Ser Ser Asp Asp Tyr Asp Trp Glu Val Thr Ser Leu
    130                 135                 140
Leu Asn Arg Ser Val Gly Leu Ala Tyr Asp Pro Pro Ile Ser Asn Gly
145                 150                 155                 160
Lys Gln Val Glu Asp Leu Val Gln Gly Gln Ser Gly Ser Arg Lys His
                165                 170                 175
Tyr Ile Phe Thr Gln Thr Glu Leu Asp Ile Gly Glu Ser Val His Gly
            180                 185                 190
Leu Gly Glu Arg Phe Gly Pro Phe Asn Arg Leu Gly Gln His Val Glu
        195                 200                 205
Ile Trp Asn Glu Asp Gly Gly Thr Ser Ser Asp Gln Ala Tyr Lys Asn
    210                 215                 220
Val Ser Phe Trp Met Ser Ser Lys Gly Tyr Gly Val Phe Ile Asp Thr
225                 230                 235                 240
Pro Glu Lys Val Asp Leu Glu Ile Gly Ser Glu Arg Cys Cys Arg Val
                245                 250                 255
Gln Thr Ser Val Glu Gly Gln Arg Leu Lys Trp Tyr Ile Ile Tyr Gly
            260                 265                 270
Pro Ser Pro Lys Glu Val Leu Thr Lys Tyr Ser Val Leu Thr Gly Arg
        275                 280                 285
Ala Pro Met Val Pro Ala Trp Ser Phe Gly Leu Trp Leu Thr Thr Ser
    290                 295                 300
Phe Thr Thr Asn Tyr Asp Glu Ala Thr Val Thr Asp Phe Leu Gln Gln
305                 310                 315                 320
Met Ser Asp Arg Ser Ile Pro Val Glu Val Phe His Tyr Asp Ser Phe
                325                 330                 335
Trp Met Arg Ala Phe His Trp Cys Asp Phe Val Phe Ser Pro Asp His
            340                 345                 350
Phe Pro Asp Pro Lys Gly Ser Ile Ala Arg Ile Lys His Ala Gly Leu
        355                 360                 365
Thr Asn Lys Val Cys Val Trp Ile Asn Pro Tyr Leu Gly Gln Ala Ser
    370                 375                 380

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Pro Val Phe Leu Glu Ala Ala Glu Lys Gly Tyr Leu Leu Lys Arg Thr
385                 390                 395                 400
Asn Gly Asp Val Trp Gln Trp Asp Leu Trp Gln Thr Gly Met Gly Leu
                405                 410                 415
Val Asp Phe Thr Asn Pro Glu Ala Val Arg Trp Tyr Glu Gly Cys Leu
            420                 425                 430
Glu Arg Leu Phe Asp Val Gly Ile Glu Ser Ile Lys Thr Asp Phe Gly
        435                 440                 445
Glu Arg Ile Pro Thr Lys Gly Val Lys Trp His Asp Glu Ser Val Asp
    450                 455                 460
Pro Ala Arg Met His Asn Tyr Tyr Ala Phe Ile Tyr Asn Lys Ile Val
465                 470                 475                 480
Tyr Asn Ala Leu Thr Arg Arg Tyr Gly Asp Gly Gln Ala Val Leu Phe
                485                 490                 495
Ala Arg Ser Ala Cys Ala Gly Val Gln Arg Phe Pro Leu Cys Trp Gly
            500                 505                 510
Gly Asp Cys Glu Ser Thr Pro Ala Ala Leu Ala Glu Ser Val Arg Gly
        515                 520                 525
Gly Leu Ser Ile Gly Leu Ser Ser Phe Ser Phe Trp Ser Cys Asp Ile
    530                 535                 540
Gly Gly Phe Glu Gly Thr Pro Pro Pro Trp Ile Tyr Lys Arg Trp Val
545                 550                 555                 560
Ala Phe Gly Leu Leu Cys Ser His Ser Arg Leu His Gly Ser Asp Ser
                565                 570                 575
Tyr Arg Val Pro Trp Leu Ile Asp Asn Asp Asp Ala Gly Pro Gln Gly
            580                 585                 590
Ser Thr Ala Val Leu Arg Thr Phe Val Arg Leu Lys Arg Arg Leu Met
        595                 600                 605
Pro Tyr Leu Tyr Thr Gln Ala Val Gln Ser Thr Arg Met Gly Trp Pro
    610                 615                 620
Leu Ser Leu Arg Ala Thr Ala Leu Glu Phe Pro His Asp Pro Thr Ala
625                 630                 635                 640
Trp Ala Ala Cys Asp Arg Gln Phe Phe Val Gly Glu Asn Leu Leu Val
                645                 650                 655
Ala Pro Val Phe Thr Glu His Gly Asp Val Glu Phe Tyr Leu Pro Glu
            660                 665                 670
Gly Gln Trp Thr Ser Leu Trp Asp Glu Lys Lys Val Val Ser Gly Pro
        675                 680                 685
Gly Trp Arg Arg Glu Lys His Gly Phe Gly Thr Leu Pro Ile Tyr Val
    690                 695                 700
Arg Glu Gly Ala Val Ile Val Met Gly Lys Glu Gln Gly Glu Gly Gly
705                 710                 715                 720
Phe Ala Tyr Asp Trp Cys Glu Ala Pro Glu Val Arg Leu Tyr Gln Thr
                725                 730                 735
Lys Gln Gly Asp Cys Ala Thr Val Val Asp Ala Ser Gly Lys Glu Val
            740                 745                 750
Gly Thr Leu Thr Val Gln Asp Asp Gly Ser Leu Lys Gly Leu Glu Cys
        755                 760                 765
Phe Arg Gly Asp Val Thr Val Arg Arg Ile Glu
    770                 775
```

<210> 255
<211> 629

<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase GAQ43980.1

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

370 375 380
Ala Arg Ser Val Ser Arg Tyr Thr Ile Asp Ser Asp Glu Phe Arg Glu
385 390 395 400
Arg Gly Ala Lys Leu Leu Ala Leu Leu Glu Thr Thr Leu Gly Gly Thr
405 410 415
Ile Phe Leu Tyr Gln Gly Gln Glu Ile Gly Met Arg Asn Phe Pro Leu
420 425 430
Glu Trp Asp Pro Asp Ile Glu Tyr Lys Asp Val Glu Ser Val Asn Phe
435 440 445
Leu Asn Lys Ser Lys Glu Leu His Pro Val Gly Thr Glu Gly Leu Ala
450 455 460
Lys Ala Arg Thr Leu Leu Gln Lys Lys Ala Arg Asp His Ala Arg Thr
465 470 475 480
Pro Met Gln Trp Ser Ala Ala Pro His Ala Gly Phe Thr Val Pro Asp
485 490 495
Ala Thr Pro Trp Met Arg Val Asn Asp Asp Tyr Glu Thr Val Asn Val
500 505 510
Glu Thr Gln Met Ser Phe Pro Trp Gln Ser Lys Gly Glu Leu Ser Val
515 520 525
Trp Gln Tyr Trp Gln Gln Ala Ile Gln His Arg Lys Leu Tyr Lys Asn
530 535 540
Ala Phe Val Tyr Gly Gly Phe Glu Asp Leu Asp Tyr His Asn Glu Lys
545 550 555 560
Val Phe Ala Tyr Leu Arg Thr Ser Ala Asp Gly Asn Asp Ser Trp Leu
565 570 575
Val Ala Met Asn Trp Thr Thr Ser Ala Val Glu Trp Thr Val Pro Ser
580 585 590
Asp Ile His Val Thr Arg Trp Val Ser Ser Thr Leu Gln Thr Ala Pro
595 600 605
Pro Val Ala Ser Lys Thr Val Ile Thr Leu Arg Ala Phe Glu Gly Val
610 615 620
Leu Gly Cys Cys Asn
625

<210> 256
<211> 963
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase GAQ43844.1

<400> 256
Met Ala Gly Thr Arg Pro Met Ser Asn Arg Trp Thr Leu Leu Leu Ser
1 5 10 15
Leu Val Ile Leu Leu Gly Cys Leu Val Ile Pro Gly Val Thr Val Lys
20 25 30
His Glu Asn Phe Lys Thr Cys Ser Gln Ser Gly Phe Cys Lys Arg Asn
35 40 45
Arg Ala Phe Ala Asp Asp Ala Ser Ala Gln Gly Pro Ser Trp Thr Ser
50 55 60
Pro Tyr Glu Leu Asp Ser Ser Ser Ile Gln Phe Lys Asp Gly Gln Leu
65 70 75 80

```
His Gly Thr Ile Leu Lys Ser Val Ser Ala Asn Glu Lys Val Lys Leu
                85                  90                  95
Pro Leu Val Val Ser Phe Leu Glu Ser Gly Ala Ala Arg Val Val Val
            100                 105                 110
Asp Glu Glu Lys Arg Leu Asn Gly Glu Ile Gln Leu Arg His Asp Ser
        115                 120                 125
Lys Ala Arg Lys Glu Arg Tyr Asn Glu Ala Glu Lys Trp Val Leu Val
    130                 135                 140
Gly Gly Leu Glu Leu Ser Lys Thr Ala Thr Leu Lys Pro Glu Thr Glu
145                 150                 155                 160
Thr Gly Phe Thr Arg Val Leu Tyr Gly Pro Asp Asn Gln Phe Glu Ala
                165                 170                 175
Val Ile Arg His Ala Pro Phe Ser Ala Asp Phe Lys Arg Asp Gly Gln
            180                 185                 190
Thr His Val Gln Leu Asn Asn Lys Gly Tyr Leu Asn Met Glu His Trp
        195                 200                 205
Arg Pro Lys Val Glu Val Glu Gly Glu Gly Glu Gln Gln Thr Gln Glu
    210                 215                 220
Asp Glu Ser Thr Trp Trp Asp Glu Ser Phe Gly Gly Asn Thr Asp Thr
225                 230                 235                 240
Lys Pro Arg Gly Pro Glu Ser Val Gly Leu Asp Ile Thr Phe Pro Gly
                245                 250                 255
Tyr Lys His Val Phe Gly Ile Pro Glu His Ala Asp Ser Leu Ser Leu
            260                 265                 270
Lys Glu Thr Arg Gly Gly Glu Gly Asn His Glu Glu Pro Tyr Arg Met
        275                 280                 285
Tyr Asn Ala Asp Val Phe Glu Tyr Glu Leu Asn Ser Pro Met Thr Leu
    290                 295                 300
Tyr Gly Ala Ile Pro Phe Met Gln Ala His Arg Lys Asp Ser Thr Val
305                 310                 315                 320
Gly Val Phe Trp Leu Asn Ala Ala Glu Thr Trp Val Asp Ile Val Lys
                325                 330                 335
Ser Thr Ser Ser Pro Asn Pro Leu Ala Leu Gly Val Gly Ala Thr Thr
            340                 345                 350
Asp Thr Gln Ser His Trp Phe Ser Glu Ser Gly Gln Leu Asp Val Phe
        355                 360                 365
Val Phe Leu Gly Pro Thr Pro Gln Glu Ile Ser Lys Thr Tyr Gly Glu
    370                 375                 380
Leu Thr Gly Tyr Thr Gln Leu Pro Gln His Phe Ala Ile Ala Tyr His
385                 390                 395                 400
Gln Cys Arg Trp Asn Tyr Ile Thr Asp Glu Asp Val Lys Glu Val Asp
                405                 410                 415
Arg Asn Phe Asp Lys Tyr Gln Ile Pro Tyr Asp Val Ile Trp Leu Asp
            420                 425                 430
Ile Glu Tyr Thr Asp Asp Arg Lys Tyr Phe Thr Trp Asp Pro Leu Thr
        435                 440                 445
Phe Pro Asp Pro Ile Ser Met Glu Glu Gln Leu Asp Glu Ser Glu Arg
    450                 455                 460
Lys Leu Val Val Ile Ile Asp Pro His Ile Lys Asn Gln Asp Lys Tyr
465                 470                 475                 480
Ser Ile Ser Gln Glu Met Thr Ser Lys Asp Leu Ala Thr Lys Asn Lys
                485                 490                 495
Asp Gly Glu Ile Tyr Asp Gly Trp Cys Trp Pro Gly Ser Ser His Trp
            500                 505                 510
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Ile Asp Thr Phe Asn Pro Ala Ala Ile Lys Trp Trp Ile Ser Leu Phe
        515                 520                 525
Lys Phe Asp Lys Phe Lys Gly Thr Leu Ser Asn Val Phe Ile Trp Asn
    530                 535                 540
Asp Met Asn Glu Pro Ser Val Phe Asn Gly Pro Glu Thr Thr Met Pro
545                 550                 555                 560
Lys Asp Asn Leu His His Gly Asn Trp Glu His Arg Asp Ile His Asn
                565                 570                 575
Val His Gly Ile Thr Leu Val Asn Ala Thr Tyr Asp Ala Leu Leu Glu
            580                 585                 590
Arg Lys Lys Gly Glu Val Arg Arg Pro Phe Ile Leu Thr Arg Ser Tyr
        595                 600                 605
Tyr Ala Gly Ala Gln Arg Met Ser Ala Met Trp Thr Gly Asp Asn Gln
    610                 615                 620
Ala Thr Trp Glu His Leu Ala Ala Ser Ile Pro Met Val Leu Asn Asn
625                 630                 635                 640
Gly Ile Ala Gly Phe Pro Phe Ala Gly Ala Asp Val Gly Gly Phe Phe
                645                 650                 655
His Asn Pro Ser Lys Glu Leu Leu Thr Arg Trp Tyr Gln Ala Gly Ile
            660                 665                 670
Trp Tyr Pro Phe Phe Arg Ala His Ala His Ile Asp Thr Arg Arg Arg
        675                 680                 685
Glu Pro Tyr Leu Ile Ala Glu Pro His Arg Ser Ile Ile Ser Gln Ala
    690                 695                 700
Ile Arg Leu Arg Tyr Gln Leu Leu Pro Ala Trp Tyr Thr Ala Phe His
705                 710                 715                 720
Glu Ala Ser Val Asn Gly Met Pro Ile Val Arg Pro Gln Tyr Tyr Ala
                725                 730                 735
His Pro Thr Asp Glu Ala Gly Phe Ala Ile Asp Asp Gln Leu Tyr Leu
            740                 745                 750
Gly Ser Thr Gly Leu Leu Ala Lys Pro Val Val Ser Glu Glu Ala Thr
        755                 760                 765
Thr Ala Asp Ile Tyr Leu Ala Asp Asp Glu Lys Tyr Tyr Asp Tyr Phe
    770                 775                 780
Asp Tyr Thr Val Tyr Gln Gly Ala Gly Lys Arg His Thr Val Pro Ala
785                 790                 795                 800
Pro Met Glu Thr Val Pro Leu Leu Met Gln Gly Gly His Val Ile Pro
                805                 810                 815
Arg Lys Asp Arg Pro Arg Arg Ser Ser Ala Leu Met Arg Trp Asp Pro
            820                 825                 830
Tyr Thr Leu Val Val Val Leu Asp Lys Asn Gly Gln Ala Asp Gly Ser
        835                 840                 845
Leu Tyr Val Asp Asp Gly Glu Thr Phe Asp Tyr Glu Arg Gly Ala Tyr
    850                 855                 860
Ile His Arg Arg Phe Arg Phe Gln Glu Ser Ala Leu Val Ser Glu Asp
865                 870                 875                 880
Val Gly Thr Lys Gly Pro Lys Thr Ala Glu Tyr Leu Lys Thr Met Ala
                885                 890                 895
Asn Val Arg Val Glu Arg Val Val Val Val Asp Pro Pro Lys Glu Trp
            900                 905                 910
Gln Gly Lys Thr Ser Val Thr Val Ile Glu Asp Gly Ala Ser Ala Ala
        915                 920                 925
Ser Thr Ala Pro Met Gln Tyr His Ser Gln Ser Asp Gly Lys Ala Ala
    930                 935                 940
```

```
Tyr Ala Val Val Lys Asn Pro Asn Val Gly Ile Gly Lys Thr Trp Arg
945                 950                 955                 960
Ile Glu Phe
```

<210> 257
<211> 1468
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase GAQ42954.1

<400> 257

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

```
305                 310                 315                 320
Leu Arg Arg Arg Trp Thr Glu Glu Gly Tyr Glu Val Trp Ser Gly Pro
                325                 330                 335
Leu Ser Asn Gly Arg Thr Val Ala Ala Val Ile Asn Trp Arg Asn Glu
            340                 345                 350
Ser Arg Asp Leu Thr Leu Asp Leu Pro Asp Ile Gly Leu Gln His Ala
        355                 360                 365
Gly Thr Val Lys Asn Ile Trp Asp Gly Thr Thr Ala Gln Asn Val Val
    370                 375                 380
Thr Ser Tyr Thr Ala Thr Val Ala Gly His Gly Thr Met Leu Leu Glu
385                 390                 395                 400
Leu Gln Asn Thr Thr Ala Val Gly Val Tyr Pro Arg Asp Val Phe Gly
                405                 410                 415
Glu Ser Ser Gly Gln Thr Thr Thr Phe Glu Asn Ile Tyr Ala Val Thr
            420                 425                 430
Thr Ser Ala Lys Tyr Thr Val Ser Val Tyr Phe Ser Gln Pro Ala Ser
        435                 440                 445
Ser Ala Glu Thr Ile Ser Ile Gly Ser Asn Ala Asn Gln Ser Ile Ile
    450                 455                 460
Ser Val Gln Val Pro Ala Ser Ser Thr Leu Val Ser Ala Asn Ile Pro
465                 470                 475                 480
Leu Thr Ala Gly Ser Ser Asn Thr Val Thr Ile Asn Thr Ser Ile Pro
                485                 490                 495
Ile Asp Ala Ile His Ile Thr Ala Pro Asn Gly Thr Tyr Tyr Pro Cys
            500                 505                 510
Thr Asn Phe Thr Leu Ala Gly Ser Thr Thr Leu Thr Thr Cys Gly Ser
        515                 520                 525
Gly Tyr Cys Gln Pro Val Gly Ser Lys Ile Gly Tyr Ile Ser Pro Ser
    530                 535                 540
Gly Thr Ala Lys Ala Thr Ile Ser Ala Thr Thr Ser Gly Ser Lys Tyr
545                 550                 555                 560
Leu Glu Ile Asp Trp Ile Asn Asn Glu Ile Ala Phe Asp Ser Ser Trp
                565                 570                 575
Gly Trp Gly Ser Asn Ser Arg Asn Leu Thr Val Thr Val Asn Ser Glu
            580                 585                 590
Glu Pro Val Arg Ile Glu Val Pro Leu Ser Gly Arg His Ser Glu Leu
        595                 600                 605
Phe Gly Pro Gly Leu Gly Trp Trp Asp Thr Ala Thr Leu Gly Leu Leu
    610                 615                 620
Thr Ser Gly Trp Lys Glu Gly Leu Asn Glu Val Ile Val Gly Asn Val
625                 630                 635                 640
Gly Gly Asp Glu Gly Phe Gln Ser Tyr Gly Ala Asp Phe Glu Ile Leu
                645                 650                 655
Arg Ser Asn Phe Glu Lys Met Lys Val Ser Leu Thr Leu Tyr Ala Ala
            660                 665                 670
Ala Leu Gln Leu Ala Asp Ala Ala Val Val Gln Lys Arg Thr Val Asp
        675                 680                 685
Val Ala Glu Leu Glu His Tyr Trp Ser Tyr Gly Arg Ser Glu Pro Val
    690                 695                 700
Tyr Pro Thr Pro Glu Thr Ser Gly Ser Gly Asp Trp Glu Glu Ala Phe
705                 710                 715                 720
Thr Lys Ala Lys Ser Leu Val Ala Gln Met Thr Asn Asp Glu Lys Asn
                725                 730                 735
Asn Ile Thr Tyr Gly Tyr Thr Ser Thr Thr Asn Gly Cys Ser Gly Met
```

```
            740                 745                 750
Ser Gly Gly Val Pro Arg Leu Gly Tyr Pro Gly Met Cys Leu Gln Asp
        755                 760                 765
Ala Ala Ser Gly Val Arg Gly Thr Asp Met Val Asn Ala Tyr Ala Ser
    770                 775                 780
Gly Leu His Ile Gly Ala Ser Trp Asn Arg Asp Leu Ala Tyr Glu His
785                 790                 795                 800
Ala His Tyr Met Gly Ala Glu Phe Lys Arg Lys Gly Ala Asn Val Ala
                805                 810                 815
Leu Gly Pro Val Val Gly Pro Leu Gly Arg Met Ala Arg Gly Gly Arg
            820                 825                 830
Asn Trp Glu Gly Tyr Ser Asn Asp Pro Tyr Leu Ser Gly Ser Leu Val
        835                 840                 845
Gln Asn Thr Ile Arg Gly Leu Gln Glu Ser Val Ile Ala Cys Val Lys
    850                 855                 860
His Phe Ile Gly Asn Glu Gln Glu Thr Asn Arg Asn Thr Pro Gln Leu
865                 870                 875                 880
Leu Glu Asp Ser Tyr Asn Gln Ser Val Ser Ser Asn Ile Asp Asp Lys
                885                 890                 895
Thr Ile His Glu Leu Tyr Leu Trp Pro Phe Gln Asp Ala Val Lys Ala
            900                 905                 910
Gly Ala Gly Ala Val Met Cys Ser Tyr Asn Arg Ile Asn Asn Ser Tyr
        915                 920                 925
Gly Cys Gln Asn Ser Lys Asn Leu Asn Gly Leu Leu Lys Gly Glu Leu
    930                 935                 940
Gly Phe Gln Gly Phe Val Val Ser Asp Trp Asn Ala Gln Gln Ser Gly
945                 950                 955                 960
Ile Ala Ser Ala Ala Ala Gly Leu Asp Met Val Met Pro Asp Ser Val
                965                 970                 975
Tyr Trp Glu Asn Gly Asn Leu Ser Leu Ala Val Arg Asn Gly Ser Leu
            980                 985                 990
Ser Ser Thr Arg Leu Asp Asp Met Ala Thr Arg Ile Val Ala Ala Trp
        995                 1000                1005
Tyr Lys Tyr Ala Glu Leu Glu Asp Pro Gly Phe Gly Met Pro Ile Ser
    1010                1015                1020
Leu Leu Glu Pro His Asp Pro Val Asp Ala Arg Asp Pro Ala Ser Lys
1025                1030                1035                1040
Ala Thr Ile Leu Gln Glu Ala Ile Glu Gly His Val Leu Val Lys Asn
                1045                1050                1055
Thr Asp Asn Ala Leu Pro Leu Lys Glu Pro Lys Phe Leu Ser Leu Phe
            1060                1065                1070
Gly Tyr Asp Ala Ile Ala Ala Gln Arg Asn Thr Met Asp Asp Leu Ser
        1075                1080                1085
Trp Ser Leu Trp Thr Met Gly Leu Asp Asn Thr Leu Ser Tyr Pro Asn
    1090                1095                1100
Gly Thr Ala Val Asp Pro Ser His Leu Lys Tyr Met Phe Leu Ser Ser
1105                1110                1115                1120
Thr Asn Pro Ser Glu Asn Gly Pro Gly Val Ser Leu Asn Gly Thr Met
                1125                1130                1135
Ile Ser Gly Gly Gly Ser Gly Ala Ser Thr Pro Ser Tyr Ile Asp Ala
            1140                1145                1150
Pro Phe Asp Ala Phe Gln Arg Gln Ala Tyr Glu Asp Asn Thr Phe Leu
        1155                1160                1165
Ala Trp Asp Phe Ala Ser Gln Ser Pro Val Val Asn Pro Ala Ser Glu
```

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    1170                1175                1180
Ala Cys Leu Val Phe Ile Asn Glu Ala Ala Ala Glu Gly Trp Asp Arg
1185                1190                1195                1200
Pro Tyr Val Ala Asp Pro Tyr Ser Asp Thr Leu Val Glu Asn Val Ala
                1205                1210                1215
Ser Gln Cys Asn Asn Thr Met Val Ile Ile His Asn Ala Gly Ile Arg
            1220                1225                1230
Leu Val Asp Arg Trp Val Asp Asn Pro Asn Val Thr Ala Val Ile Tyr
        1235                1240                1245
Gly His Leu Pro Gly Gln Asp Ser Gly Arg Ala Leu Val Glu Ile Met
    1250                1255                1260
Tyr Gly Lys Gln Ser Pro Ser Gly Arg Leu Pro Tyr Thr Val Ala Lys
1265                1270                1275                1280
Asn Ala Ser Asp Tyr Gly Ala Leu Leu Ser Pro Val Val Pro Glu Gly
                1285                1290                1295
Thr Lys Asp Leu Tyr Tyr Pro Gln Asp Asn Phe Thr Glu Gly Val Tyr
            1300                1305                1310
Ile Asp Tyr Lys Ala Phe Glu Gln Lys Asn Ile Thr Pro Arg Tyr Glu
        1315                1320                1325
Phe Gly Tyr Gly Leu Thr Tyr Ser Thr Phe Asp Tyr Ser Gly Leu Lys
    1330                1335                1340
Ile Ser Ile His Thr Gly Val Asn Thr Asp Tyr Leu Pro Pro Asn Ser
1345                1350                1355                1360
Thr Ile Glu Glu Gly Gly Ile Pro Ala Leu Trp Asp Val Val Ala Thr
                1365                1370                1375
Val Thr Cys Ser Val Ala Asn Thr Gly Ser Val Ala Ala Ala Glu Val
            1380                1385                1390
Ala Gln Leu Tyr Leu Gly Ile Pro Gly Gly Pro Ala Lys Val Leu Arg
        1395                1400                1405
Gly Phe Glu Lys Lys Leu Ile Gln Pro Gly His His Thr Lys Val Gln
    1410                1415                1420
Phe Asp Leu Thr Arg Arg Asp Leu Ser Ser Trp Asp Val Val Asn Gln
1425                1430                1435                1440
Ala Trp Val Leu Gln Lys Gly Asp Tyr Ser Val Tyr Val Gly Lys Ser
                1445                1450                1455
Val Leu Asp Thr Gln Leu Thr Gly Thr Leu Thr Ile
            1460                1465


<210> 258
<211> 1181
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase GAQ42198.1

<400> 258
Met Ala Val Ser Ala Ser Ser Pro Glu Pro Leu Gly Ala Asn Ile Asp
 1               5                  10                  15
Glu Arg Thr Pro Leu Asn Ser Ser Ala Gln His Ala Thr Pro Ser Ala
            20                  25                  30
Asn Thr Pro Asp Tyr Ser Ser Ile Thr Lys Gly Leu Thr Ser Asp Val
        35                  40                  45
```

```
His Ser Ser His Gly Ser Asp Glu Glu Gln Pro Leu Ile Asn Pro Pro
    50                  55                  60
Glu Ser Pro Gly Lys Asp Val Thr Ala Leu Thr Ser Ile Ser Thr Val
65                  70                  75                  80
Ile Gly Val Leu Leu Leu Gly Glu Phe Ile Ser Asn Ala Asp Ala Thr
                85                  90                  95
Leu Val Met Ala Ala Thr Gly Arg Ile Ser Ser Glu Phe Asn Arg Leu
            100                 105                 110
Arg Asp Ala Ser Trp Leu Ser Thr Ala Tyr Thr Leu Gly Leu Cys Ala
        115                 120                 125
Ala Gln Pro Met Tyr Gly Lys Leu Ser Asp Ile Tyr Gly Arg Lys Pro
    130                 135                 140
Leu Leu Leu Trp Ala Tyr Phe Leu Phe Gly Val Gly Cys Val Ile Ser
145                 150                 155                 160
Gly Ile Gly Pro Asp Met Ala Thr Val Ile Leu Gly Arg Ala Ile Ser
                165                 170                 175
Gly Ile Gly Gly Ala Gly Thr Met Ala Met Gly Ser Ile Ile Ile Thr
            180                 185                 190
Asp Ile Val Pro Arg Arg Asp Val Ala His Trp Arg Ala Tyr Ile Asn
        195                 200                 205
Ile Ala Met Thr Leu Gly Arg Ser Ala Gly Gly Pro Val Gly Gly Trp
    210                 215                 220
Leu Thr Asp Thr Ile Gly Trp Arg Trp Ser Phe Ile Ile Gln Gly Pro
225                 230                 235                 240
Leu Ala Ala Val Ala Ala Leu Leu Val Val Trp Lys Leu Lys Leu Val
                245                 250                 255
His Pro Val Thr Glu Lys Ser Ile Arg Arg Val Asp Phe Leu Gly Thr
            260                 265                 270
Phe Leu Leu Ala Thr Gly Ile Ile Thr Ile Thr Val Ile Met Asp Gln
        275                 280                 285
Ala Gly Gln Ser Phe Ala Trp Ala Ser Leu Ser Thr Ala Ile Leu Ser
    290                 295                 300
Thr Leu Ser Leu Ser Ala Phe Val Ala Phe Val Leu Val Glu Leu Tyr
305                 310                 315                 320
Val Ala Pro Glu Pro Ile Phe Glu Leu Arg Met Leu Arg Lys Pro Asn
                325                 330                 335
Val Thr Pro Ser Tyr Leu Ile Gly Ser Leu Gln Ile Thr Ala Gln Val
            340                 345                 350
Gly Met Met Phe Ser Val Pro Leu Tyr Phe Gln Val Thr Ser Lys Ala
        355                 360                 365
Ser Ala Thr Val Ala Gly Gly His Leu Val Pro Ala Val Ile Gly Asn
    370                 375                 380
Thr Leu Gly Gly Leu Ile Ala Gly Ala Phe Ile Arg Arg Thr Gly Gln
385                 390                 395                 400
Phe Lys Val Leu Leu Ile Leu Ala Gly Leu Val Ala Ser Val Ala Tyr
                405                 410                 415
Leu Leu Leu Phe Leu Arg Trp Asn Gly His Thr Gly Phe Trp Glu Ser
            420                 425                 430
Leu Tyr Ile Ile Pro Gly Gly Met Gly Thr Gly Phe Cys Ser Ala Ala
        435                 440                 445
Ala Phe Val Ser Met Thr Ala Phe Leu Met Pro Gln Glu Val Ala Met
    450                 455                 460
Ala Thr Gly Gly Tyr Phe Leu Leu Phe Ser Phe Ala Met Thr Ala Gly
465                 470                 475                 480
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Val Thr Val Thr Asn Ser Leu Leu Gly Thr Val Phe Lys Arg Gln Met
                485                 490                 495
Glu Gln His Leu Thr Gly Pro Gly Ala Lys Lys Ile Ile Glu Arg Ala
            500                 505                 510
Leu Ser Asp Thr Ser Tyr Ile Asn Gly Leu Gln Gly His Val Arg Asp
        515                 520                 525
Val Val Val Lys Gly Tyr Val Ala Gly Leu Arg Tyr Thr Tyr Pro Met
    530                 535                 540
Arg Val Ser Ile Ser Ser Leu Ala Leu Ser Val Tyr Leu Phe Gly Lys
545                 550                 555                 560
Leu Ala Leu Gly Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile Tyr
                565                 570                 575
Phe Leu Leu Thr Asp Arg Phe Gly Arg Ala Asp Asn Ser Thr Thr Ala
            580                 585                 590
Thr Cys Asp Thr Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln Gly
        595                 600                 605
Ile Ile Asn His Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
    610                 615                 620
Trp Ile Ser Pro Ile Thr Glu Gln Leu Pro Gln Asp Thr Ser Asp Gly
625                 630                 635                 640
Glu Ala Tyr His Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser
                645                 650                 655
Asn Phe Gly Thr Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu His
            660                 665                 670
Ala Arg Gly Met Tyr Leu Met Val Asp Val Val Pro Asn His Met Gly
        675                 680                 685
Tyr Ala Gly Asn Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe
    690                 695                 700
Asp Ser Ser Ser Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp
705                 710                 715                 720
Asn Leu Thr Met Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val Ser
                725                 730                 735
Leu Pro Asp Leu Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr
            740                 745                 750
Asp Trp Val Ala Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg
        755                 760                 765
Ile Asp Ser Val Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr Gln
    770                 775                 780
Glu Ala Ala Gly Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn Pro
785                 790                 795                 800
Ala Leu Asp Cys Pro Tyr Gln Asp Tyr Leu Asp Gly Val Leu Asn Tyr
                805                 810                 815
Pro Ile Tyr Trp Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser
            820                 825                 830
Ile Ser Asp Leu Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser
        835                 840                 845
Asp Pro Thr Leu Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg
    850                 855                 860
Phe Ala Ser Tyr Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser
865                 870                 875                 880
Tyr Ile Phe Leu Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu
                885                 890                 895
Gln His Tyr Ser Gly Gly Asp Val Pro Tyr Asn Arg Glu Ala Thr Trp
            900                 905                 910
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Leu Ser Gly Tyr Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr
        915                 920                 925
Thr Asn Ala Ile Arg Lys Leu Ala Ile Ser Ala Asp Ser Asp Tyr Ile
    930                 935                 940
Thr Tyr Ala Asn Asp Pro Ile Tyr Thr Asp Ser Asn Thr Ile Ala Met
945                 950                 955                 960
Arg Lys Gly Thr Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys
                965                 970                 975
Gly Ser Ser Gly Ser Ser Tyr Thr Leu Ser Leu Ser Gly Ser Gly Tyr
            980                 985                 990
Thr Ser Gly Thr Glu Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr
        995                 1000                1005
Val Asp Ser Asn Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro
    1010                1015                1020
Arg Val Leu Leu Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys Gly
1025                1030                1035                1040
Gly Ser Gly Ser Thr Thr Thr Thr Ala Ala Thr Ser Thr Ser Thr Ser
                1045                1050                1055
Lys Ala Thr Ser Ser Thr Thr Thr Thr Thr Ala Ile Thr Thr Thr Ser
            1060                1065                1070
Ser Ser Cys Thr Ala Thr Ser Thr Thr Leu Pro Ile Thr Phe Glu Glu
        1075                1080                1085
Leu Val Thr Thr Thr Tyr Gly Glu Glu Ile Tyr Leu Ser Gly Ser Ile
    1090                1095                1100
Ser Gln Leu Gly Glu Trp Asp Thr Ser Asp Ala Val Lys Leu Ser Ala
1105                1110                1115                1120
Asp Asp Tyr Thr Ser Ser Asn Pro Glu Trp Tyr Val Thr Val Ser Leu
                1125                1130                1135
Pro Val Gly Thr Thr Phe Glu Tyr Lys Phe Ile Lys Val Glu Glu Asp
            1140                1145                1150
Gly Ser Val Thr Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro
        1155                1160                1165
Glu Cys Gly Ser Gly Glu Thr Val Val Asp Thr Trp Arg
    1170                1175                1180


<210> 259
<211> 768
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase GAQ39994.1

<400> 259
Met Pro Leu Thr Tyr Leu Gly Ala Leu Ala Met Leu Thr Ala Leu Pro
 1               5                  10                  15
Ser Leu Gly Gln Ala Arg Ser Thr Trp Pro Leu Gly Ser Gly Leu Glu
            20                  25                  30
Leu Ser Tyr Gln Ala Ser Gln His Gln Ile Ser Ile His Gln Asp Asn
        35                  40                  45
Gln Thr Ile Phe Ser Thr Leu Pro Gly Gln Pro Phe Leu Ser Ala Gly
    50                  55                  60
Ala Gly Lys Asp Gln Ile Val Glu Asp Ser Gly Asn Phe Asn Ile Thr
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65                  70                  75                  80
Asn Val Ala Gln Ala Arg Cys Gln Gly Gln Asn Ile Thr Gln Leu Ala
                85                  90                  95
Gly Ile Pro Arg Arg Asp Ser Val Lys Asn Gln Val Ala Val Arg Gly
            100                 105                 110
Tyr Leu Leu Asp Cys Gly Gly Glu Asp Ile Ala Tyr Ala Met Asn Phe
        115                 120                 125
Trp Val Pro Lys Thr Leu Ser Asp Arg Val Ala Phe Glu Ala Thr Val
    130                 135                 140
Asp Ser Asp Ala Asn Ala Ser Val Pro Val Glu Arg Leu Tyr Leu Thr
145                 150                 155                 160
Phe Ala Ser His Ala Arg Glu Asp Phe Tyr Gly Leu Gly Ala Gln Ala
                165                 170                 175
Ser Phe Ala Ser Met Lys Asn Arg Ser Ile Pro Ile Phe Ser Arg Glu
            180                 185                 190
Gln Gly Val Gly Arg Gly Asp Gln Pro Tyr Thr Ala Ile Glu Asp Ser
        195                 200                 205
Gln Gly Phe Phe Ser Gly Gly Asp Gln Tyr Thr Thr Tyr Thr Ala Ile
    210                 215                 220
Pro Gln Tyr Val Ser Ser Asp Gly Arg Val Phe Tyr Leu Asp Glu Asn
225                 230                 235                 240
Asp Thr Ala Tyr Ala Val Phe Asp Phe Gln Arg Pro Asp Ala Val Thr
                245                 250                 255
Val Arg Tyr Asp Ser Ile Thr Val His Gly His Leu Met Gln Ala Asp
            260                 265                 270
Asn Met Leu Asp Ala Ile Thr Met Leu Thr Glu Tyr Thr Gly Arg Met
        275                 280                 285
Pro Ala Leu Pro Glu Trp Val Asp His Gly Ala Leu Leu Gly Ile Gln
    290                 295                 300
Gly Gly Gln Glu Lys Val Asn Arg Ile Val Lys Gln Gly Phe Glu His
305                 310                 315                 320
Asp Cys Pro Val Ala Gly Val Trp Leu Gln Asp Trp Ser Gly Thr His
                325                 330                 335
Leu Gln Ser Ala Pro Tyr Gly Asn Met Asn Ile Ser Arg Leu Trp Trp
            340                 345                 350
Asn Trp Glu Ser Asp Thr Ser Leu Tyr Pro Thr Trp Ala Glu Phe Val
        355                 360                 365
Gln Ala Leu Arg Glu Gln His Gly Val Arg Thr Leu Ala Tyr Val Asn
    370                 375                 380
Pro Phe Leu Ala Asp Val Ser Ser Lys Ser Asp Gly Tyr Arg Arg Asn
385                 390                 395                 400
Leu Phe Gln Glu Ala Ser Lys His Arg Tyr Met Val Gln Asn Thr Thr
                405                 410                 415
Thr Asn Ser Thr Ala Ile Ile Ser Ser Gly Lys Gly Ile Asp Ala Gly
            420                 425                 430
Ile Leu Asp Leu Thr Asn Glu Glu Thr Arg Ala Trp Phe Ala Asp Val
        435                 440                 445
Leu Arg Thr Gln Val Trp Ser Ala Asn Ile Ser Gly Cys Met Trp Asp
    450                 455                 460
Phe Gly Glu Tyr Thr Pro Ile Thr Ala Asp Thr Ser Leu Ala Asn Ile
465                 470                 475                 480
Ser Thr Ser Ala Phe Phe Tyr His Asn Gln Tyr Pro Arg Asp Trp Ala
                485                 490                 495
Ala Tyr Gln Arg Ser Val Ala Ala Glu Met Pro Leu Phe His Glu Met
```

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            500                 505                 510
Val Thr Phe His Arg Ser Ala Ser Met Gly Ala Asn Arg His Met Asn
        515                 520                 525
Leu Phe Trp Val Gly Asp Gln Ala Thr Leu Trp Thr Pro Asn Asp Gly
    530                 535                 540
Ile Lys Ser Val Val Thr Ile Gln Gly Gln Met Gly Ile Ser Gly Tyr
545                 550                 555                 560
Ala His Ser His Ser Asp Ile Gly Gly Tyr Thr Thr Val Phe Glu Pro
                565                 570                 575
Pro Thr Thr Ser Asn Ser Ser Gly Ala Ile Pro Arg Ser Ala Glu Leu
            580                 585                 590
Leu Gly Arg Trp Gly Glu Leu Gly Ala Val Ser Ser Ala Val Phe Arg
        595                 600                 605
Ser His Glu Gly Asn Val Pro Ser Val Asn Ala Gln Phe Tyr Ser Asn
    610                 615                 620
Ser Thr Thr Tyr Ala Tyr Phe Ala Tyr Asn Ala Arg Met Phe Arg Ser
625                 630                 635                 640
Leu Gly Pro Tyr Arg Arg Arg Ile Leu Asn Thr Glu Ser Gln Arg Arg
                645                 650                 655
Gly Trp Pro Leu Leu Arg Met Pro Val Leu Tyr His Pro Glu Asp Leu
            660                 665                 670
Arg Ala Arg Gln Ile Ser Tyr Glu Ser Phe Phe Leu Gly Arg Asp Leu
        675                 680                 685
Tyr Val Ala Pro Val Leu Asp Glu Gly Arg Lys Ser Val Glu Val Tyr
    690                 695                 700
Phe Pro Gly His Ser Ala Asn Arg Thr Tyr Thr His Val Trp Ser Gly
705                 710                 715                 720
Gln Thr Tyr Arg Gly Gly Gln Thr Ala Gln Val Ser Ala Pro Phe Gly
                725                 730                 735
Lys Pro Ala Val Phe Val Val Asp Gly Ala Ser Ser Pro Glu Leu Asp
            740                 745                 750
Val Phe Leu Asp Phe Val Arg Lys Glu Asn Gly Thr Val Leu Arg Ala
        755                 760                 765


<210> 260
<211> 985
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase GAQ38166.1

<400> 260
Met Val Lys Leu Thr Asp Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
 1               5                  10                  15
Ala Tyr Gly Ala Ser Gln Ser Arg Leu Ser Thr Thr Thr Ser Ser Gln
            20                  25                  30
Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
        35                  40                  45
Ala Asn Ile Asp Asp Pro Gln Ala Ala Asn Ala Gln Ser Val Cys Pro
    50                  55                  60
Gly Tyr Lys Ala Ser Lys Val Gln His Asn Ser Arg Gly Phe Thr Ala
65                  70                  75                  80
```

```
Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
                85                  90                  95
Asp Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
            100                 105                 110
Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
        115                 120                 125
Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
    130                 135                 140
Ser Val Ser Asp Ser Asp Phe Ser Val Ser Trp Ser Asn Glu Pro Ser
145                 150                 155                 160
Phe Asn Phe Lys Val Ile Arg Lys Ala Thr Gly Asp Ala Leu Phe Ser
                165                 170                 175
Thr Glu Gly Thr Val Leu Val Tyr Glu Asp Gln Phe Ile Glu Phe Val
            180                 185                 190
Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
        195                 200                 205
Thr Gln Phe Arg Leu Gln Arg Asp Ala Asn Leu Thr Ile Tyr Pro Ser
    210                 215                 220
Asp Asp Gly Thr Pro Ile Asp Lys Asn Ile Tyr Gly Gln His Pro Phe
225                 230                 235                 240
Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
                245                 250                 255
Val Pro Val Lys Ser Ser Glu Thr Asp Ala Ser Gln Lys Tyr Ile Ser
            260                 265                 270
Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
        275                 280                 285
Leu Arg Pro Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
    290                 295                 300
Leu Thr Phe Tyr Ser Gly Pro Asn Pro Ala Asp Val Thr Arg Gln Tyr
305                 310                 315                 320
Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Ser Thr Leu
                325                 330                 335
Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
            340                 345                 350
Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
        355                 360                 365
Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
    370                 375                 380
Gln Asn Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
385                 390                 395                 400
His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
                405                 410                 415
Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
            420                 425                 430
Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
        435                 440                 445
Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
    450                 455                 460
Pro Lys Ala Val Glu Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
465                 470                 475                 480
Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
                485                 490                 495
Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
            500                 505                 510
```

```
His Pro Pro Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
        515                 520                 525
Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
    530                 535                 540
Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Ser Thr Ser
545                 550                 555                 560
Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
                565                 570                 575
Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
            580                 585                 590
Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Ile Asp Gly Val
        595                 600                 605
Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
    610                 615                 620
Thr Tyr His Gly Leu Leu Glu Val Trp Ser His Glu Arg Arg Pro Phe
625                 630                 635                 640
Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
                645                 650                 655
Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
            660                 665                 670
Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
        675                 680                 685
Asp Thr Cys Gly Phe Thr Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
    690                 695                 700
Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
705                 710                 715                 720
Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
                725                 730                 735
Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
            740                 745                 750
Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
        755                 760                 765
Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
    770                 775                 780
Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Ile Pro Val Leu Glu
785                 790                 795                 800
Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
                805                 810                 815
Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
            820                 825                 830
Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
        835                 840                 845
Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
    850                 855                 860
Arg Gly Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865                 870                 875                 880
Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
                885                 890                 895
Tyr Pro Asn Ala Thr Leu Arg Val Gly Phe Thr Ala Ser Arg Ser Ser
            900                 905                 910
Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
        915                 920                 925
Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
    930                 935                 940
```

```
Asn Gly Lys Thr Val Ser Pro Gly Ser Ile Thr Tyr Asn Ser Thr Ser
945                 950                 955                 960
Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Asn Gly Gly Ala
                965                 970                 975
Trp Ala Glu Asn Trp Val Leu Glu Trp
            980                 985
```

<210> 261
<211> 866
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase GAQ36312.1

<400> 261

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

```
    290                 295                 300
Thr Asp Ile Asp Tyr Met Asp Lys Arg Arg Val Phe Thr Leu Asp Pro
305                 310                 315                 320
Gln Arg Phe Pro Leu Glu Lys Met Arg Glu Leu Val Thr Tyr Leu His
                325                 330                 335
Asn His Asp Gln His Tyr Ile Val Met Val Asp Pro Ala Val Ser Val
            340                 345                 350
Ser Asn Asn Ser Ala Tyr Leu Thr Gly Val Arg Asp Asn Val Phe Leu
        355                 360                 365
His Asn Gln Asn Gly Ser Leu Tyr Glu Gly Ala Val Trp Pro Gly Val
    370                 375                 380
Thr Val Phe Pro Asp Trp Phe Asn Glu Asp Thr Gln Asp Tyr Trp Thr
385                 390                 395                 400
Ala Gln Phe Gln Gln Phe Phe Asp Pro Lys Ser Gly Val Asp Ile Asp
                405                 410                 415
Ala Leu Trp Ile Asp Met Asn Glu Ala Ser Asn Phe Cys Pro Tyr Pro
            420                 425                 430
Cys Leu Asp Pro Ala Ala Phe Ala Ile Ser Asp Asp Leu Pro Pro Ala
        435                 440                 445
Ala Pro Pro Val Arg Pro Ser Ser Pro Ile Pro Leu Pro Gly Phe Pro
    450                 455                 460
Ala Asp Phe Gln Pro Ser Ser Lys Arg Ser Val Lys Arg Ala Gln Gly
465                 470                 475                 480
Asp Lys Gly Lys Lys Val Gly Leu Pro Asn Arg Asn Leu Thr Asp Pro
                485                 490                 495
Pro Tyr Thr Ile Arg Asn Ala Ala Gly Val Leu Ser Met Ser Thr Ile
            500                 505                 510
Glu Thr Asp Leu Ile His Ala Gly Glu Gly Tyr Ala Glu Tyr Asp Thr
        515                 520                 525
His Asn Leu Tyr Gly Thr Met Met Ser Ser Ala Ser Arg Thr Ala Met
    530                 535                 540
Gln Ala Arg Arg Pro Asp Val Arg Pro Leu Val Ile Thr Arg Ser Thr
545                 550                 555                 560
Phe Ala Gly Ala Gly Ala His Val Gly His Trp Leu Gly Asp Asn Leu
                565                 570                 575
Ser Asp Trp Val His Tyr Arg Ile Ser Ile Ala Gln Ile Leu Ser Phe
            580                 585                 590
Ala Ser Met Phe Gln Ile Pro Met Val Gly Ala Asp Val Cys Gly Phe
        595                 600                 605
Gly Ser Asn Thr Thr Glu Glu Leu Cys Gly Arg Trp Ala Ser Leu Gly
    610                 615                 620
Ala Phe Tyr Thr Phe Tyr Arg Asn His Asn Glu Leu Gly Asp Ile Pro
625                 630                 635                 640
Gln Glu Phe Tyr Arg Trp Pro Thr Val Ala Glu Ser Ala Arg Lys Ala
                645                 650                 655
Ile Asp Ile Arg Tyr Arg Leu Leu Asp Tyr Ile Tyr Thr Ala Leu His
            660                 665                 670
Arg Gln Ser Gln Thr Gly Glu Pro Phe Leu Gln Pro Gln Phe Tyr Leu
        675                 680                 685
Tyr Pro Glu Asp Ser Asn Thr Phe Ala Asn Asp Arg Gln Phe Phe Tyr
    690                 695                 700
Gly Asp Ala Leu Leu Val Ser Pro Val Leu Asn Glu Gly Ser Thr Ser
705                 710                 715                 720
Val Asp Ala Tyr Phe Pro Asp Asp Ile Phe Tyr Asp Trp Tyr Thr Gly
```

```
                725                 730                 735
Ala Val Val Arg Gly His Gly Glu Asn Ile Thr Leu Ser Asn Ile Asn
            740                 745                 750
Ile Thr His Ile Pro Leu His Ile Arg Gly Gly Asn Ile Ile Pro Val
        755                 760                 765
Arg Met Ser Ser Gly Met Thr Thr Thr Glu Val Arg Lys Gln Gly Phe
    770                 775                 780
Glu Leu Ile Ile Ala Pro Asp Leu Asp Gly Thr Ala Ser Gly Ser Leu
785                 790                 795                 800
Tyr Leu Asp Asp Gly Asp Ser Leu Asn Pro Ser Ser Val Thr Glu Leu
                805                 810                 815
Glu Phe Thr Tyr Ser Asn Gly Glu Leu His Val Gln Gly Thr Phe Gly
            820                 825                 830
Gln Lys Ala Val Pro Lys Val Glu Lys Cys Thr Leu Leu Gly Lys Ser
        835                 840                 845
Ala Arg Thr Phe Lys Gly Phe Ala Leu Asp Ala Pro Val Asn Leu Lys
    850                 855                 860
Leu Lys
865
```

<210> 262
<211> 2359
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase GAQ33831.1

<400> 262

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

```
Asp Gln Leu Gln Phe Asp Asp Ala Val Phe Pro Asn Gly Glu Asp Asp
        195                 200                 205
Val Ala Arg Leu Val Ser Lys Met Glu Asp Glu Tyr Gly Leu Leu Ser
    210                 215                 220
Leu Thr Asp Val Val Trp Asn His Thr Ala His Asn Ser Lys Trp Leu
225                 230                 235                 240
Glu Glu His Pro Glu Ala Gly Tyr Ser Val Glu Thr Ala Pro Trp Leu
                245                 250                 255
Glu Ala Ala Leu Glu Leu Asp Thr Ala Leu Leu Lys Phe Gly Gln Glu
            260                 265                 270
Leu Ser Thr Leu Gly Leu Pro Thr Glu Phe His Thr Val Asp Glu Leu
        275                 280                 285
Met Glu Val Met Asn Ala Met Arg Asp Lys Val Ile Ser Gly Ile Arg
    290                 295                 300
Leu Trp Glu Phe Tyr Ala Ile Asp Val Lys Ala Asp Thr Gln Arg Ile
305                 310                 315                 320
Leu Asp Gln Trp Lys Thr Ser Lys Asp Leu Asn Leu Thr Asp Lys Lys
                325                 330                 335
Trp Ala Gln Leu Asn Leu Ser Asp Tyr Lys Asn Trp Thr Leu Lys Gln
            340                 345                 350
Gln Ala Thr Phe Ile Arg Glu Tyr Ala Ile Pro Thr Ser Lys Gln Val
        355                 360                 365
Leu Gly Arg Phe Ser Arg Ala Val Asp Leu His Phe Gly Ala Ala Ile
    370                 375                 380
Leu Thr Ala Leu Phe Gly Pro His Asp Ser Pro Thr Ser Asp Thr Asn
385                 390                 395                 400
Thr Val Glu Glu Ser Leu Ser Lys Ile Leu Asp Glu Val Asn Leu Pro
                405                 410                 415
Phe Tyr Glu Glu Tyr Asp Gly Asp Val Ser Glu Ile Met Asn Gln Val
            420                 425                 430
Phe Asn Arg Ile Lys Tyr Leu Arg Ile Asp Asp His Gly Pro Lys Leu
        435                 440                 445
Gly Ala Val Thr Ala Gln Ser Pro Leu Ile Glu Thr Tyr Phe Thr Arg
    450                 455                 460
Leu Pro Leu Asn Asp Val Thr Lys Lys His Lys Lys Gly Ala Leu Ala
465                 470                 475                 480
Leu Val Asn Asn Gly Trp Ile Trp Asn Ala Asp Ala Leu Arg Asp Asn
                485                 490                 495
Ala Gly Pro Asp Ser Arg Ala Tyr Leu Arg Arg Glu Val Ile Val Trp
            500                 505                 510
Gly Asp Cys Val Lys Leu Arg Tyr Gly Ser Cys Arg Asp Asp Asn Pro
        515                 520                 525
Phe Leu Trp Asp Phe Met Thr Asp Tyr Thr Arg Leu Met Ala Lys Tyr
    530                 535                 540
Phe Ser Gly Phe Arg Ile Asp Asn Cys His Ser Thr Pro Leu Val Val
545                 550                 555                 560
Ala Glu Tyr Leu Leu Asp Glu Ala Arg Lys Val Arg Pro Asn Leu Thr
                565                 570                 575
Val Phe Ala Glu Leu Phe Thr Gly Ser Glu Glu Ala Asp Tyr Ile Phe
            580                 585                 590
Val Lys Arg Leu Gly Ile Asn Ala Leu Ile Arg Glu Ala Met Gln Ala
        595                 600                 605
Trp Ser Thr Gly Glu Leu Ser Arg Leu Val His Arg His Gly Gly Arg
    610                 615                 620
```

```
Pro Ile Gly Ser Phe Asp Leu Asp Leu Pro Ser Ser Gly Ser Ser His
625                 630                 635                 640
Ala Ile Ala Ser Ser Gly Leu Asp Ser Gly Lys Glu Lys Val Ala His
                645                 650                 655
Ile Arg Pro Thr Pro Val Gln Ala Leu Phe Met Asp Cys Thr His Asp
            660                 665                 670
Asn Glu Met Pro Ala Gln Lys Arg Thr Ala Lys Asp Thr Leu Pro Asn
        675                 680                 685
Gly Ala Leu Val Ala Met Cys Ala Ser Ala Ile Gly Ser Val Ile Gly
    690                 695                 700
Tyr Asp Glu Val Tyr Pro Arg Leu Val Asp Leu Val His Glu His Arg
705                 710                 715                 720
Leu Tyr Phe Ser Glu Phe Ser Glu Ala Pro Glu Thr Gly Leu Asn Ser
                725                 730                 735
Leu Glu Gly Gly Ile Gly Gly Ile Lys Lys Leu Leu Asn Asp Leu His
            740                 745                 750
Thr Arg Met Gly Val Glu Glu Tyr Asp Glu Thr His Ile His His Asp
        755                 760                 765
Gly Glu Tyr Ile Thr Val His Arg Val His Pro Arg Thr Arg Lys Gly
    770                 775                 780
Val Phe Leu Ile Ala His Thr Ala Phe Ser Gly Gln Asp Gly Lys Ser
785                 790                 795                 800
Val Leu Ala Pro Thr His Leu Val Gly Thr His Val Lys His Ile Gly
                805                 810                 815
Thr Trp Leu Leu Glu Val Asp Ala Ser Gln Thr Thr Lys Glu Arg Ile
            820                 825                 830
Gln Thr Asp Lys Ser Tyr Leu Arg Gly Leu Pro Ser Gln Val Lys Thr
        835                 840                 845
Phe Glu Gly Thr Lys Ile Glu Glu Ser Gly Lys Asp Thr Ile Ile Ser
    850                 855                 860
Val Leu Asp Ser Phe Val Ala Gly Ser Ile Ala Leu Phe Glu Thr Ser
865                 870                 875                 880
Met Pro Ser Val Glu His Ala Ser Gly Leu Asp Asn Tyr Ile Thr Glu
                885                 890                 895
Gly Val Asp His Ala Phe Ser Asp Leu Ser Leu Val Asp Leu Asn Phe
            900                 905                 910
Ala Leu Tyr Arg Cys Glu Ala Glu Glu Arg Asp Ser Ser Lys Gly Gln
        915                 920                 925
Asp Gly Val Tyr Asp Ile Pro Gly His Gly Pro Leu Val Tyr Ala Gly
    930                 935                 940
Leu Gln Gly Trp Trp Ser Val Leu Glu Asn Ile Ile Lys Tyr Asn Glu
945                 950                 955                 960
Leu Gly His Pro Leu Cys Asp His Leu Arg Asn Gly Gln Trp Ala Leu
                965                 970                 975
Asp Tyr Ile Val Ala Arg Leu Glu Lys Leu Gly His Thr Asp Glu His
            980                 985                 990
Thr Ala Leu Gly Arg Pro Ala Ala Trp Leu Gln Glu Lys Phe Gln Ala
        995                 1000                1005
Val Arg Gln Leu Pro Ser Phe Leu Leu Pro Arg Tyr Phe Ala Ile Ile
    1010                1015                1020
Val Gln Val Ala Tyr Asn Ala Ala Trp Lys Arg Gly Ile Gln Leu Leu
1025                1030                1035                1040
Gly Pro His Ile Gln Asn Gly Gln Glu Phe Ile His Gln Leu Gly Met
                1045                1050                1055
```

```
Val Ser Val Gln Gln Thr Gly Tyr Val Asn Ser Ala Ser Leu Trp Pro
            1060                1065                1070
Thr Lys Lys Val Pro Ser Leu Ala Ala Gly Leu Pro His Phe Ala Val
        1075                1080                1085
Asp Trp Ala Arg Cys Trp Gly Arg Asp Val Phe Ile Ser Leu Arg Gly
    1090                1095                1100
Leu Leu Leu Cys Thr Ser Arg Phe Glu Asp Ala Lys Glu His Ile Thr
1105                1110                1115                1120
Ala Phe Ala Ser Val Leu Lys His Gly Met Ile Pro Asn Leu Leu Ser
                1125                1130                1135
Ser Gly Lys Leu Pro Arg Tyr Asn Ser Arg Asp Ser Val Trp Phe Phe
            1140                1145                1150
Leu Gln Ser Ile Gln Asp Tyr Thr Lys Met Ala Pro Asp Gly Leu Arg
        1155                1160                1165
Leu Leu Asp His Asn Val Pro Arg Arg Phe Leu Pro Tyr Asp Asp Val
    1170                1175                1180
Trp Phe Pro Tyr Asp Asp Pro Arg Ala Tyr Ser Gln His Ser Thr Ile
1185                1190                1195                1200
Ser Glu Ile Ile Gln Glu Val Leu Gln Arg His Ala Gln Gly Leu Ser
                1205                1210                1215
Phe Arg Glu Tyr Asn Ala Gly Pro Asp Leu Asp Met Gln Met Thr Gln
            1220                1225                1230
Glu Gly Phe Gln Ile Asp Val Lys Val Asp Trp Glu Thr Gly Leu Ile
        1235                1240                1245
Phe Gly Gly Ser Gln Tyr Asn Cys Gly Thr Trp Gln Asp Lys Met Gly
    1250                1255                1260
Glu Ser Ala Lys Ala Gly Asn Lys Gly Val Pro Gly Thr Pro Arg Asp
1265                1270                1275                1280
Gly Ala Ala Ile Glu Ile Thr Gly Leu Val Tyr Ser Ala Leu Thr Trp
                1285                1290                1295
Val Ala Glu Leu His Glu Arg Gly Leu Tyr Lys His Asp Gly Val Asp
            1300                1305                1310
Ile Gly Asp Gly Lys Ser Ile Ser Phe Lys Glu Trp Ala Ser Arg Ile
        1315                1320                1325
Gln Ala Asn Phe Glu Arg Cys Tyr Tyr Val Pro Leu Gln Pro Lys Asp
    1330                1335                1340
Asp Gly Gln Tyr Asp Ile Asp Ala Asn Ile Ile Asn Arg Arg Gly Ile
1345                1350                1355                1360
Tyr Lys Asp Leu Tyr Arg Ser Gly Lys Pro Tyr Glu Asp Tyr Gln Leu
                1365                1370                1375
Arg Ser Asn Phe Pro Ile Ala Met Thr Val Ala Pro Asp Leu Phe Thr
            1380                1385                1390
Ser Ser Lys Ala Leu Ala Ala Leu Ala Leu Ala Asp Glu Val Leu Val
        1395                1400                1405
Gly Pro Val Gly Met Ala Thr Leu Asp Pro Ser Asp Leu Asn Tyr Arg
    1410                1415                1420
Pro Asn Tyr Asn Asn Ser Glu Asp Ser Thr Asp Phe Ala Thr Ala Lys
1425                1430                1435                1440
Gly Arg Asn Tyr His Gln Gly Pro Glu Trp Val Trp Gln Arg Gly Tyr
                1445                1450                1455
Phe Leu Arg Ala Phe Leu His Phe Asp Leu Ala Arg Arg Thr Thr Pro
            1460                1465                1470
Ala Glu Arg Thr Glu Thr Tyr Gln Gln Ile Thr Arg Arg Leu Glu Gly
        1475                1480                1485
```

```
Cys Lys Arg Ala Leu Arg Glu Ser Pro Trp Lys Gly Leu Thr Glu Leu
    1490                1495                1500
Thr Asn Lys Asn Gly Ala His Cys Ala Asp Ser Asn Ile Cys Phe Trp
1505                1510                1515                1520
Ser Val Met Ser Leu Thr Glu Ser Ala Ala Ala Ala Met Leu Thr Ala
                1525                1530                1535
Ala Val Val Val Asp Ser Pro Ile Asp Val His Glu Pro Arg Trp Asp
            1540                1545                1550
Asp Gln Thr Arg Gly Arg Asp Leu Tyr Thr Gln Leu Val Ile Ser Leu
        1555                1560                1565
Leu Val Gly Leu Ser Ala Phe Phe Ser Phe Cys Val Leu Arg Pro Lys
    1570                1575                1580
Trp Thr Glu Leu Tyr Ala Ala Arg Arg Arg Gln Arg Cys Ala Ala Ser
1585                1590                1595                1600
Tyr Leu Pro Glu Leu Pro Asp Ser Phe Phe Gly Trp Ile Pro Val Leu
                1605                1610                1615
Tyr Arg Ile Thr Asp Glu Gln Val Leu Glu Ser Ala Gly Leu Asp Ala
            1620                1625                1630
Phe Val Phe Leu Thr Phe Leu Lys Phe Ala Ile Arg Phe Leu Ser Ala
        1635                1640                1645
Ile Phe Phe Phe Ala Leu Val Ile Ile Leu Pro Thr His Tyr Lys Asn
    1650                1655                1660
Thr Gly Lys Ser Gly Val Pro Gly Trp Asp Asp Asp Asp Asp Glu Thr
1665                1670                1675                1680
Phe Asp Gly Asp Lys Asp Lys Lys Lys Ile Ile Ser Asp Pro Asn Tyr
                1685                1690                1695
Leu Trp Met Tyr Val Ile Phe Thr Tyr Ile Phe Thr Gly Leu Ala Val
            1700                1705                1710
Tyr Met Leu Ile Gln Glu Thr Asn Lys Val Ile Arg Thr Arg Gln Lys
        1715                1720                1725
Tyr Leu Gly Ser Gln Thr Ser Thr Thr Asp Arg Thr Ile Arg Leu Ser
    1730                1735                1740
Gly Ile Pro Pro Asp Leu Gly Thr Glu Glu Lys Ile Lys Asp Phe Met
1745                1750                1755                1760
Glu Gly Leu Lys Val Gly Lys Val Glu Ser Val Thr Leu Cys Arg Asp
                1765                1770                1775
Trp Arg Glu Leu Asp His Leu Ile Asp Glu Arg Leu Lys Leu Leu Arg
            1780                1785                1790
Asn Leu Glu Arg Ala Trp Thr Arg His Leu Gly Tyr Lys Arg Val Lys
        1795                1800                1805
Ala Ser Pro Asn Ala Leu Thr Leu Met His Gln Gln Pro Arg Gly Ser
    1810                1815                1820
Ser Ile Val Ser Asp Gly Glu Ser Glu Arg Ile Gln Leu Leu Ser Glu
1825                1830                1835                1840
Gly Gly Arg Asp His Val Thr Asp Tyr Ala His Lys Arg Pro Thr Val
                1845                1850                1855
Arg Ile Trp Tyr Gly Pro Phe Lys Leu Arg Tyr Lys Asn Ile Asp Ala
            1860                1865                1870
Ile Asp Tyr Tyr Glu Glu Lys Leu Arg Arg Leu Asp Glu Lys Ile Gln
        1875                1880                1885
Val Ala Arg Gln Lys Glu Tyr Pro Pro Thr Glu Val Ala Phe Val Thr
    1890                1895                1900
Met Glu Ser Ile Ala Ala Ser Gln Met Val Val Gln Ala Ile Leu Asp
1905                1910                1915                1920
```

```
Pro His Pro Met Gln Leu Leu Ala Arg Leu Ala Pro Ala Pro Ala Asp
                1925                1930                1935
Val Val Trp Lys Asn Thr Tyr Leu Pro Arg Ser Arg Arg Met Met Gln
            1940                1945                1950
Ser Trp Phe Ile Thr Val Val Ile Gly Phe Leu Thr Val Phe Trp Ser
        1955                1960                1965
Val Leu Leu Ile Pro Val Ala Tyr Leu Leu Glu Tyr Glu Thr Leu His
    1970                1975                1980
Lys Val Phe Pro Gln Leu Ala Asp Ala Leu Ala Arg Asn Pro Leu Ala
1985                1990                1995                2000
Lys Ser Leu Val Gln Thr Gly Leu Pro Thr Leu Val Leu Ser Leu Leu
                2005                2010                2015
Thr Val Ala Val Pro Tyr Leu Tyr Asn Trp Leu Ser Asn Gln Gln Gly
            2020                2025                2030
Met Met Ser Arg Gly Asp Ile Glu Leu Ser Val Ile Ser Lys Thr Phe
        2035                2040                2045
Phe Phe Ser Phe Phe Asn Leu Phe Leu Val Phe Thr Val Phe Gly Thr
    2050                2055                2060
Ala Thr Thr Phe Tyr Gly Phe Trp Glu Asn Leu Arg Asp Ala Phe Lys
2065                2070                2075                2080
Asp Ala Thr Thr Ile Ala Phe Ala Leu Ala Lys Thr Leu Glu Asn Phe
                2085                2090                2095
Ala Pro Phe Tyr Ile Asn Phe Leu Cys Leu Gln Gly Ile Gly Leu Phe
            2100                2105                2110
Pro Phe Arg Leu Leu Glu Phe Gly Ser Val Ala Met Tyr Pro Ile Asn
        2115                2120                2125
Phe Leu Ala Ala Lys Thr Pro Arg Asp Tyr Ala Glu Leu Ser Thr Pro
    2130                2135                2140
Pro Thr Phe Ser Tyr Gly Tyr Ser Ile Pro Gln Thr Val Leu Ser Leu
2145                2150                2155                2160
Ile Ile Cys Val Val Tyr Ser Val Phe Pro Ser Ser Trp Leu Ile Cys
                2165                2170                2175
Leu Phe Gly Leu Ile Tyr Phe Thr Ile Gly Lys Phe Ile Tyr Lys Tyr
            2180                2185                2190
Gln Leu Leu Tyr Ala Met Asp His Gln Gln His Ser Thr Gly Arg Ala
        2195                2200                2205
Trp Pro Met Ile Cys Ser Arg Ile Leu Met Gly Leu Ile Val Phe Gln
    2210                2215                2220
Leu Ala Met Ile Gly Val Leu Ala Leu Arg Arg Ala Ile Thr Arg Ser
2225                2230                2235                2240
Leu Leu Ile Val Pro Leu Leu Met Ala Thr Val Trp Phe Ser Tyr Phe
                2245                2250                2255
Phe Ala Arg Thr Tyr Glu Pro Leu Met Lys Phe Ile Ala Leu Lys Ser
            2260                2265                2270
Ile Asp Arg Glu Arg Pro Gly Gly Gly Asp Ile Ser Pro Ser Pro Ser
        2275                2280                2285
Ser Thr Phe Ser Pro Pro Ser Gly Leu Asp Arg Asp Ser Phe Pro Ile
    2290                2295                2300
Arg Ile Gly Gly Gln Glu Leu Gly Leu Arg Leu Arg Lys Tyr Val Asn
2305                2310                2315                2320
Pro Ser Leu Ile Leu Pro Leu His Asp Ala Trp Leu Pro Gly Arg Thr
                2325                2330                2335
Met Val Pro Glu Leu Gln Gly Glu Leu Glu His Arg Asn Ser Glu Asn
            2340                2345                2350
```

Asn Ala Ala Asp Glu Ser Val
2355

<210> 263
<211> 655
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase GAQ33901.1

<400> 263
Met Trp Ser Ser Trp Leu Leu Ser Ala Leu Leu Ala Thr Glu Ala Leu
1 5 10 15
Ala Val Pro Tyr Glu Glu Tyr Ile Leu Ala Pro Ser Ser Arg Asp Leu
20 25 30
Ala Pro Ala Ser Val Arg Gln Val Asn Gly Ser Val Thr Asn Ala Ala
35 40 45
Ala Leu Thr Gly Ala Gly Gly Gln Ala Thr Phe Asn Gly Val Ser Ser
50 55 60
Val Thr Tyr Asp Phe Gly Ile Asn Val Ala Gly Ile Val Ser Val Asp
65 70 75 80
Val Ala Ser Ala Ser Ser Glu Ser Ala Phe Ile Gly Val Thr Phe Thr
85 90 95
Glu Ser Ser Met Trp Ile Ser Asn Glu Ala Cys Asp Ala Thr Gln Asp
100 105 110
Ala Gly Leu Asp Thr Pro Leu Trp Phe Ala Val Gly Gln Gly Ala Gly
115 120 125
Val Tyr Ser Val Gly Lys Lys Tyr Thr Arg Gly Ala Phe Arg Tyr Met
130 135 140
Thr Val Val Ser Asn Thr Thr Ala Thr Val Ser Leu Asn Ser Val Lys
145 150 155 160
Ile Asn Tyr Thr Ala Ser Pro Ile Gln Asp Leu Arg Ala Tyr Thr Gly
165 170 175
Tyr Phe His Ser Ser Asp Glu Leu Leu Asn Arg Ile Trp Tyr Ala Gly
180 185 190
Ala Tyr Thr Leu Gln Leu Cys Ser Ile Asp Pro Thr Thr Gly Asp Ala
195 200 205
Leu Val Gly Leu Gly Val Ile Thr Ser Ser Glu Thr Ile Thr Leu Pro
210 215 220
Gln Thr Asp Lys Trp Trp Thr Asn Tyr Thr Ile Thr Asn Gly Ser Ser
225 230 235 240
Thr Leu Thr Asp Gly Ala Lys Arg Asp Arg Leu Val Trp Pro Gly Asp
245 250 255
Met Ser Ile Ala Leu Glu Ser Val Ala Val Ser Thr Glu Asp Leu Tyr
260 265 270
Ser Val Arg Thr Ala Leu Glu Ser Leu Tyr Ala Leu Gln Lys Ala Asp
275 280 285
Gly Gln Leu Pro Tyr Ala Gly Lys Pro Phe Tyr Asp Thr Val Ser Phe
290 295 300
Thr Tyr His Leu His Ser Leu Val Gly Ala Ala Ser Tyr Tyr Gln Tyr
305 310 315 320
Thr Gly Asp Arg Ala Trp Leu Thr Arg Tyr Trp Gly Gln Tyr Lys Lys

```
                325                 330                 335
Gly Val Gln Trp Ala Leu Ser Ser Val Asp Ser Thr Gly Leu Ala Asn
            340                 345                 350
Ile Thr Ala Ser Ala Asp Trp Leu Arg Phe Gly Met Gly Ala His Asn
        355                 360                 365
Ile Glu Ala Asn Ala Ile Leu Tyr Tyr Val Leu Asn Asp Ala Ile Ser
    370                 375                 380
Leu Ala Gln Ser Leu Asn Asp Asn Ala Pro Ile Arg Asn Trp Thr Ala
385                 390                 395                 400
Thr Ala Ala Arg Ile Lys Thr Val Ala Asn Glu Leu Leu Trp Asp Asp
                405                 410                 415
Lys Asn Gly Leu Tyr Thr Asp Asn Glu Thr Thr Thr Leu His Pro Gln
            420                 425                 430
Asp Gly Asn Ser Trp Ala Val Lys Ala Asn Leu Thr Leu Ser Ala Asn
        435                 440                 445
Gln Ser Ala Ile Ile Ser Glu Ser Leu Ala Ala Arg Trp Gly Pro Tyr
    450                 455                 460
Gly Ala Pro Ala Pro Glu Ala Gly Ala Thr Val Ser Pro Phe Ile Gly
465                 470                 475                 480
Gly Phe Glu Leu Gln Ala His Tyr Gln Ala Gly Gln Pro Asp Arg Ala
                485                 490                 495
Leu Asp Leu Leu Arg Leu Gln Trp Gly Phe Met Leu Asp Asp Pro Arg
            500                 505                 510
Met Thr Asn Ser Thr Phe Ile Glu Gly Tyr Ser Thr Asp Gly Ser Leu
        515                 520                 525
Val Tyr Ala Pro Tyr Thr Asn Arg Pro Arg Val Ser His Ala His Gly
    530                 535                 540
Trp Ser Thr Gly Pro Thr Ser Ala Leu Thr Ile Tyr Thr Ala Gly Leu
545                 550                 555                 560
Arg Val Thr Gly Pro Ala Gly Ala Thr Trp Leu Tyr Lys Pro Gln Pro
                565                 570                 575
Gly Asn Leu Thr Gln Val Glu Ala Gly Phe Ser Thr Arg Leu Gly Ser
            580                 585                 590
Phe Ala Ser Ser Phe Ser Arg Ser Gly Gly Arg Tyr Gln Glu Leu Ser
        595                 600                 605
Phe Thr Thr Pro Asn Gly Thr Thr Gly Ser Val Glu Leu Gly Asp Val
    610                 615                 620
Ser Gly Gln Leu Val Ser Glu Gly Gly Val Lys Val Gln Leu Val Gly
625                 630                 635                 640
Gly Lys Ala Ser Gly Leu Gln Gly Gly Lys Trp Arg Leu Asn Val
                645                 650                 655
```

<210> 264
<211> 676
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase EHA19108.1

<400> 264

```
Met Arg Trp His Lys Leu Leu Pro Gly Val Leu Ala Leu Leu Pro Leu
 1               5                  10                  15
```

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

Leu Leu Phe Gly Val Val Asp Ala Asp Arg Ala Ala Ser Ile Ser Glu
    450                 455                 460
Arg Leu Thr Asp Asn Trp Thr Pro Ile Gly Ala Val Ala Pro Glu Leu
465                 470                 475                 480
Pro Glu Asn Ile Ser Pro Phe Ile Ser Ser Phe Glu Ile Gln Gly His
                485                 490                 495
Leu Thr Val Gly Gln Pro Gln Arg Ala Leu Glu Leu Ile Arg Arg Ser
            500                 505                 510
Trp Gly Trp Tyr Tyr Asn Asn Ala Asn Gly Thr Gln Ser Thr Val Ile
        515                 520                 525
Glu Gly Tyr Leu Gln Asn Gly Thr Phe Gly Tyr Arg Ser Asp Arg Gly
    530                 535                 540
Tyr Tyr Tyr Asp Thr Ala Tyr Val Ser His Ser His Gly Trp Ser Ser
545                 550                 555                 560
Gly Pro Thr Ser Ala Leu Thr Asn Tyr Ile Val Gly Ile Ser Val Thr
                565                 570                 575
Ser Pro Leu Gly Ala Thr Trp Arg Ile Ala Pro Gln Phe Val Asp Leu
            580                 585                 590
Gln Ser Ala Glu Gly Gly Phe Thr Thr Ser Leu Gly Lys Phe Gln Ala
        595                 600                 605
Gly Trp Ser Lys Thr Asp Lys Gly Tyr Thr Leu Asp Phe Thr Val Pro
    610                 615                 620
His Gly Thr Gln Gly Asn Leu Thr Leu Pro Phe Val Ser Ala Ala Lys
625                 630                 635                 640
Pro Ser Ile Lys Ile Asp Gly Thr Glu Ile Ser Arg Gly Val Gln Tyr
                645                 650                 655
Ala Asn Ser Thr Ala Thr Val Thr Val Ser Gly Gly Gly Thr Tyr Lys
            660                 665                 670
Val Glu Val Gln
        675


<210> 265
<211> 847
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase EHA19157.1

<400> 265
Met Pro Gln Lys Glu Phe Val Pro Lys Thr Tyr Gln Glu Ser Ser Thr
 1               5                  10                  15
Gly Ala Gln Ser Ser Ser Ser Val His Leu Arg Ser Ser Pro Glu Glu
            20                  25                  30
Arg Ser Phe Asp Phe Ser Phe Glu Pro Ile Arg Glu Asn Leu Phe Arg
        35                  40                  45
Val Thr Phe Ser Ser Gln Asp His Pro Leu Pro Pro Tyr Pro Ser Val
    50                  55                  60
Thr Lys Pro Ala Thr Ser Leu Asp Gly Val His Val Ser Ala Thr Gly
65                  70                  75                  80
Gly Ser Asn Gln Lys Thr Ile Glu Val Gly Asp Val Thr Ala Ser Val
                85                  90                  95
Glu Trp Ser Asn Thr Pro Val Val Ser Leu Ser Trp Lys Gly Thr Glu

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            100                 105                 110
Lys Pro Leu Tyr Arg Asp Leu Pro Leu Arg Ser Tyr Val Ala Asp Ser
        115                 120                 125
Thr Gly Ile Ala His Tyr Thr Glu His Asp Arg Asp Cys Leu His Val
    130                 135                 140
Gly Leu Gly Glu Lys Arg Ala Pro Met Asp Leu Thr Gly Arg His Phe
145                 150                 155                 160
Gln Leu Ser Ala Thr Asp Ser Phe Gly Tyr Asp Val Tyr Asn Thr Asp
                165                 170                 175
Pro Leu Tyr Lys His Ile Pro Leu Leu Ile Lys Ala Ser Pro Asp Gly
            180                 185                 190
Cys Val Ala Ile Phe Ser Thr Thr His Gly Arg Gly Thr Trp Ser Val
        195                 200                 205
Gly Ser Glu Val Asp Gly Leu Trp Gly His Phe Lys Val Tyr Arg Gln
    210                 215                 220
Asp Tyr Gly Gly Leu Glu Gln Tyr Leu Ile Val Gly Lys Thr Leu Lys
225                 230                 235                 240
Asp Val Val Arg Ser Tyr Ala Glu Leu Val Gly Leu Pro Ile Leu Val
                245                 250                 255
Pro Arg Trp Ala Tyr Gly Tyr Ile Ser Gly Gly Tyr Lys Tyr Thr Met
            260                 265                 270
Leu Asp Asp Pro Pro Ala His Glu Ala Leu Met Glu Phe Ala Asp Lys
        275                 280                 285
Leu Glu Glu His Gly Ile Pro Cys Ser Ala His Gln Met Ser Ser Gly
    290                 295                 300
Tyr Ser Ile Ala Glu Thr Glu Pro Lys Val Arg Asn Val Phe Thr Trp
305                 310                 315                 320
Asn Lys Tyr Arg Phe Pro Asn Pro Glu Glu Trp Ile Ala Lys Tyr His
                325                 330                 335
Gly Arg Gly Ile Arg Leu Leu Ser Asn Ile Lys Pro Phe Leu Leu Ala
            340                 345                 350
Ser His Pro Asp Phe Gln Lys Leu Ile Asp Gly Asn Gly Phe Phe Lys
        355                 360                 365
Asp Pro Glu Ser Ser Lys Pro Gly Tyr Met Arg Leu Trp Ser Ala Gly
    370                 375                 380
Gly Ala Thr Gly Gly Asp Gly Cys His Ile Asp Phe Ser Ser Ala Val
385                 390                 395                 400
Ala Phe Lys Trp Trp Tyr Asp Gly Val Gln Ser Leu Lys Arg Ala Gly
                405                 410                 415
Ile Asp Ala Met Trp Asn Asp Asn Asn Glu Tyr Thr Leu Pro Asp Asp
            420                 425                 430
Asp Trp Lys Leu Ala Leu Asp Glu Pro Thr Val Ser Asp Ala Val Lys
        435                 440                 445
Lys Gly Val Glu Asn Ser Val Gly Gln Trp Gly Arg Ala Met His Thr
    450                 455                 460
Glu Leu Met Gly Lys Ala Ser His Asp Ala Leu Leu Asn Ile Glu Pro
465                 470                 475                 480
Asn His Arg Pro Phe Val Leu Thr Arg Ser Ala Thr Ala Gly Thr Met
                485                 490                 495
Arg Tyr Ala Ala Ser Thr Trp Ser Gly Asp Asn Val Thr Ser Trp Glu
            500                 505                 510
Gly Met Lys Gly Ala Asn Ala Leu Ser Leu Ser Ala Gly Ile Ser Leu
        515                 520                 525
Leu Gln Cys Cys Gly His Asp Ile Gly Gly Phe Glu Gly Pro Gln Pro
```

```
    530                 535                 540
Ser Pro Glu Leu Leu Leu Arg Trp Ile Gln Leu Gly Ile His Ser Pro
545                 550                 555                 560
Arg Phe Ala Ile Asn Cys Phe Lys Thr Ser Pro Gly Asn Ser Ser Val
                565                 570                 575
Gly Asp Val Ile Glu Pro Trp Met Tyr Pro Glu Ile Thr Pro Leu Val
            580                 585                 590
Arg Asp Thr Ile Lys Arg Arg Tyr Glu Ile Leu Pro Tyr Ile Tyr Ser
        595                 600                 605
Leu Gly Leu Glu Ser His Leu Thr Ala Ser Pro Pro Gln Arg Trp Val
    610                 615                 620
Gly Trp Gly Tyr Glu Ser Asp Pro Glu Val Trp Thr Lys Ala Leu Lys
625                 630                 635                 640
Ser Gly Asp Glu Gln Phe Trp Phe Gly Asp Thr Ile Met Val Gly Gly
                645                 650                 655
Val Tyr Glu Pro Gly Val Ser Val Ala Lys Leu Tyr Leu Pro Arg Lys
            660                 665                 670
Ala Asn Asp Gln Phe Asp Phe Gly Tyr Val Asn Met Asn Glu Pro Tyr
        675                 680                 685
Asn Tyr Leu Ala Ser Gly Gln Trp Val Glu Val Pro Ser Glu Trp Arg
    690                 695                 700
Lys Ser Ile Pro Leu Leu Ala Arg Ile Gly Gly Ala Ile Pro Val Gly
705                 710                 715                 720
Lys Pro Val His Thr Arg Val Pro Gly Asp Asp Thr Pro Ala Ser Val
                725                 730                 735
Ala Val Lys Glu Val Asp Asp Tyr Arg Gly Val Glu Ile Phe Pro Pro
            740                 745                 750
Leu Gly Ser Ser His Gly Gln Val Phe Ser Thr Thr Trp Phe Glu Asp
        755                 760                 765
Asp Gly Ile Ser Leu Glu Ala Arg Ile Ser Glu Tyr Thr Val Thr Tyr
    770                 775                 780
Ser Ser Thr Glu Glu Lys Val Ile Val Gly Phe Ser Arg Asp Glu Lys
785                 790                 795                 800
Ser Gly Phe Val Pro Ala Trp Thr Asp Leu Asp Ile Ile Leu His Asn
                805                 810                 815
Gly Asp Glu Arg Arg Val Val Ser Asp Ile Gly Lys Thr Val Glu Tyr
            820                 825                 830
Lys Gly Lys Gly Ser Arg Gly Arg Val Val Tyr Thr Leu Lys Asn
        835                 840                 845
```

<210> 266
<211> 593
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase EHA19519.1

<400> 266

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

```
    450                 455                 460
Thr Thr Ala Thr Ser Ser Ser Thr Ala Thr Ser Lys Ser Ala Ser Thr
465                 470                 475                 480
Ser Ser Thr Ser Thr Ala Cys Thr Ala Thr Ser Thr Ser Leu Ala Val
                485                 490                 495
Thr Phe Glu Glu Leu Val Thr Thr Thr Tyr Gly Glu Glu Ile Tyr Leu
            500                 505                 510
Ser Gly Ser Ile Ser Gln Leu Gly Asp Trp Asp Thr Ser Asp Ala Val
        515                 520                 525
Lys Met Ser Ala Asp Asp Tyr Thr Ser Ser Asn Pro Glu Trp Ser Val
    530                 535                 540
Thr Val Thr Leu Pro Val Gly Thr Thr Phe Glu Tyr Lys Phe Ile Lys
545                 550                 555                 560
Val Glu Ser Asp Gly Thr Val Thr Trp Glu Ser Asp Pro Asn Arg Glu
                565                 570                 575
Tyr Thr Val Pro Glu Cys Gly Ser Gly Glu Thr Val Val Asp Thr Trp
            580                 585                 590
Arg
```

<210> 267
<211> 985
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase EHA20839.1

<400> 267

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

```
Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
        195                 200                 205
Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
    210                 215                 220
Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
225                 230                 235                 240
Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
                245                 250                 255
Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
            260                 265                 270
Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
        275                 280                 285
Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
    290                 295                 300
Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
305                 310                 315                 320
Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
                325                 330                 335
Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
            340                 345                 350
Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
        355                 360                 365
Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
    370                 375                 380
Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
385                 390                 395                 400
His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
                405                 410                 415
Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
            420                 425                 430
Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
        435                 440                 445
Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
    450                 455                 460
Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
465                 470                 475                 480
Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
                485                 490                 495
Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
            500                 505                 510
His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
        515                 520                 525
Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
    530                 535                 540
Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
545                 550                 555                 560
Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
                565                 570                 575
Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
            580                 585                 590
Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
        595                 600                 605
Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
    610                 615                 620
```

```
Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
625                 630                 635                 640
Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
                645                 650                 655
Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
            660                 665                 670
Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
        675                 680                 685
Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
    690                 695                 700
Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
705                 710                 715                 720
Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
                725                 730                 735
Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
            740                 745                 750
Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
        755                 760                 765
Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
    770                 775                 780
Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
785                 790                 795                 800
Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
                805                 810                 815
Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
            820                 825                 830
Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
        835                 840                 845
Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
    850                 855                 860
Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865                 870                 875                 880
Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
                885                 890                 895
Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
            900                 905                 910
Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
        915                 920                 925
Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
    930                 935                 940
Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945                 950                 955                 960
Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
                965                 970                 975
Trp Ala Glu Asn Trp Val Leu Glu Trp
            980                 985
```

<210> 268
<211> 640
<212> PRT
<213> Artificial Sequence

<220>

<223> Transgucosidase EHA21384.1

<400> 268
Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
 1               5                  10                  15
Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
            20                  25                  30
Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
        35                  40                  45
Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
    50                  55                  60
Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
65                  70                  75                  80
Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
                85                  90                  95
Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
            100                 105                 110
Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
        115                 120                 125
Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp
    130                 135                 140
Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile
145                 150                 155                 160
Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr
                165                 170                 175
Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln
            180                 185                 190
Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser
        195                 200                 205
Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser
    210                 215                 220
Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln
225                 230                 235                 240
Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe
                245                 250                 255
Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr
            260                 265                 270
Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp
        275                 280                 285
Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu
    290                 295                 300
Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
305                 310                 315                 320
Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
                325                 330                 335
Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
            340                 345                 350
Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
        355                 360                 365
Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr
    370                 375                 380
Gly Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala
385                 390                 395                 400
Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala

```
                405                 410                 415
Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu
            420                 425                 430
Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr
        435                 440                 445
Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr
    450                 455                 460
Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly
465                 470                 475                 480
Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr
                485                 490                 495
Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr
            500                 505                 510
Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser Thr
        515                 520                 525
Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp
    530                 535                 540
Leu Thr Ala Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser
545                 550                 555                 560
Ile Ser Gln Leu Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser
                565                 570                 575
Ala Asp Lys Tyr Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr
            580                 585                 590
Leu Pro Ala Gly Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser
        595                 600                 605
Asp Asp Ser Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val
    610                 615                 620
Pro Gln Ala Cys Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
625                 630                 635                 640


<210> 269
<211> 587
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase EHA23512.1

<400> 269
Met Ala Lys Ser Ala Ser Gln Ile His Arg Ala Trp Trp Lys Glu Cys
 1               5                  10                  15
Ser Val Tyr Gln Ile Trp Pro Ala Ser Tyr Lys Asp Ser Asn Asp Asp
            20                  25                  30
Gly Ile Gly Asp Ile Pro Gly Ile Ile Ser Lys Leu Asp Tyr Ile Lys
        35                  40                  45
Asn Ile Gly Val Asp Ile Val Trp Leu Cys Pro Ser Tyr Lys Ser Pro
    50                  55                  60
Gln Val Asp Met Gly Tyr Asp Ile Ala Asp Tyr Tyr Ser Ile Ala Asp
65                  70                  75                  80
Glu Tyr Gly Thr Val Ala Asp Val Glu Lys Leu Ile Gln Gly Cys His
                85                  90                  95
Glu Arg Gly Met Lys Leu Leu Met Asp Leu Val Val Asn His Thr Ser
            100                 105                 110
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Asp Gln Asn Glu Trp Phe Lys Gln Ser Arg Ser Ser Lys Asp Asn Glu
        115                 120                 125
Tyr Arg Asn Trp Tyr Val Trp Lys Pro Ala Arg Tyr Asp Glu Gln Gly
    130                 135                 140
Asn Arg His Pro Pro Asn Asn Trp Val Ser His Phe Gln Gly Ser Ala
145                 150                 155                 160
Trp Glu Trp Asp Glu His Thr Gly Glu Tyr Tyr Leu His Leu Tyr Ala
                165                 170                 175
Thr Glu Gln Pro Asp Leu Asn Trp Glu His Pro Pro Val Arg Lys Ala
            180                 185                 190
Val His Asp Ile Met Arg Phe Trp Leu Asp Lys Gly Ala Asp Gly Phe
        195                 200                 205
Arg Met Asp Val Ile Asn Phe Ile Ser Lys Asp Gln Arg Phe Pro Asp
    210                 215                 220
Ala Pro Val Lys Asp Pro Arg Thr Pro Trp Gln Trp Gly Asp Lys Tyr
225                 230                 235                 240
Tyr Ala Asn Gly Pro Arg Leu His Glu Tyr Leu Gln Asp Leu Gly Lys
                245                 250                 255
Ile Leu Lys Glu Tyr Asp Ala Phe Ser Val Gly Glu Met Pro Phe Val
            260                 265                 270
Arg Asp Thr Glu Glu Val Leu Arg Ala Val Arg Tyr Asp Arg Asn Glu
        275                 280                 285
Ile Asn Met Ile Phe Asn Phe Glu His Val Asp Ile Asp His Gly Thr
    290                 295                 300
Tyr Asp Lys Phe Glu Pro Gly Ser Trp Lys Leu Thr Asp Leu Lys Ala
305                 310                 315                 320
Phe Phe Glu Thr Trp Gln Lys Phe Met Tyr Asn Asn Asp Gly Trp Asn
                325                 330                 335
Ala Leu Tyr Trp Glu Asn His Asp Gln Pro Arg Ser Ile Asp Arg Tyr
            340                 345                 350
Ala Gln Ala Lys Glu Glu Phe Arg Thr Glu Ala Gly Lys Met Leu Ala
        355                 360                 365
Thr Val Leu Ala Leu Gln Ser Gly Thr Pro Phe Val Tyr Gln Gly Gln
    370                 375                 380
Glu Ile Gly Met Arg Asn Val Pro Val Glu Trp Asp Met Asn Glu Tyr
385                 390                 395                 400
Lys Asp Ile Asp Cys Leu Asn His Trp His Arg Leu Leu Lys His Arg
                405                 410                 415
Pro Asp Asp Ile Glu Ala Gln Lys Ser Ala Arg Gln Glu Tyr Gln Lys
            420                 425                 430
Lys Ser Arg Asp Asn Gly Arg Thr Pro Val Gln Trp Ser Ser Ala Pro
        435                 440                 445
Asn Gly Gly Phe Thr Gly Pro Asn Ala Lys Pro Trp Met Ser Val Asn
    450                 455                 460
Pro Asp Tyr Val Arg Phe Asn Ala Glu Ala Gln Val Asn Asp Pro Asn
465                 470                 475                 480
Ser Ile Tyr His Tyr Trp Ala Ala Val Leu Gly Leu Arg Lys Lys Tyr
                485                 490                 495
Leu Asp Ile Phe Val Tyr Gly Asp Tyr Asp Leu Val Asp Lys Asp Ser
            500                 505                 510
Gln Glu Val Phe Ala Tyr Ala Arg Gln Phe Glu Asn Gln Lys Ala Leu
        515                 520                 525
Val Leu Thr Asn Trp Thr Glu Lys Thr Leu Glu Trp Asp Ala Thr Ala
    530                 535                 540
```

Asn Gly Val Lys Gly Ile Lys Asp Val Leu Leu Asn Ser Tyr Glu Ser
545 550 555 560
Ala Glu Ala Ala Lys Glu Arg Phe Thr Gly Gln Lys Trp Ser Leu Arg
565 570 575
Pro Tyr Glu Ala Val Val Leu Leu Val Glu Ala
580 585

<210> 270
<211> 768
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase EHA23680.1

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

```
    290                 295                 300
Gly Gly Gln Glu Lys Val Asn Arg Ile Val Lys Gln Gly Phe Glu His
305                 310                 315                 320
Asp Cys Pro Val Ala Gly Val Trp Leu Gln Asp Trp Ser Gly Thr His
                325                 330                 335
Leu Gln Ser Ala Pro Tyr Gly Asn Met Asn Ile Ser Arg Leu Trp Trp
            340                 345                 350
Asn Trp Glu Ser Asp Thr Ser Leu Tyr Pro Thr Trp Ala Glu Phe Val
        355                 360                 365
Gln Thr Leu Arg Glu Gln His Gly Val Arg Thr Leu Ala Tyr Val Asn
    370                 375                 380
Pro Phe Leu Ala Asn Val Ser Ser Lys Ser Asp Gly Tyr Arg Arg Asn
385                 390                 395                 400
Leu Phe Leu Glu Ala Ser Gln His Arg Tyr Met Val Gln Asn Thr Thr
                405                 410                 415
Thr Asn Ser Thr Ala Ile Ile Ser Ser Gly Lys Gly Ile Asp Ala Gly
            420                 425                 430
Ile Leu Asp Leu Thr Asn Glu Asp Thr Arg Ala Trp Phe Ala Asp Val
        435                 440                 445
Leu Arg Thr Gln Val Trp Ser Ala Asn Ile Ser Gly Cys Met Trp Asp
    450                 455                 460
Phe Gly Glu Tyr Thr Pro Ile Thr Pro Asp Thr Ser Leu Ala Asn Ile
465                 470                 475                 480
Ser Thr Ser Ala Phe Phe Tyr His Asn Gln Tyr Pro Arg Asp Trp Ala
                485                 490                 495
Ala Tyr Gln Arg Ser Val Ala Ala Glu Met Pro Leu Phe His Glu Met
            500                 505                 510
Val Thr Phe His Arg Ser Ala Ser Met Gly Ala Asn Arg His Met Asn
        515                 520                 525
Leu Phe Trp Val Gly Asp Gln Ala Thr Leu Trp Thr Arg Asn Asp Gly
    530                 535                 540
Ile Lys Ser Val Val Thr Ile Gln Gly Gln Met Gly Ile Ser Gly Tyr
545                 550                 555                 560
Ala His Ser His Ser Asp Ile Gly Gly Tyr Thr Thr Val Phe Glu Pro
                565                 570                 575
Pro Thr Thr Ser Asn Ser Ser Gly Ala Ile Pro Arg Ser Ala Glu Leu
            580                 585                 590
Leu Gly Arg Trp Gly Glu Leu Gly Ala Val Ser Ser Ala Val Phe Arg
        595                 600                 605
Ser His Glu Gly Asn Val Pro Ser Val Asn Ala Gln Phe Tyr Ser Asn
    610                 615                 620
Ser Thr Thr Tyr Ala Tyr Phe Ala Tyr Asn Ala Arg Leu Phe Arg Ser
625                 630                 635                 640
Leu Gly Pro Tyr Arg Arg Arg Ile Leu Asn Thr Glu Ser Gln Arg Arg
                645                 650                 655
Gly Trp Pro Leu Leu Arg Met Pro Val Leu Tyr His Pro Glu Asp Leu
            660                 665                 670
Arg Ala Arg Gln Ile Ser Tyr Glu Ser Phe Phe Leu Gly Arg Asp Leu
        675                 680                 685
Tyr Val Ala Pro Val Leu Asp Glu Gly His Lys Ser Val Asp Val Tyr
    690                 695                 700
Phe Pro Gly His Gly Ala Asn Arg Thr Tyr Thr His Val Trp Thr Gly
705                 710                 715                 720
Gln Thr Tyr Arg Ala Gly Gln Thr Ala Lys Val Ser Ala Pro Phe Gly
```

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                725                 730                 735
Lys Pro Ala Val Phe Leu Val Asn Gly Ala Ser Ser Pro Glu Leu Asp
            740                 745                 750
Val Phe Leu Asn Phe Val Arg Lys Glu Asn Gly Thr Val Leu His Ala
        755                 760                 765


<210> 271
<211> 680
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase EHA25759.1

<400> 271
Met Asp Pro Ala Asn Glu Tyr Cys Gly Leu Glu Asp Tyr Gly Leu Val
 1               5                  10                  15
Gly Asp Met His Thr Cys Ala Leu Val Ser Lys Asn Gly Ser Val Asp
            20                  25                  30
Ser Met Cys Trp Pro Val Phe Asp Ser Pro Ser Ile Phe Cys Arg Ile
        35                  40                  45
Leu Asp Lys Glu Lys Gly Gly His Phe Ser Ile Thr Pro Asp Arg Arg
    50                  55                  60
Leu Lys Asn Pro Leu Ser Lys Gln Arg Tyr Arg Pro Tyr Thr Asn Met
65                  70                  75                  80
Leu Glu Thr Arg Trp Ile His Glu Glu Gly Val Met Asn Ile Leu Asp
                85                  90                  95
Tyr Phe Pro Ile Ala Lys Pro Lys Pro His Val Val Glu Lys Gly Leu
            100                 105                 110
Pro Gln Trp Cys Arg Cys Tyr Gln Asn Lys Gly Ser Ala Gln Tyr Gln
        115                 120                 125
Ala Cys Arg Ser Gly Met Val Arg Lys Ala Glu Cys Val Arg Gly Glu
    130                 135                 140
Met Glu Ile Glu Ile Glu Leu Phe Pro Ala Phe Asn Tyr Ala Arg Asp
145                 150                 155                 160
Ser His Val Ala Gln Gln Ser Ser Ala Ser Asp Asp Ala Ile Gln Val
                165                 170                 175
Tyr His Phe Gln Ala Glu Ser Gln Asn Leu Val Val Ser Val Leu Gly
            180                 185                 190
Asp Lys Gly Asp Ile Ser Glu Asp Asp Ser Asp Leu Ser Ile Glu Phe
        195                 200                 205
Glu Leu Ser Asp Arg Pro Gly His Leu Gly Pro Gly Leu Val Gly Lys
    210                 215                 220
Val Ile Leu Lys Glu Gly Gln Ser Ile Thr Met Leu Leu His Asp Gln
225                 230                 235                 240
Glu Ser Ile Thr Cys Asp Val Asp Asp Leu Ala Pro Tyr Leu Gln Gln
                245                 250                 255
Ile Glu Arg Thr Thr Gly Asp Phe Trp Ser Asp Trp Thr Ser Lys Cys
            260                 265                 270
Thr Phe Arg Gly His Tyr Arg Glu Gln Val Glu Arg Ser Leu Leu Val
        275                 280                 285
Leu Lys Leu Leu Thr Tyr Lys Pro Thr Gly Ala Ile Val Ala Ala Pro
    290                 295                 300
```

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Thr Phe Ser Leu Pro Glu His Ile Gly Gly Ser Arg Asn Trp Asp Tyr
305                 310                 315                 320
Arg Tyr Ser Trp Val Arg Asp Ala Ala Phe Thr Val Tyr Val Phe Leu
                325                 330                 335
Lys Asn Gly Tyr Pro Glu Glu Ala Glu Ser Tyr Ile Asn Phe Ile Phe
            340                 345                 350
Glu Arg Ile Phe Pro Pro Met Asp Lys Asn Pro Lys Pro Gly Glu Pro
        355                 360                 365
Phe Leu Pro Ile Met Ile Thr Ile His Gly Glu Arg Glu Ile Pro Glu
    370                 375                 380
Met Glu Leu Asp His Leu Glu Gly Tyr Arg Gly Ser Arg Pro Val Arg
385                 390                 395                 400
Ile Gly Asn Gly Ala Ala Thr His Ile Gln Leu Asp Ile Tyr Gly Glu
                405                 410                 415
Leu Met Asp Ser Ile Tyr Leu Tyr Asn Lys His Ala Ala Asp Ile Ser
            420                 425                 430
Tyr Asp Gln Trp Arg Ala Ile Arg Arg Met Ile Asp Phe Val Ile Gln
        435                 440                 445
Ile Arg His Gln Pro Asp Gln Ser Ile Trp Glu Val Arg Gly Pro Pro
    450                 455                 460
Gln Asn Phe Val Tyr Ser Lys Ile Met Leu Trp Val Ala Leu Asp Arg
465                 470                 475                 480
Gly Leu Arg Leu Ala Glu Lys Arg Ser Asn Leu Pro Cys Pro Asp Arg
                485                 490                 495
Ala Arg Trp Met His Glu Arg Asp Ala Leu Tyr Asp Glu Ile Met Thr
            500                 505                 510
Lys Gly Tyr Asn Ala Glu Lys Gly Phe Phe Cys Met Ser Tyr Glu Asn
        515                 520                 525
Gln Asp Ala Met Asp Ala Ala Val Leu Ile Ala Pro Leu Val Phe Phe
    530                 535                 540
Val Ala Pro Asn Asp Pro Arg Leu Leu Ser Thr Ile Gln Arg Ile Thr
545                 550                 555                 560
Glu Val Pro Ala Lys Gly Gly Leu Ser Val Ala Asn Met Val Ser Arg
                565                 570                 575
Tyr Asp Thr Gly Lys Val Asp Asp Gly Val Gly Gly Asn Glu Gly Ala
            580                 585                 590
Phe Leu Met Val Thr Phe Trp Leu Val Glu Ala Met Met Arg Ala Ala
        595                 600                 605
Arg Ser Lys Ser Tyr Leu Pro His Asp Pro Phe Phe Gln Gln Leu Arg
    610                 615                 620
Lys Thr Ala Thr Ser Gln Phe Asp Ser Ile Leu Ser Phe Ala Asn His
625                 630                 635                 640
Leu Gly Met Phe Ser Glu Glu Val Ala Thr Ser Gly Glu Gln Ile Gly
                645                 650                 655
Asn Met Pro Gln Ala Phe Ser His Leu Ala Cys Val Ser Ala Ala Met
            660                 665                 670
Asn Leu Gly Gly Gly Gly Asp Arg
        675                 680
```

<210> 272
<211> 1539
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase EHA26514.1

<400> 272
Met Ser Ser Pro Gln Gln Val Tyr Leu Leu Pro Leu Lys Asp Asp Gly
 1               5                  10                  15
Ser Pro Asp Val Pro Gly Gly Tyr Ile Tyr Leu Pro Ala Pro Thr Asn
            20                  25                  30
Pro Pro Tyr Leu Leu Arg Phe Val Ile Glu Gly Ser Ser Ser Ile Cys
        35                  40                  45
Arg Glu Gly Ala Leu Trp Val Asn Ile Pro Glu Lys Gly Glu Ser Phe
    50                  55                  60
Asn Arg Ser Ala Phe Arg Ser Phe Ser Leu Ser Pro Asp Phe Asn Lys
65                  70                  75                  80
Asn Ile Gln Ile Asp Val Pro Ile Thr Ser Ala Gly Ser Phe Ala Phe
                85                  90                  95
Tyr Val Thr Phe Ser Pro Leu Pro Glu Phe Ser Val Ile Ser Thr Pro
            100                 105                 110
Thr Pro Glu Pro Thr Arg Thr Pro Thr His Tyr Ile Asp Val Ser Pro
        115                 120                 125
Lys Leu Thr Leu Arg Gly Gln Asp Leu Pro Leu Asn Ala Leu Ser Ile
    130                 135                 140
Tyr Ser Val Ile Ser Lys Phe Met Gly Gln Tyr Pro Lys Glu Trp Glu
145                 150                 155                 160
Lys His Leu Asn Gly Ile Ser Gln Arg Asn Tyr Asn Met Val His Phe
                165                 170                 175
Thr Pro Leu Met Lys Arg Gly Ala Ser Asn Ser Pro Tyr Ser Ile Phe
            180                 185                 190
Asp Gln Leu Gln Phe Asp Asp Ala Val Phe Pro Asn Gly Glu Asp Asp
        195                 200                 205
Val Ala Arg Leu Ile Ser Lys Met Glu Asn Glu Tyr Gly Leu Leu Ser
    210                 215                 220
Leu Thr Asp Val Val Trp Asn His Thr Ala His Asn Ser Lys Trp Leu
225                 230                 235                 240
Glu Glu His Pro Glu Ala Gly Tyr Ser Val Glu Thr Ala Pro Trp Leu
                245                 250                 255
Glu Ala Ala Leu Glu Leu Asp Thr Ala Leu Leu Lys Phe Gly Gln Asp
            260                 265                 270
Leu Gln Asn Leu Gly Leu Pro Thr Glu Phe Gln Thr Val Asp Glu Leu
        275                 280                 285
Met Lys Val Met Asn Val Met Arg Asp Lys Val Ile Ala Gly Ile Arg
    290                 295                 300
Leu Trp Glu Phe Tyr Ala Ile Asp Val Lys Ser Asp Thr His Lys Ile
305                 310                 315                 320
Leu Asp Lys Trp Lys Thr Ser Lys Asp Ile Asp Leu Thr Asp Thr Asn
                325                 330                 335
Trp Ala Gln Leu Asn Leu Gln Asp Tyr Lys Asn Trp Thr Leu Lys Gln
            340                 345                 350
Gln Ala Thr Phe Ile Arg Asp His Ala Ile Pro Thr Ser Lys Gln Val
        355                 360                 365
Leu Asp Arg Phe Ser Arg Ala Val Asp Leu Gln Phe Gly Ala Ala Ile
    370                 375                 380
Leu Thr Ala Leu Phe Gly Pro His Asn Pro Ser Thr Ser Asp Thr Ser

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385                 390                 395                 400
Ile Val Glu Glu Ser Leu Ser Lys Ile Leu Asp Glu Val Asn Leu Pro
                405                 410                 415
Phe Tyr Glu Glu Tyr Asp Gly Asp Val Ser Glu Ile Met Asn Gln Val
            420                 425                 430
Phe Asn Arg Ile Lys Tyr Leu Arg Ile Asp Asp His Gly Pro Lys Leu
        435                 440                 445
Gly Ala Val Thr Ala Gln Ser Pro Leu Ile Glu Thr Tyr Phe Thr Arg
    450                 455                 460
Leu Pro Leu Asn Asp Val Thr Lys Lys His Lys Lys Glu Ala Leu Ala
465                 470                 475                 480
Leu Val Asn Asn Gly Trp Ile Trp Asn Ala Asp Ala Leu Arg Asp Asn
                485                 490                 495
Ala Gly Pro Asp Ser Arg Ala Tyr Leu Arg Arg Glu Val Ile Val Trp
            500                 505                 510
Gly Asp Cys Val Lys Leu Arg Tyr Gly Ser Cys Arg Asp Asp Asn Pro
        515                 520                 525
Phe Leu Trp Asp Phe Met Thr Asp Tyr Thr Arg Leu Met Ala Lys Tyr
    530                 535                 540
Phe Ser Gly Phe Arg Ile Asp Asn Cys His Ser Thr Pro Leu Val Val
545                 550                 555                 560
Ala Glu Tyr Leu Leu Asp Glu Ala Arg Lys Val Arg Pro Asn Leu Thr
                565                 570                 575
Val Phe Ala Glu Leu Phe Thr Gly Ser Glu Glu Ala Asp Tyr Ile Phe
            580                 585                 590
Val Lys Arg Leu Gly Ile Asn Ala Leu Ile Arg Glu Ala Met Gln Ala
        595                 600                 605
Trp Ser Thr Gly Glu Leu Ser Arg Leu Val His Arg His Gly Gly Arg
    610                 615                 620
Pro Ile Gly Ser Phe Asp Leu Asp Leu Pro Ser Ser Gly Ser Ser His
625                 630                 635                 640
Ala Ile Ala Ser Ser Gly Leu Asp Ser Gly Lys Glu Lys Val Val His
                645                 650                 655
Ile Arg Pro Thr Pro Val Gln Ala Leu Phe Met Asp Cys Thr His Asp
            660                 665                 670
Asn Glu Met Pro Ala Gln Lys Arg Thr Ala Lys Asp Thr Leu Pro Asn
        675                 680                 685
Gly Ala Leu Val Ala Met Cys Ala Ser Ala Ile Gly Ser Val Ile Gly
    690                 695                 700
Tyr Asp Glu Val Tyr Pro Arg Leu Val Asp Leu Val His Glu His Arg
705                 710                 715                 720
Leu Tyr Phe Ser Glu Phe Ser Glu Ala Pro Glu Thr Gly Leu Asn Ser
                725                 730                 735
Leu Glu Gly Gly Ile Gly Gly Ile Lys Lys Leu Leu Asn Glu Leu His
            740                 745                 750
Thr Lys Met Gly Ile Glu Gly Tyr Asp Glu Thr His Ile His His Asp
        755                 760                 765
Gly Glu Tyr Ile Thr Val His Arg Val His Pro Arg Thr Arg Lys Gly
    770                 775                 780
Val Phe Leu Ile Ala His Thr Ala Phe Pro Gly Gln Asp Ser Arg Ser
785                 790                 795                 800
Val Leu Ala Pro Thr His Leu Val Gly Thr Gln Val Lys His Ile Gly
                805                 810                 815
Thr Trp Leu Leu Glu Val Asp Thr Ser Gln Thr Thr Lys Glu Arg Ile
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            820                 825                 830
Gln Ala Asp Lys Ser Tyr Leu Arg Gly Leu Pro Ser Gln Val Lys Thr
        835                 840                 845
Phe Glu Gly Thr Lys Ile Glu Glu Ser Gly Lys Asp Thr Ile Ile Ser
    850                 855                 860
Val Leu Asn Ser Phe Val Ala Gly Ser Ile Ala Leu Phe Glu Thr Ser
865                 870                 875                 880
Met Pro Ser Val Glu His Ala Ser Gly Leu Asp Asn Tyr Ile Thr Glu
                885                 890                 895
Gly Val Asp His Ala Phe Ser Asp Leu Ser Leu Val Asp Leu Asn Phe
            900                 905                 910
Ala Leu Tyr Arg Cys Glu Ala Glu Glu Arg Asp Ser Ser Lys Gly Gln
        915                 920                 925
Asp Gly Ala Tyr Asp Ile Pro Gly His Gly Pro Leu Val Tyr Ala Gly
    930                 935                 940
Leu Gln Gly Trp Trp Ser Val Leu Glu Asn Ile Ile Lys Tyr Asn Glu
945                 950                 955                 960
Leu Gly His Pro Leu Cys Asp His Leu Arg Asn Gly Gln Trp Ala Leu
                965                 970                 975
Asp Tyr Ile Val Ala Arg Leu Glu Lys Leu Ser His Lys Glu Glu His
            980                 985                 990
Pro Ala Leu Gly Arg Pro Ala Ala Trp Leu Gln Glu Lys Phe Gln Ala
        995                 1000                1005
Val Arg Gln Leu Pro Ser Phe Leu Leu Pro Arg Tyr Phe Ala Ile Ile
    1010                1015                1020
Val Gln Val Ala Tyr Asn Ala Ala Trp Lys Arg Gly Ile Gln Leu Leu
1025                1030                1035                1040
Gly Ser His Ile Gln Lys Gly Gln Glu Phe Ile His Gln Leu Gly Met
                1045                1050                1055
Val Ser Val Gln Gln Thr Gly Tyr Val Asn Ser Ala Ser Leu Trp Pro
            1060                1065                1070
Thr Lys Lys Val Pro Ser Leu Ala Ala Gly Leu Pro His Phe Ala Val
        1075                1080                1085
Asp Trp Ala Arg Cys Trp Gly Arg Asp Val Phe Ile Ser Leu Arg Gly
    1090                1095                1100
Leu Leu Leu Cys Thr Gly Arg Phe Glu Asp Ala Lys Glu His Ile Thr
1105                1110                1115                1120
Ala Phe Ala Ser Val Leu Lys His Gly Met Ile Pro Asn Leu Leu Ser
                1125                1130                1135
Ser Gly Lys Leu Pro Arg Tyr Asn Ser Arg Asp Ser Val Trp Phe Phe
            1140                1145                1150
Leu Gln Ser Ile Gln Asp Tyr Thr Glu Met Ala Pro Asp Gly Leu Glu
        1155                1160                1165
Ile Leu Asp His Lys Val Pro Arg Arg Phe Leu Pro Tyr Asp Asp Val
    1170                1175                1180
Trp Phe Pro Phe Asp Asp Pro Arg Ala Tyr Ser Gln Gln Ser Thr Ile
1185                1190                1195                1200
Ser Glu Ile Ile Gln Glu Val Phe Gln Arg His Ala Gln Gly Leu Ser
                1205                1210                1215
Phe Arg Glu Tyr Asn Ala Gly Pro Asp Leu Asp Met Gln Met Thr Gln
            1220                1225                1230
Asp Gly Phe Gln Ile Asp Val Lys Val Asp Trp Glu Thr Gly Leu Ile
        1235                1240                1245
Phe Gly Gly Ser Gln Tyr Asn Cys Gly Thr Trp Gln Asp Lys Met Gly
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    1250                1255                1260
Glu Ser Ala Lys Ala Gly Asn Lys Gly Val Pro Gly Thr Pro Arg Asp
1265                1270                1275                1280
Gly Ala Ala Ile Glu Ile Thr Gly Leu Val Tyr Ser Ala Leu Thr Trp
                1285                1290                1295
Val Ala Lys Leu His Glu Arg Gly Ile Tyr Lys His Asp Gly Val Asp
            1300                1305                1310
Ile Gly Gly Gly Lys Ser Ile Ser Phe Glu Asp Trp Ala Ser Arg Ile
        1315                1320                1325
Arg Ala Asn Phe Glu Arg Cys Tyr Tyr Val Pro Leu Gln Pro Lys Asp
    1330                1335                1340
Asp Gly Gln Tyr Asp Ile Asp Ala Asn Ile Ile Asn Arg Arg Gly Ile
1345                1350                1355                1360
Tyr Lys Asp Leu Tyr Arg Ser Gly Lys Pro Tyr Glu Asp Tyr Gln Leu
                1365                1370                1375
Arg Ser Asn Phe Pro Ile Ala Met Thr Val Ala Pro Asp Leu Phe Thr
            1380                1385                1390
Ala Ser Lys Ala Leu Ala Ala Leu Ala Leu Ala Asp Glu Val Leu Val
        1395                1400                1405
Gly Pro Val Gly Met Ala Thr Leu Asp Pro Ser Asp Leu Asn Tyr Arg
    1410                1415                1420
Pro Asn Tyr Asn Asn Ser Glu Asp Ser Thr Asp Phe Ala Thr Ala Lys
1425                1430                1435                1440
Gly Arg Asn Tyr His Gln Gly Pro Glu Trp Val Trp Gln Arg Gly Tyr
                1445                1450                1455
Phe Leu Arg Ala Phe Leu His Phe Asp Leu Ala Arg Arg Thr Thr Pro
            1460                1465                1470
Ala Glu Arg Thr Glu Thr Tyr Gln Gln Ile Thr Arg Arg Leu Glu Gly
        1475                1480                1485
Cys Lys Arg Ala Leu Arg Glu Ser Pro Trp Lys Gly Leu Thr Glu Leu
    1490                1495                1500
Thr Asn Lys Asn Gly Ala Tyr Cys Ala Asp Ser Ser Pro Thr Gln Ala
1505                1510                1515                1520
Trp Ser Ala Gly Cys Leu Leu Asp Leu Tyr Tyr Asp Ala Ser Arg His
                1525                1530                1535
Ser Gln Ser
```

<210> 273
<211> 656
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase EHA26552.1

<400> 273

```
Met Trp Ser Ser Trp Leu Leu Ser Ala Leu Leu Ala Thr Glu Ala Leu
 1               5                  10                  15
Ala Val Pro Tyr Glu Glu Tyr Ile Leu Ala Pro Ser Ser Arg Asp Leu
            20                  25                  30
Ala Pro Ala Ser Val Arg Gln Val Asn Gly Ser Val Thr Asn Ala Ala
        35                  40                  45
```

```
Ala Leu Thr Gly Ala Gly Gly Gln Ala Thr Phe Asn Gly Val Ser Ser
    50                  55                  60
Val Thr Tyr Asp Phe Gly Ile Asn Val Ala Gly Ile Val Ser Val Asp
65                  70                  75                  80
Val Ala Ser Ala Ser Ser Glu Ser Ala Phe Ile Gly Val Thr Phe Thr
                85                  90                  95
Glu Ser Ser Met Trp Ile Ser Ser Glu Ala Cys Asp Ala Thr Gln Asp
            100                 105                 110
Ala Gly Leu Asp Thr Pro Leu Trp Phe Ala Val Gly Gln Gly Ala Gly
        115                 120                 125
Leu Tyr Thr Val Glu Lys Lys Tyr Asn Arg Gly Ala Phe Arg Tyr Met
    130                 135                 140
Thr Val Val Ser Asn Thr Thr Ala Thr Val Ser Leu Asn Ser Val Lys
145                 150                 155                 160
Ile Asn Tyr Thr Ala Ser Pro Thr Gln Asp Leu Arg Ala Tyr Thr Gly
                165                 170                 175
Tyr Phe His Ser Asn Asp Glu Leu Leu Asn Arg Ile Trp Tyr Ala Gly
            180                 185                 190
Ala Tyr Thr Leu Gln Leu Cys Ser Ile Asp Pro Thr Thr Gly Asp Ala
        195                 200                 205
Leu Val Gly Leu Gly Val Ile Thr Ser Ser Glu Thr Ile Ser Leu Pro
    210                 215                 220
Gln Thr Asp Lys Trp Trp Thr Asn Tyr Thr Ile Thr Asn Gly Ser Ser
225                 230                 235                 240
Thr Leu Thr Asp Gly Ala Lys Arg Asp Arg Leu Val Trp Pro Gly Asp
                245                 250                 255
Met Ser Ile Ala Leu Glu Ser Val Ala Val Ser Thr Glu Asp Leu Tyr
            260                 265                 270
Ser Val Arg Thr Ala Leu Glu Ser Leu Tyr Ala Leu Gln Lys Pro Asp
        275                 280                 285
Gly Arg Leu Pro Tyr Ala Gly Lys Pro Phe Phe Asp Thr Val Ser Phe
    290                 295                 300
Thr Tyr His Leu His Ser Leu Val Gly Ala Ala Ser Tyr Tyr Gln Tyr
305                 310                 315                 320
Thr Gly Asp Arg Ala Trp Leu Thr Arg Tyr Trp Gly Gln Tyr Lys Lys
                325                 330                 335
Gly Val Gln Trp Ala Leu Ser Ser Val Asp Ser Thr Gly Leu Ala Asn
            340                 345                 350
Ile Thr Ala Ser Ala Asp Trp Leu Arg Phe Gly Met Gly Ala His Asn
        355                 360                 365
Ile Glu Ala Asn Ala Ile Leu Tyr Tyr Val Leu Asn Asp Ala Ile Ser
    370                 375                 380
Leu Ala Gln Thr Leu Asn Asp Asn Ala Pro Ile Arg Asn Trp Thr Thr
385                 390                 395                 400
Thr Ala Ala Arg Ile Lys Thr Val Ala Asn Glu Leu Leu Trp Asp Asp
                405                 410                 415
Lys Asn Gly Leu Tyr Thr Asp Asn Glu Thr Thr Thr Leu His Pro Gln
            420                 425                 430
Asp Gly Asn Ser Trp Ala Val Lys Ala Asn Leu Thr Leu Ser Ala Asn
        435                 440                 445
Gln Ser Ala Ile Val Ser Glu Ser Leu Ala Ala Arg Trp Gly Pro Tyr
    450                 455                 460
Gly Ala Pro Ala Pro Glu Ala Gly Ala Thr Val Ser Pro Phe Ile Gly
465                 470                 475                 480
```

Gly Phe Glu Leu Gln Ala His Tyr Gln Ala Gly Gln Pro Asp Arg Ala
485 490 495
Leu Asp Leu Leu Arg Leu Gln Trp Gly Phe Met Leu Asp Asp Pro Arg
500 505 510
Met Thr Asn Ser Thr Phe Ile Glu Gly Tyr Ser Thr Asp Gly Ser Leu
515 520 525
Ala Tyr Ala Pro Tyr Thr Asn Thr Pro Arg Val Ser His Ala His Gly
530 535 540
Trp Ala Thr Gly Pro Thr Ser Ala Leu Thr Ile Tyr Thr Ala Gly Leu
545 550 555 560
Arg Val Thr Gly Pro Ala Gly Ala Thr Trp Leu Tyr Lys Pro Gln Pro
565 570 575
Gly Asn Leu Thr Gln Val Glu Ala Gly Phe Ser Thr Arg Leu Gly Ser
580 585 590
Phe Ala Ser Ser Phe Ser Arg Ser Gly Gly Arg Tyr Gln Glu Leu Ser
595 600 605
Phe Ser Thr Pro Asn Gly Thr Thr Gly Ser Val Glu Leu Gly Asp Val
610 615 620
Ser Gly Gln Leu Val Ser Asp Arg Gly Val Lys Val Gln Leu Val Gly
625 630 635 640
Gly Lys Ala Ser Gly Leu Gln Gly Gly Lys Trp Lys Leu Ser Asn Asn
645 650 655

<210> 274
<211> 790
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase EHA26885.1

<400> 274
Met Leu Gly Ser Leu Leu Leu Leu Leu Pro Leu Val Gly Ala Ala Val
1 5 10 15
Ile Gly Pro Arg Ala Asn Ser Gln Ser Cys Pro Gly Tyr Lys Ala Ser
20 25 30
Asn Val Gln Lys Gln Ala Arg Ser Leu Thr Ala Asp Leu Thr Leu Ala
35 40 45
Gly Thr Pro Cys Asn Ser Tyr Gly Lys Asp Leu Glu Asp Leu Lys Leu
50 55 60
Leu Val Glu Tyr Gln Thr Asp Glu Arg Leu His Val Met Ile Tyr Asp
65 70 75 80
Ala Asp Glu Glu Val Tyr Gln Val Pro Glu Ser Val Leu Pro Arg Val
85 90 95
Gly Ser Asp Glu Asp Ser Glu Asp Ser Val Leu Glu Phe Asp Tyr Val
100 105 110
Glu Glu Pro Phe Ser Phe Thr Ile Ser Lys Gly Asp Glu Val Leu Phe
115 120 125
Asp Ser Ser Ala Ser Pro Leu Val Phe Gln Ser Gln Tyr Val Asn Leu
130 135 140
Arg Thr Trp Leu Pro Asp Asp Pro Tyr Val Tyr Gly Leu Gly Glu His
145 150 155 160
Ser Asp Pro Met Arg Leu Pro Thr Tyr Asn Tyr Thr Arg Thr Leu Trp

```
                165                 170                 175
Asn Arg Asp Ala Tyr Gly Thr Pro Asn Asn Thr Asn Leu Tyr Gly Ser
            180                 185                 190
His Pro Val Tyr Tyr Asp His Arg Gly Lys Ser Gly Thr Tyr Gly Val
        195                 200                 205
Phe Leu Leu Asn Ser Asn Gly Met Asp Ile Lys Ile Asn Gln Thr Thr
    210                 215                 220
Asp Gly Lys Gln Tyr Leu Glu Tyr Asn Leu Leu Gly Gly Val Leu Asp
225                 230                 235                 240
Phe Tyr Phe Phe Tyr Gly Glu Asp Pro Lys Gln Ala Ser Met Glu Tyr
                245                 250                 255
Ser Lys Ile Val Gly Leu Pro Ala Met Gln Ser Tyr Trp Thr Phe Gly
            260                 265                 270
Phe His Gln Cys Arg Tyr Gly Tyr Arg Asp Val Tyr Glu Leu Ala Glu
        275                 280                 285
Val Val Tyr Asn Tyr Ser Gln Ala Lys Ile Pro Leu Glu Thr Met Trp
    290                 295                 300
Thr Asp Ile Asp Tyr Met Asp Lys Arg Arg Val Phe Thr Leu Asp Pro
305                 310                 315                 320
Gln Arg Phe Pro Leu Glu Lys Met Arg Glu Leu Val Thr Tyr Leu His
                325                 330                 335
Asn His Asp Gln His Tyr Ile Val Met Val Asp Pro Ala Val Ser Val
            340                 345                 350
Ser Asn Asn Thr Ala Tyr Ile Thr Gly Val Arg Asp Asp Val Phe Leu
        355                 360                 365
His Asn Gln Asn Gly Ser Leu Tyr Glu Gly Ala Val Trp Pro Gly Val
    370                 375                 380
Thr Val Phe Pro Asp Trp Phe Asn Glu Gly Thr Gln Asp Tyr Trp Thr
385                 390                 395                 400
Ala Gln Phe Gln Gln Phe Phe Asp Pro Lys Ser Gly Val Asp Ile Asp
                405                 410                 415
Ala Leu Trp Ile Asp Met Asn Glu Ala Ser Asn Phe Cys Pro Tyr Pro
            420                 425                 430
Cys Leu Asp Pro Ala Ala Tyr Ala Ile Ser Ala Asp Leu Pro Pro Ala
        435                 440                 445
Ala Pro Pro Val Arg Pro Ser Ser Pro Ile Pro Leu Pro Gly Phe Pro
    450                 455                 460
Ala Asp Phe Gln Pro Ser Ser Lys Arg Ser Val Lys Arg Ala Gln Gly
465                 470                 475                 480
Asp Lys Gly Lys Lys Val Gly Leu Pro Asn Arg Asn Leu Thr Asp Pro
                485                 490                 495
Pro Tyr Thr Ile Arg Asn Ala Ala Gly Val Leu Ser Met Ser Thr Ile
            500                 505                 510
Glu Thr Asp Leu Ile His Ala Gly Glu Gly Tyr Ala Glu Tyr Asp Thr
        515                 520                 525
His Asn Leu Tyr Gly Thr Thr His Ile Pro Met Val Gly Ala Asp Val
    530                 535                 540
Cys Gly Phe Gly Ser Asn Thr Thr Glu Glu Leu Cys Ala Arg Trp Ala
545                 550                 555                 560
Ser Leu Gly Ala Phe Tyr Thr Phe Tyr Arg Asn His Asn Glu Leu Gly
                565                 570                 575
Asp Ile Ser Gln Glu Phe Tyr Arg Trp Pro Thr Val Ala Glu Ser Ala
            580                 585                 590
Arg Lys Ala Ile Asp Ile Arg Tyr Lys Leu Leu Asp Tyr Ile Tyr Thr
```

```
        595                 600                 605
Ala Leu His Arg Gln Ser Gln Ser Gly Glu Pro Phe Leu Gln Pro Gln
    610                 615                 620
Phe Tyr Leu Tyr Pro Glu Asp Ser Asn Thr Phe Ala Asn Asp Arg Gln
625                 630                 635                 640
Phe Phe Tyr Gly Asp Ala Leu Leu Val Ser Pro Val Leu Asn Glu Gly
                645                 650                 655
Ser Thr Ser Val Asp Ala Tyr Phe Pro Asp Asp Ile Phe Tyr Asp Trp
            660                 665                 670
Tyr Thr Gly Ala Val Val Arg Gly His Gly Glu Asn Ile Thr Leu Ser
        675                 680                 685
Asn Ile Asn Ile Thr His Ile Pro Leu His Ile Arg Gly Gly Asn Ile
    690                 695                 700
Ile Pro Val Arg Thr Ser Ser Gly Met Thr Thr Thr Glu Val Arg Lys
705                 710                 715                 720
Gln Gly Phe Glu Leu Ile Ile Ala Pro Asp Leu Asp Asp Thr Ala Ser
                725                 730                 735
Gly Ser Leu Tyr Leu Asp Asp Gly Asp Ser Leu Asn Pro Ser Ser Val
            740                 745                 750
Thr Glu Leu Glu Phe Thr Tyr Ser Lys Gly Glu Leu His Val Lys Gly
        755                 760                 765
Thr Phe Gly Gln Lys Ala Val Pro Lys Val Glu Lys Cys Thr Leu Leu
    770                 775                 780
Gly Lys Ser Ala Arg Thr
785                 790
```

<210> 275
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase EHA27488.1

<400> 275

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

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Phe Asp Glu Ala Gly Asn Pro Val Pro Pro Asn Asn Trp Ala Gln Ile
145                 150                 155                 160
Leu Gly Asp Thr Leu Ser Ala Trp Thr Trp His Glu Glu Thr Gln Glu
                165                 170                 175
Phe Tyr Leu Thr Leu His Thr Ser Ala Gln Ala Glu Leu Asn Trp Glu
            180                 185                 190
Asn Pro Asp Val Val Thr Ala Val Tyr Asp Val Met Glu Phe Trp Leu
        195                 200                 205
Arg Arg Gly Ile Cys Gly Phe Arg Met Asp Val Ile Asn Phe Ile Ser
    210                 215                 220
Lys Asp Gln Ser Phe Pro Asp Ala Pro Ile Ile Asp Pro Ala Ser Lys
225                 230                 235                 240
Tyr Gln Pro Gly Glu Gln Phe Tyr Thr Asn Gly Pro Arg Phe His Glu
                245                 250                 255
Phe Met His Gly Ile Tyr Asp Asn Val Leu Ser Lys Tyr Asp Thr Ile
            260                 265                 270
Thr Val Gly Glu Thr Pro Tyr Val Thr Asp Met Lys Glu Ile Ile Lys
        275                 280                 285
Thr Val Gly Ser Thr Ala Lys Glu Leu Asn Met Ala Phe Asn Phe Asp
    290                 295                 300
His Met Glu Ile Glu Asp Ile Lys Thr Lys Gly Glu Ser Lys Trp Ser
305                 310                 315                 320
Leu Arg Asp Trp Lys Leu Thr Glu Leu Lys Gly Ile Leu Ser Gly Trp
                325                 330                 335
Gln Lys Arg Met Arg Glu Trp Asp Gly Trp Asn Ala Ile Phe Leu Glu
            340                 345                 350
Cys His Asp Gln Ala Arg Ser Val Ser Arg Tyr Thr Asn Asp Ser Asp
        355                 360                 365
Glu Phe Arg Asp Arg Gly Ala Lys Leu Leu Ala Leu Leu Glu Thr Thr
    370                 375                 380
Leu Gly Gly Thr Ile Phe Leu Tyr Gln Gly Gln Glu Ile Gly Met Arg
385                 390                 395                 400
Asn Phe Pro Val Glu Trp Gly Pro Asp Thr Glu Tyr Lys Asp Ile Glu
                405                 410                 415
Ser Val Asn Phe Trp Lys Lys Ser Lys Glu Leu His Pro Val Gly Ser
            420                 425                 430
Glu Gly Leu Ala Gln Ala Arg Thr Leu Leu Gln Lys Lys Ala Arg Asp
        435                 440                 445
His Ala Arg Thr Pro Met Gln Trp Ser Ala Asp Pro His Ala Gly Phe
    450                 455                 460
Thr Val Pro Asp Ala Thr Pro Trp Met Arg Val Asn Asp Asp Tyr Arg
465                 470                 475                 480
Thr Val Asn Val Glu Ala Gln Met Ser Phe Pro Trp Glu Met Lys Gly
                485                 490                 495
Glu Leu Ser Val Trp Gln Tyr Trp Gln Gln Ala Leu Gln Arg Arg Lys
            500                 505                 510
Leu His Lys Gly Ala Phe Val Tyr Gly Asp Phe Glu Asp Leu Asp Tyr
        515                 520                 525
His Asn Glu Ser Val Phe Ala Tyr Ser Arg Thr Ser Ala Asp Gly Lys
    530                 535                 540
Glu Thr Trp Leu Pro Val Pro Ser Trp Ser Leu Pro Lys Lys Arg Thr
545                 550                 555                 560
Leu Ser
```

<210> 276
<211> 957
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase EHA28539.1

<400> 276
Met Ser Asn Arg Trp Thr Leu Leu Leu Ser Leu Val Ile Leu Leu Gly
 1               5                  10                  15
Cys Leu Val Ile Pro Gly Val Thr Val Lys His Glu Asn Phe Lys Thr
            20                  25                  30
Cys Ser Gln Ser Gly Phe Cys Lys Arg Asn Arg Ala Phe Ala Asp Asp
        35                  40                  45
Ala Ala Ala Gln Gly Ser Ser Trp Ala Ser Pro Tyr Glu Leu Asp Ser
    50                  55                  60
Ser Ser Ile Gln Phe Lys Asp Gly Gln Leu His Gly Thr Ile Leu Lys
65                  70                  75                  80
Ser Val Ser Pro Asn Glu Lys Val Lys Leu Pro Leu Val Val Ser Phe
                85                  90                  95
Leu Glu Ser Gly Ala Ala Arg Val Val Val Asp Glu Glu Lys Arg Met
            100                 105                 110
Asn Gly Asp Ile Gln Leu Arg His Asp Ser Lys Ala Arg Lys Glu Arg
        115                 120                 125
Tyr Asn Glu Ala Glu Lys Trp Val Leu Val Gly Gly Leu Glu Leu Ser
    130                 135                 140
Lys Thr Ala Thr Leu Arg Pro Glu Thr Glu Ser Gly Phe Thr Arg Val
145                 150                 155                 160
Leu Tyr Gly Pro Asp Asn Gln Phe Glu Ala Val Ile Arg His Ala Pro
                165                 170                 175
Phe Ser Ala Asp Phe Lys Arg Asp Gly Gln Thr His Val Gln Leu Asn
            180                 185                 190
Asn Lys Gly Tyr Leu Asn Met Glu His Trp Arg Pro Lys Val Glu Val
        195                 200                 205
Glu Gly Glu Gly Glu Gln Gln Thr Gln Glu Asp Glu Ser Thr Trp Trp
    210                 215                 220
Asp Glu Ser Phe Gly Gly Asn Thr Asp Thr Lys Pro Arg Gly Pro Glu
225                 230                 235                 240
Ser Val Gly Leu Asp Ile Thr Phe Pro Gly Tyr Lys His Val Phe Gly
                245                 250                 255
Ile Pro Glu His Ala Asp Ser Leu Ser Leu Lys Glu Thr Arg Gly Gly
            260                 265                 270
Glu Gly Asn His Glu Glu Pro Tyr Arg Met Tyr Asn Ala Asp Val Phe
        275                 280                 285
Glu Tyr Glu Leu Ser Ser Pro Met Thr Leu Tyr Gly Ala Ile Pro Phe
    290                 295                 300
Met Gln Ala His Arg Lys Asp Ser Thr Val Gly Val Phe Trp Leu Asn
305                 310                 315                 320
Ala Ala Glu Thr Trp Val Asp Ile Val Lys Ser Thr Ser Ser Pro Asn
                325                 330                 335
Pro Leu Ala Leu Gly Val Gly Ala Thr Thr Asp Thr Gln Ser His Trp

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            340                 345                 350
Phe Ser Glu Ser Gly Gln Leu Asp Val Phe Val Phe Leu Gly Pro Thr
        355                 360                 365
Pro Gln Glu Ile Ser Lys Thr Tyr Gly Glu Leu Thr Gly Tyr Thr Gln
    370                 375                 380
Leu Pro Gln His Phe Ala Ile Ala Tyr His Gln Cys Arg Trp Asn Tyr
385                 390                 395                 400
Ile Thr Asp Glu Asp Val Lys Glu Val Asp Arg Asn Phe Asp Lys Tyr
                405                 410                 415
Gln Ile Pro Tyr Asp Val Ile Trp Leu Asp Ile Glu Tyr Thr Asp Asp
            420                 425                 430
Arg Lys Tyr Phe Thr Trp Asp Pro Leu Ser Phe Pro Asp Pro Ile Ser
        435                 440                 445
Met Glu Glu Gln Leu Asp Glu Ser Glu Arg Lys Leu Val Val Ile Ile
    450                 455                 460
Asp Pro His Ile Lys Asn Gln Asp Lys Tyr Ser Ile Val Gln Glu Met
465                 470                 475                 480
Lys Ser Lys Asp Leu Ala Thr Lys Asn Lys Asp Gly Glu Ile Tyr Asp
                485                 490                 495
Gly Trp Cys Trp Pro Gly Ser Ser His Trp Ile Asp Thr Phe Asn Pro
            500                 505                 510
Ala Ala Ile Lys Trp Trp Val Ser Leu Phe Lys Phe Asp Lys Phe Lys
        515                 520                 525
Gly Thr Leu Ser Asn Val Phe Ile Trp Asn Asp Met Asn Glu Pro Ser
    530                 535                 540
Val Phe Asn Gly Pro Glu Thr Thr Met Pro Lys Asp Asn Leu His His
545                 550                 555                 560
Gly Asn Trp Glu His Arg Asp Ile His Asn Val His Gly Ile Thr Leu
                565                 570                 575
Val Asn Ala Thr Tyr Asp Ala Leu Leu Glu Arg Lys Lys Gly Glu Ile
            580                 585                 590
Arg Arg Pro Phe Ile Leu Thr Arg Ser Tyr Tyr Ala Gly Ala Gln Arg
        595                 600                 605
Met Ser Ala Met Trp Thr Gly Asp Asn Gln Ala Thr Trp Glu His Leu
    610                 615                 620
Ala Ala Ser Ile Pro Met Val Leu Asn Asn Gly Ile Ala Gly Phe Pro
625                 630                 635                 640
Phe Ala Gly Ala Asp Val Gly Gly Phe Phe Gln Asn Pro Ser Lys Glu
                645                 650                 655
Leu Leu Thr Arg Trp Tyr Gln Ala Gly Ile Trp Tyr Pro Phe Phe Arg
            660                 665                 670
Ala His Ala His Ile Asp Thr Arg Arg Arg Glu Pro Tyr Leu Ile Ala
        675                 680                 685
Glu Pro His Arg Ser Ile Ile Ser Gln Ala Ile Arg Leu Arg Tyr Gln
    690                 695                 700
Leu Leu Pro Ala Trp Tyr Thr Ala Phe His Glu Ala Ser Val Asn Gly
705                 710                 715                 720
Met Pro Ile Val Arg Pro Gln Tyr Tyr Ala His Pro Trp Asp Glu Ala
                725                 730                 735
Gly Phe Ala Ile Asp Asp Gln Leu Tyr Leu Gly Ser Thr Gly Leu Leu
            740                 745                 750
Ala Lys Pro Val Val Ser Glu Glu Ala Thr Thr Ala Asp Ile Tyr Leu
        755                 760                 765
Ala Asp Asp Glu Lys Tyr Tyr Asp Tyr Phe Asp Tyr Thr Val Tyr Gln
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    770                 775                 780
Gly Ala Gly Lys Arg His Thr Val Pro Ala Pro Met Glu Thr Val Pro
785                 790                 795                 800
Leu Leu Met Gln Gly Gly His Val Ile Pro Arg Lys Asp Arg Pro Arg
                805                 810                 815
Arg Ser Ser Ala Leu Met Arg Trp Asp Pro Tyr Thr Leu Val Val Val
            820                 825                 830
Leu Asp Lys Asn Gly Gln Ala Asp Gly Ser Leu Tyr Val Asp Asp Gly
        835                 840                 845
Glu Thr Phe Asp Tyr Lys Arg Gly Ala Tyr Ile His Arg Arg Phe Arg
    850                 855                 860
Phe Gln Glu Ser Ala Leu Val Ser Glu Asp Val Gly Thr Lys Gly Pro
865                 870                 875                 880
Lys Thr Ala Glu Tyr Leu Lys Thr Met Ala Asn Val Arg Val Glu Arg
                885                 890                 895
Val Val Val Val Asp Pro Pro Lys Glu Trp Gln Gly Lys Thr Ser Val
            900                 905                 910
Thr Val Ile Glu Asp Gly Ala Ser Ala Ala Ser Thr Ala Ser Met Gln
        915                 920                 925
Tyr His Ser Gln Pro Asp Gly Lys Ala Ala Tyr Ala Val Val Lys Asn
    930                 935                 940
Pro Asn Val Gly Ile Gly Lys Thr Trp Arg Ile Glu Phe
945                 950                 955


<210> 277
<211> 656
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase XP_001389086.1

<400> 277
Met Trp Ser Ser Trp Leu Leu Ser Ala Leu Leu Ala Thr Glu Ala Leu
 1               5                  10                  15
Ala Val Pro Tyr Glu Glu Tyr Ile Leu Ala Pro Ser Ser Arg Asp Leu
            20                  25                  30
Ala Pro Ala Ser Val Arg Gln Val Asn Gly Ser Val Thr Asn Ala Ala
        35                  40                  45
Ala Leu Thr Gly Ala Gly Gly Gln Ala Thr Phe Asn Gly Val Ser Ser
    50                  55                  60
Val Thr Tyr Asp Phe Gly Ile Asn Val Ala Gly Ile Val Ser Val Asp
65                  70                  75                  80
Val Ala Ser Ala Ser Ser Asp Ser Ala Phe Ile Gly Val Thr Phe Thr
                85                  90                  95
Glu Ser Ser Met Trp Ile Ser Ser Glu Ala Cys Asp Ala Thr Gln Asp
            100                 105                 110
Ala Gly Leu Asp Thr Pro Leu Trp Phe Ala Val Gly Gln Gly Ala Gly
        115                 120                 125
Leu Tyr Thr Val Glu Lys Lys Tyr Asn Arg Gly Ala Phe Arg Tyr Met
    130                 135                 140
Thr Val Val Ser Asn Thr Thr Ala Thr Val Ser Leu Asn Ser Val Lys
145                 150                 155                 160
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Ile Asn Tyr Thr Ala Ser Pro Thr Gln Asp Leu Arg Ala Tyr Thr Gly
                165                 170                 175
Tyr Phe His Ser Asn Asp Glu Leu Leu Asn Arg Ile Trp Tyr Ala Gly
            180                 185                 190
Ala Tyr Thr Leu Gln Leu Cys Ser Ile Asp Pro Thr Thr Gly Asp Ala
        195                 200                 205
Leu Val Gly Leu Gly Val Ile Thr Ser Ser Glu Thr Ile Ser Leu Pro
    210                 215                 220
Gln Thr Asp Lys Trp Trp Thr Asn Tyr Thr Ile Thr Asn Gly Ser Ser
225                 230                 235                 240
Thr Leu Thr Asp Gly Ala Lys Arg Asp Arg Leu Val Trp Pro Gly Asp
                245                 250                 255
Met Ser Ile Ala Leu Glu Ser Val Ala Val Ser Thr Glu Asp Leu Tyr
            260                 265                 270
Ser Val Arg Thr Ala Leu Glu Ser Leu Tyr Ala Leu Gln Lys Pro Asp
        275                 280                 285
Gly Arg Leu Pro Tyr Ala Gly Lys Pro Phe Phe Asp Thr Val Ser Phe
    290                 295                 300
Thr Tyr His Leu His Ser Leu Val Gly Ala Ala Ser Tyr Tyr Gln Tyr
305                 310                 315                 320
Thr Gly Asp Arg Ala Trp Leu Thr Arg Tyr Trp Gly Gln Tyr Lys Lys
                325                 330                 335
Gly Val Gln Trp Ala Leu Ser Ser Val Asp Ser Thr Gly Leu Ala Asn
            340                 345                 350
Ile Thr Ala Ser Ala Asp Trp Leu Arg Phe Gly Met Gly Ala His Asn
        355                 360                 365
Ile Glu Ala Asn Ala Ile Leu Tyr Tyr Val Leu Asn Asp Ala Ile Ser
    370                 375                 380
Leu Ala Gln Thr Leu Asn Asp Asn Ala Pro Ile Arg Asn Trp Thr Thr
385                 390                 395                 400
Thr Ala Ala Arg Ile Lys Thr Val Ala Asn Glu Leu Leu Trp Asp Asp
                405                 410                 415
Lys Asn Gly Leu Tyr Thr Asp Asn Glu Thr Thr Thr Leu His Pro Gln
            420                 425                 430
Asp Gly Asn Ser Trp Ala Val Lys Ala Asn Leu Thr Leu Ser Ala Asn
        435                 440                 445
Gln Ser Ala Ile Val Ser Glu Ser Leu Ala Ala Arg Trp Gly Pro Tyr
    450                 455                 460
Gly Ala Pro Ala Pro Glu Ala Gly Ala Thr Val Ser Pro Phe Ile Gly
465                 470                 475                 480
Gly Phe Glu Leu Gln Ala His Tyr Gln Ala Gly Gln Pro Asp Arg Ala
                485                 490                 495
Leu Asp Leu Leu Arg Leu Gln Trp Gly Phe Met Leu Asp Asp Pro Arg
            500                 505                 510
Met Thr Asn Ser Thr Phe Ile Glu Gly Tyr Ser Thr Asp Gly Ser Leu
        515                 520                 525
Ala Tyr Ala Pro Tyr Thr Asn Thr Pro Arg Val Ser His Ala His Gly
    530                 535                 540
Trp Ala Thr Gly Pro Thr Ser Ala Leu Thr Ile Tyr Thr Ala Gly Leu
545                 550                 555                 560
Arg Val Thr Gly Pro Ala Gly Ala Thr Trp Leu Tyr Lys Pro Gln Pro
                565                 570                 575
Gly Asn Leu Thr Gln Val Glu Ala Gly Phe Ser Thr Arg Leu Gly Ser
            580                 585                 590
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Phe Ala Ser Ser Phe Ser Arg Ser Gly Gly Arg Tyr Gln Glu Leu Ser
        595                 600                 605
Phe Ser Thr Pro Asn Gly Thr Thr Gly Ser Val Glu Leu Gly Asp Val
    610                 615                 620
Ser Gly Gln Leu Val Ser Asp Arg Gly Val Lys Val Gln Leu Val Gly
625                 630                 635                 640
Gly Lys Ala Ser Gly Leu Gln Gly Gly Lys Trp Lys Leu Ser Asn Asn
                645                 650                 655


<210> 278
<211> 587
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase XP_001400455.1

<400> 278
Met Ala Lys Ser Ala Ser Gln Ile His Arg Ala Trp Trp Lys Glu Cys
 1               5                  10                  15
Ser Val Tyr Gln Ile Trp Pro Ala Ser Tyr Lys Asp Ser Asn Asp Asp
            20                  25                  30
Gly Ile Gly Asp Ile Pro Gly Ile Ile Ser Lys Leu Asp Tyr Ile Lys
        35                  40                  45
Asn Ile Gly Val Asp Ile Val Trp Leu Cys Pro Ser Tyr Lys Ser Pro
    50                  55                  60
Gln Val Asp Met Gly Tyr Asp Ile Ala Asp Tyr Tyr Ser Ile Ala Asp
65                  70                  75                  80
Glu Tyr Gly Thr Val Ala Asp Val Glu Lys Leu Ile Gln Gly Cys His
                85                  90                  95
Glu Arg Gly Met Lys Leu Leu Met Asp Leu Val Val Asn His Thr Ser
            100                 105                 110
Asp Gln Asn Glu Trp Phe Lys Gln Ser Arg Ser Ser Lys Asp Asn Lys
        115                 120                 125
Tyr Arg Asn Trp Tyr Val Trp Lys Pro Ala Arg Tyr Asp Glu Gln Gly
    130                 135                 140
Asn Arg His Pro Pro Asn Asn Trp Val Ser His Phe Gln Gly Ser Ala
145                 150                 155                 160
Trp Glu Trp Asp Glu His Thr Gly Glu Tyr Tyr Leu His Leu Tyr Ala
                165                 170                 175
Thr Glu Gln Pro Asp Leu Asn Trp Glu His Pro Pro Val Arg Lys Ala
            180                 185                 190
Val His Asp Ile Met Arg Phe Trp Leu Asp Lys Gly Ala Asp Gly Phe
        195                 200                 205
Arg Met Asp Val Ile Asn Phe Ile Ser Lys Asp Gln Arg Phe Pro Asp
    210                 215                 220
Ala Pro Val Lys Asp Pro Arg Thr Pro Trp Gln Trp Gly Asp Lys Tyr
225                 230                 235                 240
Tyr Ala Asn Gly Pro Arg Leu His Glu Tyr Leu Gln Asp Leu Gly Lys
                245                 250                 255
Ile Leu Lys Glu Tyr Asp Ala Phe Ser Val Gly Glu Met Pro Phe Val
            260                 265                 270
Arg Asp Thr Glu Glu Val Leu Arg Ala Val Arg Tyr Asp Arg Asn Glu
```

```
        275                 280                 285
Ile Asn Met Ile Phe Asn Phe Glu His Val Asp Ile Asp His Gly Thr
    290                 295                 300
Tyr Asp Lys Phe Glu Pro Gly Ser Trp Lys Leu Thr Asp Leu Lys Ala
305                 310                 315                 320
Phe Phe Glu Thr Trp Gln Lys Phe Met Tyr Asn Asn Asp Gly Trp Asn
                325                 330                 335
Ala Leu Tyr Trp Glu Asn His Asp Gln Pro Arg Ser Ile Asp Arg Tyr
            340                 345                 350
Ala Gln Ala Lys Glu Glu Phe Arg Thr Glu Ala Gly Lys Met Leu Ala
        355                 360                 365
Thr Val Leu Ala Leu Gln Ser Gly Thr Pro Phe Val Tyr Gln Gly Gln
    370                 375                 380
Glu Ile Gly Met Arg Asn Val Pro Val Glu Trp Asp Met Asn Glu Tyr
385                 390                 395                 400
Lys Asp Ile Asp Cys Leu Asn His Trp His Arg Leu Leu Lys His Arg
                405                 410                 415
Pro Asp Asp Ile Glu Ala Gln Lys Ser Ala Arg Gln Glu Tyr Gln Lys
            420                 425                 430
Lys Ser Arg Asp Asn Gly Arg Thr Pro Val Gln Trp Ser Ser Ala Pro
        435                 440                 445
Asn Gly Gly Phe Thr Gly Pro Asn Ala Lys Pro Trp Met Ser Val Ser
    450                 455                 460
Pro Asp Tyr Val Arg Phe Asn Ala Glu Ala Gln Val Asn Asp Pro Asn
465                 470                 475                 480
Ser Ile Tyr His Tyr Trp Ala Ala Val Leu Gly Leu Arg Lys Lys Tyr
                485                 490                 495
Leu Asp Ile Phe Val Tyr Gly Asp Tyr Asp Leu Val Asp Lys Asp Ser
            500                 505                 510
Gln Glu Ile Phe Ala Tyr Ala Arg Gln Tyr Glu Asn Lys Lys Ala Leu
        515                 520                 525
Val Leu Thr Asn Trp Thr Glu Lys Thr Leu Glu Trp Asp Ala Thr Thr
    530                 535                 540
Asn Gly Val Lys Gly Val Lys Asp Val Leu Leu Asn Ser Tyr Glu Ser
545                 550                 555                 560
Ala Glu Ala Ala Lys Gly Arg Phe Ser Gly Gln Lys Trp Ser Leu Arg
                565                 570                 575
Pro Tyr Glu Ala Val Val Leu Leu Val Glu Ala
            580                 585
```

<210> 279
<211> 640
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase XP_001390530.1

<400> 279

```
Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
 1               5                  10                  15
Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
            20                  25                  30
```

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

```
Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly
465                 470                 475                 480
Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr
                485                 490                 495
Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr
            500                 505                 510
Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser Thr
        515                 520                 525
Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp
    530                 535                 540
Leu Thr Ala Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser
545                 550                 555                 560
Ile Ser Gln Leu Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser
                565                 570                 575
Ala Asp Lys Tyr Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr
            580                 585                 590
Leu Pro Ala Gly Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser
        595                 600                 605
Asp Asp Ser Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val
    610                 615                 620
Pro Gln Ala Cys Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
625                 630                 635                 640
```

<210> 280
<211> 957
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase XP_001393899.1

<400> 280

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

```
                165                 170                 175
Phe Ser Ala Asp Phe Lys Arg Asp Gly Gln Thr His Val Gln Leu Asn
            180                 185                 190
Asn Lys Gly Tyr Leu Asn Met Glu His Trp Arg Pro Lys Val Glu Val
        195                 200                 205
Glu Gly Glu Gly Glu Gln Gln Thr Gln Glu Asp Glu Ser Thr Trp Trp
    210                 215                 220
Asp Glu Ser Phe Gly Gly Asn Thr Asp Thr Lys Pro Arg Gly Pro Glu
225                 230                 235                 240
Ser Val Gly Leu Asp Ile Thr Phe Pro Gly Tyr Lys His Val Phe Gly
                245                 250                 255
Ile Pro Glu His Ala Asp Ser Leu Ser Leu Lys Glu Thr Arg Gly Gly
            260                 265                 270
Glu Gly Asn His Glu Glu Pro Tyr Arg Met Tyr Asn Ala Asp Val Phe
        275                 280                 285
Glu Tyr Glu Leu Ser Ser Pro Met Thr Leu Tyr Gly Ala Ile Pro Phe
    290                 295                 300
Met Gln Ala His Arg Lys Asp Ser Thr Val Gly Val Phe Trp Leu Asn
305                 310                 315                 320
Ala Ala Glu Thr Trp Val Asp Ile Val Lys Ser Thr Ser Ser Pro Asn
                325                 330                 335
Pro Leu Ala Leu Gly Val Gly Ala Thr Thr Asp Thr Gln Ser His Trp
            340                 345                 350
Phe Ser Glu Ser Gly Gln Leu Asp Val Phe Val Phe Leu Gly Pro Thr
        355                 360                 365
Pro Gln Glu Ile Ser Lys Thr Tyr Gly Glu Leu Thr Gly Tyr Thr Gln
    370                 375                 380
Leu Pro Gln His Phe Ala Ile Ala Tyr His Gln Cys Arg Trp Asn Tyr
385                 390                 395                 400
Ile Thr Asp Glu Asp Val Lys Glu Val Asp Arg Asn Phe Asp Lys Tyr
                405                 410                 415
Gln Ile Pro Tyr Asp Val Ile Trp Leu Asp Ile Glu Tyr Thr Asp Asp
            420                 425                 430
Arg Lys Tyr Phe Thr Trp Asp Pro Leu Ser Phe Pro Asp Pro Ile Ser
        435                 440                 445
Met Glu Glu Gln Leu Asp Glu Ser Glu Arg Lys Leu Val Val Ile Ile
    450                 455                 460
Asp Pro His Ile Lys Asn Gln Asp Lys Tyr Ser Ile Val Gln Glu Met
465                 470                 475                 480
Lys Ser Lys Asp Leu Ala Thr Lys Asn Lys Asp Gly Glu Ile Tyr Asp
                485                 490                 495
Gly Trp Cys Trp Pro Gly Ser Ser His Trp Ile Asp Thr Phe Asn Pro
            500                 505                 510
Ala Ala Ile Lys Trp Trp Val Ser Leu Phe Lys Phe Asp Lys Phe Lys
        515                 520                 525
Gly Thr Leu Ser Asn Val Phe Ile Trp Asn Asp Met Asn Glu Pro Ser
    530                 535                 540
Val Phe Asn Gly Pro Glu Thr Thr Met Pro Lys Asp Asn Leu His His
545                 550                 555                 560
Gly Asn Trp Glu His Arg Asp Ile His Asn Val His Gly Ile Thr Leu
                565                 570                 575
Val Asn Ala Thr Tyr Asp Ala Leu Leu Glu Arg Lys Lys Gly Glu Ile
            580                 585                 590
Arg Arg Pro Phe Ile Leu Thr Arg Ser Tyr Tyr Ala Gly Ala Gln Arg
```

```
        595                 600                 605
Met Ser Ala Met Trp Thr Gly Asp Asn Gln Ala Thr Trp Glu His Leu
    610                 615                 620
Ala Ala Ser Ile Pro Met Val Leu Asn Asn Gly Ile Ala Gly Phe Pro
625                 630                 635                 640
Phe Ala Gly Ala Asp Val Gly Gly Phe Phe Gln Asn Pro Ser Lys Glu
                645                 650                 655
Leu Leu Thr Arg Trp Tyr Gln Ala Gly Ile Trp Tyr Pro Phe Phe Arg
            660                 665                 670
Ala His Ala His Ile Asp Thr Arg Arg Arg Glu Pro Tyr Leu Ile Ala
        675                 680                 685
Glu Pro His Arg Ser Ile Ile Ser Gln Ala Ile Arg Leu Arg Tyr Gln
    690                 695                 700
Leu Leu Pro Ala Trp Tyr Thr Ala Phe His Glu Ala Ser Val Asn Gly
705                 710                 715                 720
Met Pro Ile Val Arg Pro Gln Tyr Tyr Ala His Pro Trp Asp Glu Ala
                725                 730                 735
Gly Phe Ala Ile Asp Asp Gln Leu Tyr Leu Gly Ser Thr Gly Leu Leu
            740                 745                 750
Ala Lys Pro Val Val Ser Glu Glu Ala Thr Thr Ala Asp Ile Tyr Leu
        755                 760                 765
Ala Asp Asp Glu Lys Tyr Tyr Asp Tyr Phe Asp Tyr Thr Val Tyr Gln
    770                 775                 780
Gly Ala Gly Lys Arg His Thr Val Pro Ala Pro Met Glu Thr Val Pro
785                 790                 795                 800
Leu Leu Met Gln Gly Gly His Val Ile Pro Arg Lys Asp Arg Pro Arg
                805                 810                 815
Arg Ser Ser Ala Leu Met Arg Trp Asp Pro Tyr Thr Leu Val Val Val
            820                 825                 830
Leu Asp Lys Asn Gly Gln Ala Asp Gly Ser Leu Tyr Val Asp Asp Gly
        835                 840                 845
Glu Thr Phe Asp Tyr Glu Arg Gly Ala Tyr Ile His Arg Arg Phe Arg
    850                 855                 860
Phe Gln Glu Ser Ala Leu Val Ser Glu Asp Val Gly Thr Lys Gly Pro
865                 870                 875                 880
Lys Thr Ala Glu Tyr Leu Lys Thr Met Ala Asn Val Arg Val Glu Arg
                885                 890                 895
Val Val Val Val Asp Pro Pro Lys Glu Trp Gln Gly Lys Thr Ser Val
            900                 905                 910
Thr Val Ile Glu Asp Gly Ala Ser Ala Ala Ser Thr Ala Ser Met Gln
        915                 920                 925
Tyr His Ser Gln Pro Asp Gly Lys Ala Ala Tyr Ala Val Val Lys Asn
    930                 935                 940
Pro Asn Val Gly Ile Gly Lys Thr Trp Arg Ile Glu Phe
945                 950                 955
```

<210> 281
<211> 847
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase XP_001399012.1

<400> 281
Met Pro Gln Lys Glu Phe Val Pro Lys Thr Tyr Gln Glu Ser Ser Thr
 1               5                  10                  15
Gly Ala Gln Ser Ser Ser Ser Val His Leu Arg Ser Ser Pro Glu Glu
            20                  25                  30
Arg Ser Phe Asp Phe Ser Phe Glu Pro Ile Arg Glu Asn Leu Phe Arg
        35                  40                  45
Val Thr Phe Ser Ser Gln Asp His Pro Leu Pro Pro Tyr Pro Ser Val
    50                  55                  60
Thr Lys Pro Ala Thr Ser Leu Asp Gly Val His Val Ser Ala Thr Gly
65                  70                  75                  80
Gly Ser Asn Gln Lys Thr Ile Glu Val Gly Asp Val Thr Ala Ser Val
                85                  90                  95
Glu Trp Ser Asn Thr Pro Val Val Ser Leu Ser Trp Lys Gly Thr Glu
            100                 105                 110
Lys Pro Leu Tyr Arg Asp Leu Pro Leu Arg Ser Tyr Val Ala Asp Ser
        115                 120                 125
Thr Gly Ile Ala His Tyr Thr Glu His Asp Arg Asp Cys Leu His Val
    130                 135                 140
Gly Leu Gly Glu Lys Arg Ala Pro Met Asp Leu Thr Gly Arg His Phe
145                 150                 155                 160
Gln Leu Ser Ala Thr Asp Ser Phe Gly Tyr Asp Val Tyr Asn Thr Asp
                165                 170                 175
Pro Leu Tyr Lys His Ile Pro Leu Leu Ile Lys Ala Ser Pro Asp Gly
            180                 185                 190
Cys Val Ala Ile Phe Ser Thr Thr His Gly Arg Gly Thr Trp Ser Val
        195                 200                 205
Gly Ser Glu Val Asp Gly Leu Trp Gly His Phe Lys Val Tyr Arg Gln
    210                 215                 220
Asp Tyr Gly Gly Leu Glu Gln Tyr Leu Ile Val Gly Lys Thr Leu Lys
225                 230                 235                 240
Asp Val Val Arg Ser Tyr Ala Glu Leu Val Gly Leu Pro Ile Leu Val
                245                 250                 255
Pro Arg Trp Ala Tyr Gly Tyr Ile Ser Gly Gly Tyr Lys Tyr Thr Met
            260                 265                 270
Leu Asp Asp Pro Pro Ala His Glu Ala Leu Met Glu Phe Ala Asp Lys
        275                 280                 285
Leu Glu Glu His Gly Ile Pro Cys Ser Ala His Gln Met Ser Ser Gly
    290                 295                 300
Tyr Ser Ile Ala Glu Thr Glu Pro Lys Val Arg Asn Val Phe Thr Trp
305                 310                 315                 320
Asn Lys Tyr Arg Phe Pro Asn Pro Glu Glu Trp Ile Ala Lys Tyr His
                325                 330                 335
Gly Arg Gly Ile Arg Leu Leu Ser Asn Ile Lys Pro Phe Leu Leu Ala
            340                 345                 350
Ser His Pro Asp Phe Gln Lys Leu Ile Asp Gly Asn Gly Phe Phe Lys
        355                 360                 365
Asp Pro Glu Ser Ser Lys Pro Gly Tyr Met Arg Leu Trp Ser Ala Gly
    370                 375                 380
Gly Ala Thr Gly Gly Asp Gly Cys His Ile Asp Phe Ser Ser Ala Val
385                 390                 395                 400
Ala Phe Lys Trp Trp Tyr Asp Gly Val Gln Ser Leu Lys Arg Ala Gly
                405                 410                 415

```
Ile Asp Ala Met Trp Asn Asp Asn Asn Glu Tyr Thr Leu Pro Asp Asp
            420                 425                 430
Asp Trp Lys Leu Ala Leu Asp Glu Pro Thr Val Ser Asp Ala Val Lys
        435                 440                 445
Lys Gly Val Glu Asn Ser Val Gly Gln Trp Gly Arg Ala Met His Thr
    450                 455                 460
Glu Leu Met Gly Lys Ala Ser His Asp Ala Leu Leu Asn Ile Glu Pro
465                 470                 475                 480
Asn His Arg Pro Phe Val Leu Thr Arg Ser Ala Thr Ala Gly Thr Met
                485                 490                 495
Arg Tyr Ala Ala Ser Thr Trp Ser Gly Asp Asn Val Thr Ser Trp Glu
            500                 505                 510
Gly Met Lys Gly Ala Asn Ala Leu Ser Leu Ser Ala Gly Ile Ser Leu
        515                 520                 525
Leu Gln Cys Cys Gly His Asp Ile Gly Gly Phe Glu Gly Pro Gln Pro
    530                 535                 540
Ser Pro Glu Leu Leu Leu Arg Trp Ile Gln Leu Gly Ile His Ser Pro
545                 550                 555                 560
Arg Phe Ala Ile Asn Cys Phe Lys Thr Ser Pro Gly Asn Ser Ser Val
                565                 570                 575
Gly Asp Val Ile Glu Pro Trp Met Tyr Pro Glu Ile Thr Pro Leu Val
            580                 585                 590
Arg Asp Thr Ile Lys Arg Arg Tyr Glu Ile Leu Pro Tyr Ile Tyr Ser
        595                 600                 605
Leu Gly Leu Glu Ser His Leu Thr Ala Ser Pro Pro Gln Arg Trp Val
    610                 615                 620
Gly Trp Gly Tyr Glu Ser Asp Pro Glu Val Trp Thr Lys Ala Leu Lys
625                 630                 635                 640
Ser Gly Asp Glu Gln Phe Trp Phe Gly Asp Thr Ile Met Val Gly Gly
                645                 650                 655
Val Tyr Glu Pro Gly Val Ser Val Ala Lys Leu Tyr Leu Pro Arg Lys
            660                 665                 670
Ala Asn Asp Gln Phe Asp Phe Gly Tyr Val Asn Met Asn Glu Pro Tyr
        675                 680                 685
Asn Tyr Leu Ala Ser Gly Gln Trp Val Glu Val Pro Ser Glu Trp Arg
    690                 695                 700
Lys Ser Ile Pro Leu Leu Ala Arg Ile Gly Gly Ala Ile Pro Val Gly
705                 710                 715                 720
Lys Pro Val His Thr Arg Val Pro Gly Asp Asp Thr Pro Ala Ser Val
                725                 730                 735
Ala Val Lys Glu Val Asp Asp Tyr Arg Gly Val Glu Ile Phe Pro Pro
            740                 745                 750
Leu Gly Ser Ser His Gly Gln Val Phe Ser Thr Thr Trp Phe Glu Asp
        755                 760                 765
Asp Gly Ile Ser Leu Glu Ala Arg Ile Ser Glu Tyr Thr Val Thr Tyr
    770                 775                 780
Ser Ser Thr Glu Glu Lys Val Ile Val Gly Phe Ser Arg Asp Glu Lys
785                 790                 795                 800
Ser Gly Phe Val Pro Ala Trp Thr Asp Leu Asp Ile Ile Leu His Asn
                805                 810                 815
Gly Asp Glu Arg Arg Val Val Ser Asp Ile Gly Lys Thr Val Glu Tyr
            820                 825                 830
Lys Gly Lys Gly Ser Arg Gly Arg Val Val Tyr Thr Leu Lys Asn
        835                 840                 845
```

<210> 282
<211> 985
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase XP_001402053.1

<400> 282
Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
 1               5                  10                  15
Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
            20                  25                  30
Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
        35                  40                  45
Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
    50                  55                  60
Gly Tyr Lys Ala Ser Lys Val Gln His Asn Ser Arg Gly Phe Thr Ala
65                  70                  75                  80
Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
                85                  90                  95
Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
            100                 105                 110
Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
        115                 120                 125
Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
    130                 135                 140
Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
145                 150                 155                 160
Phe Asn Phe Lys Val Ile Arg Lys Ala Thr Gly Asp Ala Leu Phe Ser
                165                 170                 175
Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
            180                 185                 190
Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
        195                 200                 205
Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
    210                 215                 220
Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
225                 230                 235                 240
Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
                245                 250                 255
Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
            260                 265                 270
Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
        275                 280                 285
Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
    290                 295                 300
Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
305                 310                 315                 320
Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
                325                 330                 335
Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Asp Leu Ala

```
            340                 345                 350
Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
        355                 360                 365
Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
    370                 375                 380
Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
385                 390                 395                 400
His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
                405                 410                 415
Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
            420                 425                 430
Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
        435                 440                 445
Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
    450                 455                 460
Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
465                 470                 475                 480
Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
                485                 490                 495
Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
            500                 505                 510
His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
        515                 520                 525
Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
    530                 535                 540
Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
545                 550                 555                 560
Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
                565                 570                 575
Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
            580                 585                 590
Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
        595                 600                 605
Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
    610                 615                 620
Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
625                 630                 635                 640
Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
                645                 650                 655
Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
            660                 665                 670
Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
        675                 680                 685
Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
    690                 695                 700
Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
705                 710                 715                 720
Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
                725                 730                 735
Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
            740                 745                 750
Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
        755                 760                 765
Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
```

```
    770                 775                 780
Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
785                 790                 795                 800
Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
                805                 810                 815
Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
            820                 825                 830
Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
        835                 840                 845
Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
    850                 855                 860
Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865                 870                 875                 880
Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
                885                 890                 895
Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
            900                 905                 910
Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
        915                 920                 925
Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
    930                 935                 940
Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945                 950                 955                 960
Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
                965                 970                 975
Trp Ala Glu Asn Trp Val Leu Glu Trp
            980                 985


<210> 283
<211> 416
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase A2RAR6.1

<400> 283
Met Phe Val Glu Ser Ala Lys Lys Ala Leu Leu Ala Leu Ser Leu Leu
 1               5                  10                  15
Ala Ala Ser Ala Gln Ala Val Pro Arg Val Arg Arg Gln Gly Ala Ser
            20                  25                  30
Ser Ser Phe Asp Tyr Lys Ser Gln Ile Val Arg Gly Val Asn Leu Gly
        35                  40                  45
Gly Trp Leu Val Thr Glu Pro Trp Ile Thr Pro Ser Leu Tyr Asp Ser
    50                  55                  60
Thr Gly Gly Gly Ala Val Asp Glu Trp Thr Leu Cys Gln Ile Leu Gly
65                  70                  75                  80
Lys Asp Glu Ala Gln Ala Lys Leu Ser Ser His Trp Ser Ser Phe Ile
                85                  90                  95
Thr Gln Ser Asp Phe Asp Arg Met Ala Gln Ala Gly Leu Asn His Val
            100                 105                 110
Arg Ile Pro Ile Gly Tyr Trp Ala Val Ala Pro Ile Asp Gly Glu Pro
        115                 120                 125
```

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

<210> 284
<211> 830
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase A2QX52.1

<400> 284

```
Met Pro Gly His Ser Arg Ser Arg Asp Arg Leu Ser Pro Ser Ser Glu
 1               5                  10                  15
Leu Asp Asp Ala Asp Pro Val Tyr Ser Pro Ser Val Tyr Gln Arg Glu
            20                  25                  30
His Tyr Tyr Asn Asn Asp Ser Leu Phe Asp Ser Ala Asp Asp Asp Tyr
        35                  40                  45
Thr Arg Thr Pro Arg Asn Val Tyr Ser Tyr Glu Thr His Asp Glu Tyr
```

```
    50                  55                  60
His Asp Asp Asp Asp Asp Asp Asp Asp Val His Glu His Asp His Asp
65                  70                  75                  80
His Glu Tyr Asp Asp Lys Phe Glu Glu Pro Trp Val Pro Leu Arg Ala
                85                  90                  95
Gln Val Glu Gly Asp Gln Trp Arg Glu Gly Phe Glu Thr Ala Ile Pro
            100                 105                 110
Lys Glu Glu Asp Val Thr Gln Ala Lys Glu Tyr Gln Tyr Gln Met Ser
        115                 120                 125
Gly Ala Leu Gly Asp Asp Gly Pro Pro Pro Leu Pro Ser Asp Ala Leu
    130                 135                 140
Gly Arg Gly Lys Gly Lys Lys Arg Leu Asp Arg Glu Thr Arg Arg Gln
145                 150                 155                 160
Arg Arg Lys Glu Arg Leu Ala Ala Phe Phe Lys His Lys Asn Gly Ser
                165                 170                 175
Ala Ser Ala Gly Leu Val Ser Gly Asp Ala Leu Ala Lys Leu Leu Gly
            180                 185                 190
Ser Gln Asp Gly Asp Glu Asp Cys Leu Ser His Leu Gly Thr Glu Arg
        195                 200                 205
Ala Asp Ser Met Ser Gln Lys Asn Leu Glu Gly Gly Arg Gln Arg Lys
    210                 215                 220
Leu Pro Val Leu Ser Glu Glu Pro Met Met Leu Arg Pro Phe Pro Ala
225                 230                 235                 240
Val Ala Pro Thr Gly Gln Thr Gln Gly Arg Val Val Ser Gly Ala Gln
                245                 250                 255
Leu Glu Glu Gly Gly Pro Gly Met Glu Met Arg His Arg Gly Gly Gly
            260                 265                 270
Gly Pro Pro Ala Glu Gly Leu Leu Gln Lys Glu Gly Asp Trp Asp Gly
        275                 280                 285
Ser Thr Lys Gly Ser Ser Thr Ser Ala Arg Pro Ser Phe Trp Lys Arg
    290                 295                 300
Tyr His Lys Thr Phe Ile Phe Phe Ala Ile Leu Ile Val Leu Ala Ala
305                 310                 315                 320
Ile Ala Ile Pro Val Gly Ile Ile Glu Ala Arg Arg Leu His Gly Thr
                325                 330                 335
Ser Gly Gly Asp Asn Ser Ser Asn Ser Asn Leu Lys Gly Ile Ser Arg
            340                 345                 350
Asp Ser Ile Pro Ala Tyr Ala Arg Gly Thr Tyr Leu Asp Pro Phe Thr
        355                 360                 365
Trp Tyr Asp Thr Thr Asp Phe Asn Val Thr Phe Thr Asn Ala Thr Val
    370                 375                 380
Gly Gly Leu Ser Ile Met Gly Leu Asn Ser Thr Trp Asn Asp Ser Ala
385                 390                 395                 400
Gln Ala Asn Glu Asn Val Pro Pro Leu Asn Glu Lys Phe Pro Tyr Gly
                405                 410                 415
Ser Gln Pro Ile Arg Gly Val Asn Leu Gly Gly Trp Leu Ser Ile Glu
            420                 425                 430
Pro Phe Ile Val Pro Ser Leu Phe Asp Thr Tyr Thr Ser Ser Glu Gly
        435                 440                 445
Ile Ile Asp Glu Trp Thr Leu Ser Glu Lys Leu Gly Asp Ser Ala Ala
    450                 455                 460
Ser Val Ile Glu Lys His Tyr Ala Thr Phe Ile Thr Glu Gln Asp Phe
465                 470                 475                 480
Ala Asp Ile Arg Asp Ala Gly Leu Asp His Val Arg Ile Gln Phe Ser
```

```
                485                 490                 495
Tyr Trp Ala Ile Lys Thr Tyr Asp Gly Asp Pro Tyr Val Pro Lys Ile
            500                 505                 510
Ala Trp Arg Tyr Leu Leu Arg Ala Ile Glu Tyr Cys Arg Lys Tyr Gly
        515                 520                 525
Leu Arg Val Asn Leu Asp Pro His Gly Ile Pro Gly Ser Gln Asn Gly
    530                 535                 540
Trp Asn His Ser Gly Arg Gln Gly Thr Ile Gly Trp Leu Asn Gly Thr
545                 550                 555                 560
Asp Gly Glu Leu Asn Arg Gln Arg Ser Leu Glu Met His Asp Gln Leu
                565                 570                 575
Ser Gln Phe Phe Ala Gln Asp Arg Tyr Lys Asn Val Val Thr Ile Tyr
            580                 585                 590
Gly Leu Val Asn Glu Pro Leu Met Leu Ser Leu Pro Val Glu Lys Val
        595                 600                 605
Leu Asn Trp Thr Thr Glu Ala Thr Asn Leu Val Gln Lys Asn Gly Ile
    610                 615                 620
Lys Ala Trp Val Thr Val His Asp Gly Phe Leu Asn Leu Asp Lys Trp
625                 630                 635                 640
Asp Lys Met Leu Lys Thr Arg Pro Ser Asn Met Met Leu Asp Thr His
                645                 650                 655
Gln Tyr Thr Val Phe Asn Thr Gly Glu Ile Val Leu Asn His Thr Arg
            660                 665                 670
Arg Val Glu Leu Ile Cys Glu Ser Trp Tyr Ser Met Ile Gln Gln Ile
        675                 680                 685
Asn Ile Thr Ser Thr Gly Trp Gly Pro Thr Ile Cys Gly Glu Trp Ser
    690                 695                 700
Gln Ala Asp Thr Asp Cys Ala Gln Tyr Val Asn Asn Val Gly Arg Gly
705                 710                 715                 720
Thr Arg Trp Glu Gly Thr Phe Ser Leu Thr Asp Ser Thr Gln Tyr Cys
                725                 730                 735
Pro Thr Ala Ser Glu Gly Thr Cys Ser Cys Thr Gln Ala Asn Ala Val
            740                 745                 750
Pro Gly Val Tyr Ser Glu Gly Tyr Lys Thr Phe Leu Gln Thr Tyr Ala
        755                 760                 765
Glu Ala Gln Met Ser Ala Phe Glu Ser Ala Met Gly Trp Phe Tyr Trp
    770                 775                 780
Thr Trp Ala Thr Glu Ser Ala Ala Gln Trp Ser Tyr Arg Thr Ala Trp
785                 790                 795                 800
Lys Asn Gly Tyr Met Pro Lys Lys Ala Tyr Ser Pro Ser Phe Lys Cys
                805                 810                 815
Gly Asp Thr Ile Pro Ser Phe Gly Asn Leu Pro Glu Tyr Tyr
            820                 825                 830
```

<210> 285
<211> 2042
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase XP_001389036.2

<400> 285

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

```
Phe Asn Arg Ile Lys Tyr Leu Arg Ile Asp Asp His Gly Pro Lys Leu
        435                 440                 445
Gly Ala Val Thr Ala Gln Ser Pro Leu Ile Glu Thr Tyr Phe Thr Arg
    450                 455                 460
Leu Pro Leu Asn Asp Val Thr Lys Lys His Lys Lys Glu Ala Leu Ala
465                 470                 475                 480
Leu Val Asn Asn Gly Trp Ile Trp Asn Ala Asp Ala Leu Arg Asp Asn
                485                 490                 495
Ala Gly Pro Asp Ser Arg Ala Tyr Leu Arg Arg Glu Val Ile Val Trp
            500                 505                 510
Gly Asp Cys Val Lys Leu Arg Tyr Gly Ser Cys Arg Asp Asp Asn Pro
        515                 520                 525
Phe Leu Trp Asp Phe Met Thr Asp Tyr Thr Arg Leu Met Ala Lys Tyr
    530                 535                 540
Phe Ser Gly Phe Arg Ile Asp Asn Cys His Ser Thr Pro Leu Val Val
545                 550                 555                 560
Ala Glu Tyr Leu Leu Asp Glu Ala Arg Lys Val Arg Pro Asn Leu Thr
                565                 570                 575
Val Phe Ala Glu Leu Phe Thr Gly Ser Glu Glu Ala Asp Tyr Ile Phe
            580                 585                 590
Val Lys Arg Leu Gly Ile Asn Ala Leu Ile Arg Glu Ala Met Gln Ala
        595                 600                 605
Trp Ser Thr Gly Glu Leu Ser Arg Leu Val His Arg His Gly Gly Arg
    610                 615                 620
Pro Ile Gly Ser Phe Asp Leu Asp Leu Pro Ser Ser Gly Ser Ser His
625                 630                 635                 640
Ala Ile Ala Ser Ser Gly Leu Asp Ser Gly Lys Glu Lys Val Val His
                645                 650                 655
Ile Arg Pro Thr Pro Val Gln Ala Leu Phe Met Asp Cys Thr His Asp
            660                 665                 670
Asn Glu Met Pro Ala Gln Lys Arg Thr Ala Lys Asp Thr Leu Pro Asn
        675                 680                 685
Gly Ala Leu Val Ala Met Cys Ala Ser Ala Ile Gly Ser Val Ile Gly
    690                 695                 700
Tyr Asp Glu Val Tyr Pro Arg Leu Val Asp Leu Val His Glu His Arg
705                 710                 715                 720
Leu Tyr Phe Ser Glu Phe Ser Glu Ala Pro Glu Thr Gly Leu Asn Ser
                725                 730                 735
Leu Glu Gly Gly Ile Gly Gly Ile Lys Lys Leu Leu Asn Glu Leu His
            740                 745                 750
Thr Lys Met Gly Ile Glu Gly Tyr Asp Glu Thr His Ile His His Asp
        755                 760                 765
Gly Glu Tyr Ile Thr Val His Arg Val His Pro Arg Thr Arg Lys Gly
    770                 775                 780
Val Phe Leu Ile Ala His Thr Ala Phe Pro Gly Gln Asp Ser Arg Ser
785                 790                 795                 800
Val Leu Ala Pro Thr His Leu Val Gly Thr Gln Val Lys His Ile Gly
                805                 810                 815
Thr Trp Leu Leu Glu Val Asp Thr Ser Gln Thr Thr Lys Glu Arg Ile
            820                 825                 830
Gln Ala Asp Lys Ser Tyr Leu Arg Gly Leu Pro Ser Gln Val Lys Thr
        835                 840                 845
Phe Glu Gly Thr Lys Ile Glu Glu Ser Gly Lys Asp Thr Ile Ile Ser
    850                 855                 860
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Val Leu Asn Ser Phe Val Ala Gly Ser Ile Ala Leu Phe Glu Thr Ser
865                 870                 875                 880
Met Pro Ser Val Glu His Ala Ser Gly Leu Asp Asn Tyr Ile Thr Glu
                885                 890                 895
Gly Val Asp His Ala Phe Ser Asp Leu Ser Leu Val Asp Leu Asn Phe
            900                 905                 910
Ala Leu Tyr Arg Cys Glu Ala Glu Glu Arg Asp Ser Ser Lys Gly Gln
        915                 920                 925
Asp Gly Ala Tyr Asp Ile Pro Gly His Gly Pro Leu Val Tyr Ala Gly
    930                 935                 940
Leu Gln Gly Trp Trp Ser Val Leu Glu Asn Ile Ile Lys Tyr Asn Glu
945                 950                 955                 960
Leu Gly His Pro Leu Cys Asp His Leu Arg Asn Gly Gln Trp Ala Leu
                965                 970                 975
Asp Tyr Ile Val Ala Arg Leu Glu Lys Leu Ser His Lys Glu Glu His
            980                 985                 990
Pro Ala Leu Gly Arg Pro Ala Ala Trp Leu Gln Glu Lys Phe Gln Ala
        995                 1000                1005
Val Arg Gln Leu Pro Ser Phe Leu Leu Pro Arg Tyr Phe Ala Ile Ile
    1010                1015                1020
Val Gln Val Ala Tyr Asn Ala Ala Trp Lys Arg Gly Ile Gln Leu Leu
1025                1030                1035                1040
Gly Pro His Ile Gln Lys Gly Gln Glu Phe Ile His Gln Leu Gly Met
                1045                1050                1055
Val Ser Val Gln Gln Thr Gly Tyr Val Asn Ser Ala Ser Leu Trp Pro
            1060                1065                1070
Thr Lys Lys Val Pro Ser Leu Ala Ala Gly Leu Pro His Phe Ala Val
        1075                1080                1085
Asp Trp Ala Arg Cys Trp Gly Arg Asp Val Phe Ile Ser Leu Arg Gly
    1090                1095                1100
Leu Leu Leu Cys Thr Gly Arg Phe Glu Asp Ala Lys Glu His Ile Thr
1105                1110                1115                1120
Ala Phe Ala Ser Val Leu Lys His Gly Met Ile Pro Asn Leu Leu Ser
                1125                1130                1135
Ser Gly Lys Leu Pro Arg Tyr Asn Ser Arg Asp Ser Val Trp Phe Phe
            1140                1145                1150
Leu Gln Ser Ile Gln Asp Tyr Thr Glu Met Ala Pro Asp Gly Leu Glu
        1155                1160                1165
Ile Leu Asp His Lys Val Pro Arg Arg Phe Leu Pro Tyr Asp Asp Val
    1170                1175                1180
Trp Phe Pro Phe Asp Asp Pro Arg Ala Tyr Ser Gln Gln Ser Thr Ile
1185                1190                1195                1200
Ser Glu Ile Ile Gln Glu Val Phe Gln Arg His Ala Gln Gly Leu Ser
                1205                1210                1215
Phe Arg Glu Tyr Asn Ala Gly Pro Asp Leu Asp Met Gln Met Thr Gln
            1220                1225                1230
Asp Gly Phe Gln Ile Asp Val Lys Val Asp Trp Glu Thr Gly Leu Ile
        1235                1240                1245
Phe Gly Gly Ser Gln Tyr Asn Cys Gly Thr Trp Gln Asp Lys Met Gly
    1250                1255                1260
Glu Ser Ala Lys Ala Gly Asn Lys Gly Val Pro Gly Thr Pro Arg Asp
1265                1270                1275                1280
Gly Ala Ala Ile Glu Ile Thr Gly Leu Val Tyr Ser Ala Leu Thr Trp
                1285                1290                1295
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Val Ala Lys Leu His Glu Arg Gly Ile Tyr Lys His Asp Gly Val Asp
            1300                1305                1310
Ile Gly Gly Gly Lys Ser Ile Ser Phe Glu Asp Trp Ala Ser Arg Ile
        1315                1320                1325
Arg Ala Asn Phe Glu Arg Cys Tyr Tyr Val Pro Leu Gln Pro Lys Asp
    1330                1335                1340
Asp Gly Gln Tyr Asp Ile Asp Ala Asn Ile Ile Asn Arg Arg Gly Ile
1345                1350                1355                1360
Tyr Lys Asp Leu Tyr Arg Ser Gly Lys Pro Tyr Glu Asp Tyr Gln Leu
                1365                1370                1375
Arg Ser Asn Phe Pro Ile Ala Met Thr Val Ala Pro Asp Leu Phe Thr
            1380                1385                1390
Ala Ser Lys Ala Leu Ala Ala Leu Ala Leu Ala Asp Glu Val Leu Val
        1395                1400                1405
Gly Pro Val Gly Met Ala Thr Leu Asp Pro Ser Asp Leu Asn Tyr Arg
    1410                1415                1420
Pro Asn Tyr Asn Asn Ser Glu Asp Ser Thr Asp Phe Ala Thr Ala Lys
1425                1430                1435                1440
Gly Arg Asn Tyr His Gln Gly Pro Glu Trp Val Trp Gln Arg Gly Tyr
                1445                1450                1455
Phe Leu Arg Ala Phe Leu His Phe Asp Leu Ala Arg Arg Thr Thr Pro
            1460                1465                1470
Ala Glu Arg Thr Glu Thr Tyr Gln Gln Ile Thr Arg Arg Leu Glu Gly
        1475                1480                1485
Cys Lys Arg Ala Leu Arg Glu Ser Pro Trp Lys Gly Leu Thr Glu Leu
    1490                1495                1500
Thr Asn Lys Asn Gly Ala Tyr Cys Ala Asp Ser Ser Pro Thr Gln Ala
1505                1510                1515                1520
Trp Ser Ala Gly Cys Leu Leu Asp Leu Tyr Tyr Asp Ala Ser Arg His
                1525                1530                1535
Ser Gln Met Arg Ile Trp Tyr Gly Pro Phe Lys Leu Arg Tyr Lys Asn
            1540                1545                1550
Ile Asp Ala Ile Asp Tyr Tyr Glu Glu Lys Leu Arg Arg Leu Asp Glu
        1555                1560                1565
Lys Ile Gln Val Ala Arg Gln Lys Glu Tyr Pro Pro Thr Glu Val Ala
    1570                1575                1580
Phe Val Thr Met Glu Ser Ile Ala Ala Ser Gln Met Val Val Gln Ala
1585                1590                1595                1600
Ile Leu Asp Pro His Pro Met Gln Leu Leu Ala Arg Leu Ala Pro Ala
                1605                1610                1615
Pro Ala Asp Val Val Trp Lys Asn Thr Tyr Leu Pro Arg Ser Arg Arg
            1620                1625                1630
Met Met Gln Ser Trp Phe Ile Thr Val Val Ile Gly Phe Leu Thr Val
        1635                1640                1645
Phe Trp Ser Val Leu Leu Ile Pro Val Ala Tyr Leu Leu Glu Tyr Glu
    1650                1655                1660
Thr Leu His Lys Val Phe Pro Gln Leu Ala Asp Ala Leu Ala Arg Asn
1665                1670                1675                1680
Pro Leu Ala Lys Ser Leu Val Gln Thr Gly Leu Pro Thr Leu Val Leu
                1685                1690                1695
Ser Leu Leu Thr Val Ala Val Pro Tyr Leu Tyr Asn Trp Leu Ser Asn
            1700                1705                1710
Gln Gln Gly Met Met Ser Arg Gly Asp Ile Glu Leu Ser Val Ile Ser
        1715                1720                1725
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Lys Thr Phe Phe Phe Ser Phe Phe Asn Leu Phe Leu Val Phe Thr Val
    1730                1735                1740
Phe Gly Thr Ala Thr Thr Phe Tyr Gly Phe Trp Glu Asn Leu Arg Asp
1745                1750                1755                1760
Ala Phe Lys Asp Ala Thr Thr Ile Ala Phe Ala Leu Ala Lys Thr Leu
                1765                1770                1775
Glu Asn Phe Ala Pro Phe Tyr Ile Asn Phe Leu Cys Leu Gln Gly Ile
            1780                1785                1790
Gly Leu Phe Pro Phe Arg Leu Leu Glu Phe Gly Ser Val Ala Met Tyr
        1795                1800                1805
Pro Ile Asn Phe Leu Ala Ala Lys Thr Pro Arg Asp Tyr Ala Glu Leu
    1810                1815                1820
Ser Thr Pro Pro Thr Phe Ser Tyr Gly Tyr Ser Ile Pro Gln Thr Val
1825                1830                1835                1840
Leu Ser Leu Ile Ile Cys Val Val Tyr Ser Val Phe Pro Ser Ser Trp
                1845                1850                1855
Leu Ile Cys Leu Phe Gly Leu Ile Tyr Phe Thr Ile Gly Lys Phe Ile
            1860                1865                1870
Tyr Lys Tyr Gln Leu Leu Tyr Ala Met Asp His Gln Gln His Ser Thr
        1875                1880                1885
Gly Arg Ala Trp Pro Met Ile Cys Ser Arg Ile Leu Met Gly Leu Met
    1890                1895                1900
Val Phe Gln Leu Ala Met Ile Gly Val Leu Ala Leu Arg Arg Ala Ile
1905                1910                1915                1920
Thr Arg Ser Leu Leu Ile Val Pro Leu Leu Met Ala Thr Val Trp Phe
                1925                1930                1935
Ser Tyr Phe Phe Ala Arg Thr Tyr Glu Pro Leu Met Lys Phe Ile Ala
            1940                1945                1950
Leu Lys Ser Ile Asp Arg Glu Arg Pro Gly Gly Gly Asp Ile Ser Pro
        1955                1960                1965
Ser Pro Ser Ser Thr Phe Ser Pro Pro Ser Gly Leu Asp Arg Asp Ser
    1970                1975                1980
Phe Pro Ile Arg Ile Gly Gly Gln Glu Leu Gly Leu Arg Leu Arg Lys
1985                1990                1995                2000
Tyr Val Asn Pro Ser Leu Ile Leu Pro Leu His Asp Ala Trp Leu Pro
                2005                2010                2015
Gly Arg Thr Met Val Pro Glu Leu Gln Gly Glu Leu Glu His Arg Asn
            2020                2025                2030
Pro Gly Asn Asn Ala Ala Asp Glu Ser Val
        2035                2040


<210> 286
<211> 866
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase XP_001389510.2

<400> 286
Met Leu Gly Ser Leu Leu Leu Leu Leu Pro Leu Val Gly Ala Ala Val
 1               5                  10                  15
Ile Gly Pro Arg Ala Asn Ser Gln Ser Cys Pro Gly Tyr Lys Ala Ser
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            20                  25                  30
Asn Val Gln Lys Gln Ala Arg Ser Leu Thr Ala Asp Leu Thr Leu Ala
        35                  40                  45
Gly Thr Pro Cys Asn Ser Tyr Gly Lys Asp Leu Glu Asp Leu Lys Leu
    50                  55                  60
Leu Val Glu Tyr Gln Thr Asp Glu Arg Leu His Val Met Ile Tyr Asp
65                  70                  75                  80
Ala Asp Glu Glu Val Tyr Gln Val Pro Glu Ser Val Leu Pro Arg Val
                85                  90                  95
Gly Ser Asp Glu Asp Ser Glu Asp Ser Val Leu Glu Phe Asp Tyr Val
            100                 105                 110
Glu Glu Pro Phe Ser Phe Thr Ile Ser Lys Gly Asp Glu Val Leu Phe
        115                 120                 125
Asp Ser Ser Ala Ser Pro Leu Val Phe Gln Ser Gln Tyr Val Asn Leu
    130                 135                 140
Arg Thr Trp Leu Pro Asp Asp Pro Tyr Val Tyr Gly Leu Gly Glu His
145                 150                 155                 160
Ser Asp Pro Met Arg Leu Pro Thr Tyr Asn Tyr Thr Arg Thr Leu Trp
                165                 170                 175
Asn Arg Asp Ala Tyr Gly Thr Pro Asn Asn Thr Asn Leu Tyr Gly Ser
            180                 185                 190
His Pro Val Tyr Tyr Asp His Arg Gly Lys Ser Gly Thr Tyr Gly Val
        195                 200                 205
Phe Leu Leu Asn Ser Asn Gly Met Asp Ile Lys Ile Asn Gln Thr Thr
    210                 215                 220
Asp Gly Lys Gln Tyr Leu Glu Tyr Asn Leu Leu Gly Gly Val Leu Asp
225                 230                 235                 240
Phe Tyr Phe Phe Tyr Gly Glu Asp Pro Lys Gln Ala Ser Met Glu Tyr
                245                 250                 255
Ser Lys Ile Val Gly Leu Pro Ala Met Gln Ser Tyr Trp Thr Phe Gly
            260                 265                 270
Phe His Gln Cys Arg Tyr Gly Tyr Arg Asp Val Tyr Glu Leu Ala Glu
        275                 280                 285
Val Val Tyr Asn Tyr Ser Gln Ala Lys Ile Pro Leu Glu Thr Met Trp
    290                 295                 300
Thr Asp Ile Asp Tyr Met Asp Lys Arg Arg Val Phe Thr Leu Asp Pro
305                 310                 315                 320
Gln Arg Phe Pro Leu Glu Lys Met Arg Glu Leu Val Thr Tyr Leu His
                325                 330                 335
Asn His Asp Gln His Tyr Ile Val Met Val Asp Pro Ala Val Ser Val
            340                 345                 350
Ser Asn Asn Thr Ala Tyr Ile Thr Gly Val Arg Asp Asp Val Phe Leu
        355                 360                 365
His Asn Gln Asn Gly Ser Leu Tyr Glu Gly Ala Val Trp Pro Gly Val
    370                 375                 380
Thr Val Phe Pro Asp Trp Phe Asn Glu Gly Thr Gln Asp Tyr Trp Thr
385                 390                 395                 400
Ala Gln Phe Gln Gln Phe Phe Asp Pro Lys Ser Gly Val Asp Ile Asp
                405                 410                 415
Ala Leu Trp Ile Asp Met Asn Glu Ala Ser Asn Phe Cys Pro Tyr Pro
            420                 425                 430
Cys Leu Asp Pro Ala Ala Tyr Ala Ile Ser Ala Asp Leu Pro Pro Ala
        435                 440                 445
Ala Pro Pro Val Arg Pro Ser Ser Pro Ile Pro Leu Pro Gly Phe Pro
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    450                 455                 460
Ala Asp Phe Gln Pro Ser Ser Lys Arg Ser Val Lys Arg Ala Gln Gly
465                 470                 475                 480
Asp Lys Gly Lys Lys Val Gly Leu Pro Asn Arg Asn Leu Thr Asp Pro
                485                 490                 495
Pro Tyr Thr Ile Arg Asn Ala Ala Gly Val Leu Ser Met Ser Thr Ile
            500                 505                 510
Glu Thr Asp Leu Ile His Ala Gly Glu Gly Tyr Ala Glu Tyr Asp Thr
        515                 520                 525
His Asn Leu Tyr Gly Thr Met Met Ser Ser Ala Ser Arg Thr Ala Met
    530                 535                 540
Gln Ala Arg Arg Pro Asp Val Arg Pro Leu Val Ile Thr Arg Ser Thr
545                 550                 555                 560
Phe Ala Gly Ala Gly Ala His Val Gly His Trp Leu Gly Asp Asn Phe
                565                 570                 575
Ser Asp Trp Val His Tyr Arg Ile Ser Ile Ala Gln Ile Leu Ser Phe
            580                 585                 590
Ala Ser Met Phe Gln Ile Pro Met Val Gly Ala Asp Val Cys Gly Phe
        595                 600                 605
Gly Ser Asn Thr Thr Glu Glu Leu Cys Ala Arg Trp Ala Ser Leu Gly
    610                 615                 620
Ala Phe Tyr Thr Phe Tyr Arg Asn His Asn Glu Leu Gly Asp Ile Ser
625                 630                 635                 640
Gln Glu Phe Tyr Arg Trp Pro Thr Val Ala Glu Ser Ala Arg Lys Ala
                645                 650                 655
Ile Asp Ile Arg Tyr Lys Leu Leu Asp Tyr Ile Tyr Thr Ala Leu His
            660                 665                 670
Arg Gln Ser Gln Thr Gly Glu Pro Phe Leu Gln Pro Gln Phe Tyr Leu
        675                 680                 685
Tyr Pro Glu Asp Ser Asn Thr Phe Ala Asn Asp Arg Gln Phe Phe Tyr
    690                 695                 700
Gly Asp Ala Leu Leu Val Ser Pro Val Leu Asn Glu Gly Ser Thr Ser
705                 710                 715                 720
Val Asp Ala Tyr Phe Pro Asp Asp Ile Phe Tyr Asp Trp Tyr Thr Gly
                725                 730                 735
Ala Val Val Arg Gly His Gly Glu Asn Ile Thr Leu Ser Asn Ile Asn
            740                 745                 750
Ile Thr His Ile Pro Leu His Ile Arg Gly Gly Asn Ile Ile Pro Val
        755                 760                 765
Arg Thr Ser Ser Gly Met Thr Thr Thr Glu Val Arg Lys Gln Gly Phe
    770                 775                 780
Glu Leu Ile Ile Ala Pro Asp Leu Asp Asp Thr Ala Ser Gly Ser Leu
785                 790                 795                 800
Tyr Leu Asp Asp Gly Asp Ser Leu Asn Pro Ser Ser Val Thr Glu Leu
                805                 810                 815
Glu Phe Thr Tyr Ser Lys Gly Glu Leu His Val Lys Gly Thr Phe Gly
            820                 825                 830
Gln Lys Ala Val Pro Lys Val Glu Lys Cys Thr Leu Leu Gly Lys Ser
        835                 840                 845
Ala Arg Thr Phe Lys Gly Phe Ala Leu Asp Ala Pro Val Asn Phe Lys
    850                 855                 860
Leu Lys
865
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<210> 287
<211> 742
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase XP_001391128.2

<400> 287
Met Pro Ser Thr Tyr Leu Gly Ala Leu Ala Thr Leu Ala Val Phe Pro
 1               5                  10                  15
Cys Leu Gly Gln Ala Arg Ser Thr Trp Pro Leu Gly Ser Gly Leu Glu
            20                  25                  30
Leu Ser Tyr Gln Ala Ser Gln His Gln Ile Ser Ile His Gln Asp Asn
        35                  40                  45
Gln Thr Ile Phe Ser Thr Ile Pro Gly Gln Pro Phe Leu Ser Ala Ser
    50                  55                  60
Ala Gly Lys Asp Gln Phe Val Glu Asp Ser Gly Asn Phe Asn Ile Thr
65                  70                  75                  80
Asn Val Asn Gln Ala Arg Cys Arg Gly Gln Asn Ile Thr Gln Leu Ala
                85                  90                  95
Gly Ile Pro Arg Ser Asp Ser Val Lys Asn Gln Val Ala Val Arg Gly
            100                 105                 110
Tyr Leu Leu Asp Cys Gly Gly Glu Asp Ile Ala Tyr Gly Met Asn Phe
        115                 120                 125
Trp Val Pro Arg Arg Phe Ser Asp Arg Val Ala Phe Glu Ala Ser Val
    130                 135                 140
Asp Ser Glu Ala Asn Ala Ser Phe Ala Ser Met Lys Asn Arg Ser Ile
145                 150                 155                 160
Pro Ile Phe Ser Arg Glu Gln Gly Val Gly Arg Gly Asp Gln Pro Tyr
                165                 170                 175
Thr Ala Ile Glu Asp Ser Gln Gly Phe Phe Ser Gly Gly Asp Gln Tyr
            180                 185                 190
Thr Thr Tyr Thr Ala Ile Pro Gln Tyr Val Ser Ser Asp Gly Arg Val
        195                 200                 205
Phe Tyr Leu Asp Glu Asn Asp Thr Ala Tyr Ala Val Phe Asp Phe Gln
    210                 215                 220
Arg Ser Asp Ala Val Thr Val Arg Tyr Asp Ser Leu Ser Val His Gly
225                 230                 235                 240
His Leu Met Gln Ala Asp Thr Met Leu Asp Ala Ile Thr Met Leu Thr
                245                 250                 255
Glu Tyr Thr Gly Arg Met Pro Thr Leu Pro Glu Trp Val Asp His Gly
            260                 265                 270
Ala Leu Leu Gly Ile Gln Gly Gly Gln Glu Lys Val Asn Arg Ile Val
        275                 280                 285
Lys Gln Gly Phe Glu His Asp Cys Pro Val Ala Gly Val Trp Leu Gln
    290                 295                 300
Asp Trp Ser Gly Thr His Leu Gln Ser Ala Pro Tyr Gly Asn Met Asn
305                 310                 315                 320
Ile Ser Arg Leu Trp Trp Asn Trp Glu Ser Asp Thr Ser Leu Tyr Pro
                325                 330                 335
Thr Trp Ala Glu Phe Val Gln Thr Leu Arg Glu Gln His Gly Val Arg
            340                 345                 350

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Thr Leu Ala Tyr Val Asn Pro Phe Leu Ala Asn Val Ser Ser Lys Ser
        355                 360                 365
Asp Gly Tyr Arg Arg Asn Leu Phe Leu Glu Ala Ser Gln His Arg Tyr
    370                 375                 380
Met Val Gln Asn Thr Thr Thr Asn Ser Thr Ala Ile Ile Ser Ser Gly
385                 390                 395                 400
Lys Gly Ile Asp Ala Gly Ile Leu Asp Leu Thr Asn Glu Asp Thr Arg
                405                 410                 415
Ala Trp Phe Ala Asp Val Leu Arg Thr Gln Val Trp Ser Ala Asn Ile
            420                 425                 430
Ser Gly Cys Met Trp Asp Phe Gly Glu Tyr Thr Pro Ile Thr Pro Asp
        435                 440                 445
Thr Ser Leu Ala Asn Ile Ser Thr Ser Ala Phe Phe Tyr His Asn Gln
    450                 455                 460
Tyr Pro Arg Asp Trp Ala Ala Tyr Gln Arg Ser Val Ala Ala Glu Met
465                 470                 475                 480
Pro Leu Phe His Glu Met Val Thr Phe His Arg Ser Ala Ser Met Gly
                485                 490                 495
Ala Asn Arg His Met Asn Leu Phe Trp Val Gly Asp Gln Ala Thr Leu
            500                 505                 510
Trp Thr Arg Asn Asp Gly Ile Lys Ser Val Val Thr Ile Gln Gly Gln
        515                 520                 525
Met Gly Ile Ser Gly Tyr Ala His Ser His Ser Asp Ile Gly Gly Tyr
    530                 535                 540
Thr Thr Val Phe Glu Pro Pro Thr Thr Ser Asn Ser Ser Gly Ala Ile
545                 550                 555                 560
Pro Arg Ser Ala Glu Leu Leu Gly Arg Trp Gly Glu Leu Gly Ala Val
                565                 570                 575
Ser Ser Ala Val Phe Arg Ser His Glu Gly Asn Val Pro Ser Val Asn
            580                 585                 590
Ala Gln Phe Tyr Ser Asn Ser Thr Thr Tyr Ala Tyr Phe Ala Tyr Asn
        595                 600                 605
Ala Arg Leu Phe Arg Ser Leu Gly Pro Tyr Arg Arg Arg Ile Leu Asn
    610                 615                 620
Thr Glu Ser Gln Arg Arg Gly Trp Pro Leu Leu Arg Met Pro Val Leu
625                 630                 635                 640
Tyr His Pro Glu Asp Leu Arg Ala Arg Gln Ile Ser Tyr Glu Ser Phe
                645                 650                 655
Phe Leu Gly Arg Asp Leu Tyr Val Ala Pro Val Leu Asp Glu Gly His
            660                 665                 670
Lys Ser Val Glu Val Tyr Phe Pro Gly His Ser Ala Asn Arg Thr Tyr
        675                 680                 685
Thr His Val Trp Thr Gly Gln Thr Tyr Arg Ala Gly Gln Thr Ala Lys
    690                 695                 700
Val Ser Ala Pro Phe Gly Lys Pro Ala Val Phe Leu Val Asp Gly Ala
705                 710                 715                 720
Ser Ser Pro Glu Leu Asp Val Phe Leu Asp Phe Val Arg Lys Glu Asn
                725                 730                 735
Gly Thr Val Leu Tyr Ala
            740
```

<210> 288
<211> 680

<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase XP_001395384.2

<400> 288
Met Asp Pro Ala Asn Glu Tyr Cys Gly Leu Glu Asp Tyr Gly Leu Val
 1               5                  10                  15
Gly Asp Met His Thr Cys Ala Leu Val Ser Lys Asn Gly Ser Val Asp
            20                  25                  30
Ser Met Cys Trp Pro Val Phe Asp Ser Pro Ser Ile Phe Cys Arg Ile
        35                  40                  45
Leu Asp Lys Glu Lys Gly Gly His Phe Ser Ile Thr Pro Asp Arg Arg
    50                  55                  60
Leu Lys Asn Pro Leu Ser Lys Gln Arg Tyr Arg Pro Tyr Thr Asn Met
65                  70                  75                  80
Leu Glu Thr Arg Trp Ile His Glu Glu Gly Val Met Asn Ile Leu Asp
                85                  90                  95
Tyr Phe Pro Ile Ala Lys Pro Lys Pro His Val Val Glu Lys Gly Leu
            100                 105                 110
Pro Gln Trp Cys Arg Cys Tyr Gln Asn Lys Gly Ser Ala Gln Tyr Gln
        115                 120                 125
Ala Cys Arg Ser Gly Met Val Arg Lys Ala Glu Cys Val Arg Gly Glu
    130                 135                 140
Met Glu Ile Glu Ile Glu Leu Phe Pro Ala Phe Asn Tyr Ala Arg Asp
145                 150                 155                 160
Ser His Val Ala Gln Gln Ser Ser Ala Ser Asp Asp Ala Ile Gln Val
                165                 170                 175
Tyr His Phe Gln Ala Glu Ser Gln Asn Leu Val Val Ser Val Leu Gly
            180                 185                 190
Asp Arg Gly Asp Ile Ser Gly Asp Asp Ser Asp Leu Ser Ile Glu Phe
        195                 200                 205
Glu Leu Ser Asp Arg Pro Gly His Leu Gly Pro Gly Leu Val Gly Lys
    210                 215                 220
Val Thr Leu Lys Glu Gly Gln Ser Ile Thr Met Leu Leu His Asp Gln
225                 230                 235                 240
Glu Ser Ile Thr Cys Asn Val Glu Asp Leu Ala Pro Tyr Leu Gln Gln
                245                 250                 255
Ile Glu Arg Thr Thr Gly Asp Phe Trp Ser Asp Trp Thr Ser Lys Cys
            260                 265                 270
Thr Phe Arg Gly His Tyr Arg Glu Gln Val Glu Arg Ser Leu Leu Val
        275                 280                 285
Leu Lys Leu Leu Thr Tyr Lys Pro Thr Gly Ala Ile Val Ala Ala Pro
    290                 295                 300
Thr Phe Ser Leu Pro Glu His Ile Gly Gly Ser Arg Asn Trp Asp Tyr
305                 310                 315                 320
Arg Tyr Ser Trp Val Arg Asp Ala Ala Phe Thr Val Tyr Val Phe Leu
                325                 330                 335
Lys Asn Gly Tyr Pro Glu Glu Ala Glu Ser Tyr Ile Asn Phe Ile Phe
            340                 345                 350
Glu Arg Ile Phe Pro Pro Met Asp Lys Asn Pro Lys Pro Gly Glu Pro
        355                 360                 365
Phe Leu Pro Ile Met Ile Thr Ile His Gly Glu Arg Glu Ile Pro Glu

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    370                 375                 380
Met Glu Leu Glu His Leu Glu Gly Tyr Arg Gly Ser Arg Pro Val Arg
385                 390                 395                 400
Ile Gly Asn Gly Ala Ala Thr His Ile Gln Leu Asp Ile Tyr Gly Glu
                405                 410                 415
Leu Met Asp Ser Ile Tyr Leu Tyr Asn Lys His Ala Ala Asp Ile Ser
            420                 425                 430
Tyr Asp Gln Trp Arg Ala Ile Arg Arg Met Ile Asp Phe Val Ile Gln
        435                 440                 445
Ile Arg His Gln Pro Asp Gln Ser Ile Trp Glu Val Arg Gly Pro Pro
    450                 455                 460
Gln Asn Phe Val Tyr Ser Lys Ile Met Leu Trp Val Ala Leu Asp Arg
465                 470                 475                 480
Gly Leu Arg Leu Ala Glu Lys Arg Ser Asn Leu Pro Cys Pro Asp Arg
                485                 490                 495
Ala Arg Trp Met His Glu Arg Asp Ala Leu Tyr Asp Glu Ile Met Thr
            500                 505                 510
Lys Gly Tyr Asn Ser Glu Lys Gly Phe Phe Cys Met Ser Tyr Glu Asn
        515                 520                 525
Gln Asp Ala Met Asp Ala Ala Val Leu Ile Ala Pro Leu Val Phe Phe
    530                 535                 540
Val Ala Pro Asn Asp Pro Arg Leu Leu Ser Thr Ile Gln Lys Ile Thr
545                 550                 555                 560
Glu Val Pro Ala Lys Gly Gly Leu Ser Val Ala Asn Met Val Ser Arg
                565                 570                 575
Tyr Asp Thr Gly Lys Val Asp Asp Gly Val Gly Gly Asn Glu Gly Ala
            580                 585                 590
Phe Leu Met Val Thr Phe Trp Leu Val Glu Ala Met Met Arg Ala Ala
        595                 600                 605
Arg Ser Lys Ala Tyr Leu Pro His Asp Pro Phe Phe Gln Gln Leu Arg
    610                 615                 620
Lys Thr Ala Thr Ser Gln Phe Asp Ser Ile Leu Ser Phe Ala Asn His
625                 630                 635                 640
Leu Gly Met Phe Ser Glu Glu Val Ala Thr Ser Gly Glu Gln Ile Gly
                645                 650                 655
Asn Met Pro Gln Ala Phe Ser His Leu Ala Cys Val Ser Ala Ala Met
            660                 665                 670
Asn Leu Gly Gly Gly Gly Asp Arg
        675                 680


<210> 289
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase XP_001396506.2

<400> 289
Met Cys Asn Lys Ser Asn Tyr Ser Ser Pro Lys Trp Trp Lys Glu Ser
 1               5                  10                  15
Val Val Tyr Gln Val Tyr Pro Ala Ser Phe Asn Cys Gly Lys Ser Thr
            20                  25                  30
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Thr Asn Thr Asn Gly Trp Gly Asp Val Thr Gly Ile Ile Glu Lys Val
        35                  40                  45
Pro Tyr Leu Glu Ser Leu Gly Val Asp Ile Val Trp Leu Ser Pro Ile
    50                  55                  60
Tyr Thr Ser Pro Gln Val Asp Met Gly Tyr Asp Ile Ala Asp Tyr Glu
65                  70                  75                  80
Ser Ile Asp Pro Arg Tyr Gly Thr Leu Ala Asp Val Asp Leu Leu Ile
                85                  90                  95
Lys Thr Leu Lys Asp His Asp Met Lys Leu Met Met Asp Leu Val Val
            100                 105                 110
Asn His Thr Ser Asp Gln His Ser Trp Phe Val Glu Ser Ala Asn Ser
        115                 120                 125
Lys Asp Ser Pro Lys Arg Asp Trp Tyr Ile Trp Arg Pro Ala Lys Gly
    130                 135                 140
Phe Asp Glu Ala Gly Asn Pro Val Pro Pro Asn Asn Trp Ala Gln Ile
145                 150                 155                 160
Leu Gly Asp Thr Leu Ser Ala Trp Thr Trp His Ala Glu Thr Gln Glu
                165                 170                 175
Phe Tyr Leu Thr Leu His Thr Ser Ala Gln Ala Glu Leu Asn Trp Glu
            180                 185                 190
Asn Pro Asp Val Val Thr Ala Val Tyr Asp Val Met Glu Phe Trp Leu
        195                 200                 205
Arg Arg Gly Ile Cys Gly Phe Arg Met Asp Val Ile Asn Phe Ile Ser
    210                 215                 220
Lys Asp Gln Ser Phe Pro Asp Ala Pro Ile Ile Asp Pro Ala Ser Lys
225                 230                 235                 240
Tyr Gln Pro Gly Glu Gln Phe Tyr Thr Asn Gly Pro Arg Phe His Glu
                245                 250                 255
Phe Met His Gly Ile Tyr Asp Asn Val Leu Ser Lys Tyr Asp Thr Ile
            260                 265                 270
Thr Val Gly Glu Thr Pro Tyr Val Thr Asp Met Lys Glu Ile Ile Lys
        275                 280                 285
Thr Val Gly Ser Thr Ala Lys Glu Leu Asn Met Ala Phe Asn Phe Asp
    290                 295                 300
His Met Glu Ile Glu Asp Ile Lys Thr Lys Gly Glu Ser Lys Trp Ser
305                 310                 315                 320
Leu Arg Asp Trp Lys Leu Thr Glu Leu Lys Gly Ile Leu Ser Gly Trp
                325                 330                 335
Gln Lys Arg Met Arg Glu Trp Asp Gly Trp Asn Ala Ile Phe Leu Glu
            340                 345                 350
Cys His Asp Gln Ala Arg Ser Val Ser Arg Tyr Thr Asn Asp Ser Asp
        355                 360                 365
Glu Phe Arg Asp Arg Gly Ala Lys Leu Leu Ala Leu Leu Glu Thr Thr
    370                 375                 380
Leu Gly Gly Thr Ile Phe Leu Tyr Gln Gly Gln Glu Ile Gly Met Arg
385                 390                 395                 400
Asn Phe Pro Val Glu Trp Asp Pro Asp Thr Glu Tyr Lys Asp Ile Glu
                405                 410                 415
Ser Val Asn Phe Trp Lys Lys Ser Lys Glu Leu His Pro Val Gly Ser
            420                 425                 430
Glu Gly Leu Ala Gln Ala Arg Thr Leu Leu Gln Lys Lys Ala Arg Asp
        435                 440                 445
His Ala Arg Thr Pro Met Gln Trp Ser Ala Asp Pro His Ala Gly Phe
    450                 455                 460
```

Thr Val Pro Asp Ala Thr Pro Trp Met Arg Val Asn Asp Asp Tyr Gly
465 470 475 480
Thr Val Asn Val Glu Ala Gln Met Ser Phe Pro Trp Glu Met Lys Gly
485 490 495
Glu Leu Ser Val Trp Gln Tyr Trp Gln Gln Ala Leu Gln Arg Arg Lys
500 505 510
Leu His Lys Gly Ala Phe Val Tyr Gly Asp Phe Glu Asp Leu Asp Tyr
515 520 525
His Asn Glu Leu Val Phe Ala Tyr Ser Arg Thr Ser Ala Asp Gly Lys
530 535 540
Glu Thr Trp Leu Val Ala Met Asn Trp Thr Thr Asp Ala Val Glu Trp
545 550 555 560
Thr Val Pro Ser Gly Ile His Val Thr Arg Trp Val Ser Ser Thr Leu
565 570 575
Gln Thr Ala Pro Leu Met Ala Gly Gln Ser Thr Val Thr Leu Arg Ala
580 585 590
Leu Glu Gly Val Val Gly Cys Cys Ser
595 600

<210> 290
<211> 704
<212> PRT
<213> Artificial Sequence

<220>
<223> Transgucosidase XP_001398938.2

<400> 290
Met Gly Leu Cys Val Gly Trp Arg Trp Ile Leu Leu Cys Val Val Met
1 5 10 15
Gly Ala Ala Val Cys Gly Thr Asp Lys Thr Ala Thr Met Arg Trp His
20 25 30
Lys Leu Leu Pro Gly Val Leu Ala Leu Leu Pro Leu Ser Val Ala Gln
35 40 45
Ser Cys Trp Arg Asn Thr Thr Cys Ser Gly Pro Thr Glu Ser Ala Phe
50 55 60
Ser Gly Pro Trp Glu Lys Asn Ile Phe Ala Pro Ser Ser Arg Thr Val
65 70 75 80
Asn Pro Glu Lys Leu Phe Leu Ile Thr Gln Pro Asp Lys Thr Glu Glu
85 90 95
Tyr Ser Pro Phe Ala Leu His Gly Asn Gly Ser Leu Val Val Tyr Asp
100 105 110
Phe Gly Lys Glu Val Gly Gly Ile Val Ser Val Asn Phe Ser Ser Thr
115 120 125
Gly Ser Gly Ala Leu Gly Val Ala Phe Thr Glu Ala Lys Asn Trp Ile
130 135 140
Gly Glu Trp Ser Asp Ser Ser Asn Gly Gly Phe Lys Gly Pro Asp Gly
145 150 155 160
Ala Leu Tyr Gly Asn Phe Thr Glu Ala Gly Ser His Tyr Tyr Val Met
165 170 175
Pro Asp Lys Ser Leu Arg Gly Gly Phe Arg Tyr Leu Thr Leu Phe Leu
180 185 190
Ile Thr Ser Asp Asn Ser Thr Ile Gln Ile Glu Asp Val Asn Leu Glu

```
        195                 200                 205
Ile Gly Phe Gln Pro Thr Trp Ser Asn Leu Lys Ala Tyr Gln Gly Tyr
    210                 215                 220
Phe His Ser Asn Asp Asp Leu Leu Asn Lys Ile Trp Tyr Thr Gly Ala
225                 230                 235                 240
Tyr Thr Leu Gln Thr Asn Glu Val Pro Thr Asp Thr Gly Arg Gln Ile
                245                 250                 255
Pro Ala Met Ala Val Gly Trp Ala Asn Asn Cys Thr Leu Gly Pro Gly
            260                 265                 270
Asp Thr Ile Ile Val Asp Gly Ala Lys Arg Asp Arg Ala Val Trp Pro
        275                 280                 285
Gly Asp Met Gly Ile Ala Val Pro Ser Ala Phe Val Ser Leu Gly Asp
    290                 295                 300
Leu Asp Ser Val Lys Asn Ala Leu Gln Val Met Tyr Asp Thr Gln Asn
305                 310                 315                 320
Asn Ser Thr Gly Ala Phe Asp Glu Ser Gly Pro Pro Leu Ser Gln Lys
                325                 330                 335
Asp Ser Asp Thr Tyr His Met Trp Thr Met Val Gly Thr Tyr Asn Tyr
            340                 345                 350
Met Leu Phe Thr Asn Asp Ser Asp Phe Leu Glu Arg Asn Trp Glu Gly
        355                 360                 365
Tyr Gln Lys Ala Met Asp Tyr Ile Tyr Gly Lys Val Thr Tyr Pro Ser
    370                 375                 380
Gly Leu Leu Asn Val Thr Gly Thr Arg Asp Trp Ala Arg Trp Gln Gln
385                 390                 395                 400
Gly Tyr Asn Asn Ser Glu Ala Gln Met Ile Leu Tyr His Thr Leu Asn
                405                 410                 415
Thr Gly Ala Glu Leu Ala Thr Trp Ala Gly Asp Ser Gly Asp Leu Ser
            420                 425                 430
Ser Thr Trp Thr Ser Arg Ala Glu Lys Leu Arg Gln Ala Ile Asn Glu
        435                 440                 445
Tyr Cys Trp Asp Asp Ser Tyr Gly Ala Phe Lys Asp Asn Ala Thr Asp
    450                 455                 460
Thr Thr Leu His Pro Gln Asp Ala Asn Ser Met Ala Leu Leu Phe Gly
465                 470                 475                 480
Val Val Asp Ala Asp Arg Ala Ala Ser Ile Ser Glu Arg Leu Thr Asp
                485                 490                 495
Asn Trp Thr Pro Ile Gly Ala Val Ala Pro Glu Leu Pro Glu Asn Ile
            500                 505                 510
Ser Pro Phe Ile Ser Ser Phe Glu Ile Gln Gly His Leu Thr Val Gly
        515                 520                 525
Gln Pro Gln Arg Ala Leu Glu Leu Ile Arg Arg Ser Trp Gly Trp Tyr
    530                 535                 540
Tyr Asn Asn Ala Asn Gly Thr Gln Ser Thr Val Ile Glu Gly Tyr Leu
545                 550                 555                 560
Gln Asn Gly Thr Phe Gly Tyr Arg Ser Asp Arg Gly Tyr Tyr Tyr Asp
                565                 570                 575
Thr Ala Tyr Val Ser His Ser His Gly Trp Ser Ser Gly Pro Thr Ser
            580                 585                 590
Ala Leu Thr Asn Tyr Ile Val Gly Ile Ser Val Thr Ser Pro Leu Gly
        595                 600                 605
Ala Thr Trp Arg Ile Ala Pro Gln Phe Val Asp Leu Gln Ser Ala Glu
    610                 615                 620
Gly Gly Phe Thr Thr Ser Leu Gly Lys Phe Gln Ala Gly Trp Ser Lys
```

625 630 635 640
Thr Asp Lys Gly Tyr Thr Leu Asp Phe Thr Val Pro His Gly Thr Gln
645 650 655
Gly Asn Leu Thr Leu Pro Phe Val Ser Ala Ala Lys Pro Ser Ile Lys
660 665 670
Ile Asp Gly Thr Glu Ile Ser Arg Gly Val Gln Tyr Ala Asn Ser Thr
675 680 685
Ala Thr Val Thr Val Ser Gly Gly Gly Thr Tyr Lys Val Glu Val Gln
690 695 700

<210> 291

<220>
<223> Transgucosidase XP_001398938.2

<400> 291
000

<210> 292
<211> 542
<212> PRT
<213> Artificial Sequence

<220>
<223> Betaglucosidase>tr|H9ZGE3|H9ZGE3_PRUDU Prunasin
hydrolase OS=Prunus dulcis GN=Ph692 PE=2

<400> 292
Met Ala Met Gln Leu Arg Ser Leu Leu Leu Cys Val Leu Leu Leu Leu
1 5 10 15
Leu Gly Phe Ala Leu Ala Asp Thr Asn Ala Ala Ala Arg Ile His Pro
20 25 30
Pro Val Val Cys Ala Asn Leu Ser Arg Ala Asn Phe Asp Thr Leu Val
35 40 45
Pro Gly Phe Val Phe Gly Ala Ala Thr Ala Ser Tyr Gln Val Glu Gly
50 55 60
Ala Ala Asn Leu Asp Gly Arg Gly Pro Ser Ile Trp Asp Thr Phe Thr
65 70 75 80
His Lys His Pro Glu Lys Ile Ala Asp Gly Ser Asn Gly Asp Val Ala
85 90 95
Ile Asp Gln Tyr His Arg Tyr Lys Glu Asp Val Ala Ile Met Lys Asp
100 105 110
Met Gly Leu Glu Ser Tyr Arg Phe Ser Ile Ser Trp Ser Arg Val Leu
115 120 125
Pro Asn Gly Thr Leu Ser Gly Gly Ile Asn Lys Lys Gly Ile Glu Tyr
130 135 140
Tyr Asn Asn Leu Ile Asn Glu Leu Leu His Asn Gly Ile Glu Pro Leu
145 150 155 160
Val Thr Leu Phe His Trp Asp Val Pro Gln Thr Leu Glu Asp Glu Tyr
165 170 175
Gly Gly Phe Leu Ser Asn Arg Ile Val Asn Asp Phe Glu Glu Tyr Ala
180 185 190
Glu Leu Cys Phe Lys Lys Phe Gly Asp Arg Val Lys His Trp Thr Thr

```
        195                 200                 205
Leu Asn Glu Pro Tyr Thr Phe Ser Ser His Gly Tyr Ala Lys Gly Thr
    210                 215                 220
His Ala Pro Gly Arg Cys Ser Ala Trp Tyr Asn Gln Thr Cys Phe Gly
225                 230                 235                 240
Gly Asp Ser Ala Thr Glu Pro Tyr Leu Val Thr His Asn Leu Leu Leu
                245                 250                 255
Ala His Ala Ala Ala Val Lys Leu Tyr Lys Thr Lys Tyr Gln Ala Tyr
            260                 265                 270
Gln Lys Gly Val Ile Gly Ile Thr Val Val Thr Pro Trp Phe Glu Pro
        275                 280                 285
Ala Ser Glu Ala Lys Glu Asp Ile Asp Ala Val Phe Arg Ala Leu Asp
    290                 295                 300
Phe Ile Tyr Gly Trp Phe Met Asp Pro Leu Thr Arg Gly Asp Tyr Pro
305                 310                 315                 320
Gln Ser Met Arg Ser Leu Val Gly Glu Arg Leu Pro Asn Phe Thr Lys
                325                 330                 335
Lys Glu Ser Lys Ser Leu Ser Gly Ser Phe Asp Tyr Ile Gly Ile Asn
            340                 345                 350
Tyr Tyr Ser Ala Arg Tyr Ala Ser Ala Ser Lys Asn Tyr Ser Gly His
        355                 360                 365
Pro Ser Tyr Leu Asn Asp Val Asn Val Asp Val Lys Thr Glu Leu Asn
    370                 375                 380
Gly Val Pro Ile Gly Pro Gln Ala Ala Ser Ser Trp Leu Tyr Phe Tyr
385                 390                 395                 400
Pro Lys Gly Leu Tyr Asp Leu Leu Cys Tyr Thr Lys Glu Lys Tyr Asn
                405                 410                 415
Asp Pro Ile Ile Tyr Ile Thr Glu Asn Gly Val Asp Glu Phe Asn Gln
            420                 425                 430
Pro Asn Pro Lys Leu Ser Leu Cys Gln Leu Leu Asp Asp Ser Asn Arg
        435                 440                 445
Ile Tyr Tyr Tyr Tyr His His Leu Cys Tyr Leu Gln Ala Ala Ile Lys
    450                 455                 460
Glu Gly Val Lys Val Lys Gly Tyr Phe Ala Trp Ser Leu Leu Asp Asn
465                 470                 475                 480
Phe Glu Trp Asp Asn Gly Tyr Thr Val Arg Phe Gly Ile Asn Tyr Val
                485                 490                 495
Asp Tyr Asp Asn Gly Leu Lys Arg His Ser Lys His Ser Thr His Trp
            500                 505                 510
Phe Lys Ser Phe Leu Lys Lys Ser Ser Arg Asn Thr Lys Lys Ile Arg
        515                 520                 525
Arg Cys Gly Asn Asn Asn Thr Ser Ala Thr Lys Phe Val Phe
    530                 535                 540
```

<210> 293
<211> 502
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT73-251_5

<400> 293

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

```
Val Arg Glu Ala Ile Glu Arg Ala Met Asp Gly Asp Glu Arg Glu Glu
        435                 440                 445
Arg Arg Glu Arg Cys Lys Glu Leu Ala Glu Met Ala Lys Arg Ala Val
    450                 455                 460
Glu Glu Gly Gly Ser Ser His Arg Asn Leu Thr Leu Leu Thr Glu Asp
465                 470                 475                 480
Ile Leu Val Asn Gly Gly Gly Gln Glu Arg Met Asp Asp Ala Asp Asp
                485                 490                 495
Phe Pro Thr Ile Val Asn
            500
```

<210> 294
<211> 488
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT73-251-6

<400> 294

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

```
            260                 265                 270
Ile Lys Trp Leu Gly Gly Gln Gln Pro Ser Ser Val Val Tyr Ala Ser
        275                 280                 285
Leu Gly Ser Leu Cys Asn Leu Val Thr Ala Gln Phe Ile Glu Leu Gly
    290                 295                 300
Leu Gly Leu Glu Ala Ser Asn Lys Pro Phe Ile Trp Val Ile Arg Lys
305                 310                 315                 320
Gly Asn Ile Thr Glu Glu Leu Gln Lys Trp Leu Val Glu Tyr Asp Phe
                325                 330                 335
Glu Glu Lys Thr Lys Gly Arg Gly Leu Val Ile Leu Gly Trp Ala Pro
            340                 345                 350
Gln Val Leu Ile Leu Ser His Pro Ser Ile Gly Cys Phe Leu Thr His
        355                 360                 365
Cys Gly Trp Asn Ser Ser Ile Glu Gly Ile Ser Ala Gly Val Pro Met
    370                 375                 380
Val Thr Trp Pro Leu Phe Ser Asp Gln Val Phe Asn Glu Lys Leu Ile
385                 390                 395                 400
Val Gln Ile Leu Arg Ile Gly Val Ser Val Gly Ala Glu Thr Ala Met
                405                 410                 415
Asn Trp Gly Glu Glu Glu Glu Lys Gly Val Val Val Lys Arg Glu Lys
            420                 425                 430
Val Arg Glu Ala Ile Glu Arg Met Met Asp Gly Asp Glu Arg Glu Glu
        435                 440                 445
Arg Arg Glu Arg Cys Lys Glu Leu Ala Glu Thr Ala Lys Arg Ala Ile
    450                 455                 460
Glu Glu Gly Gly Ser Ser His Arg Asn Leu Thr Leu Leu Ile Glu Asp
465                 470                 475                 480
Ile Gly Thr Ser Leu Arg Arg Leu
                485
```

<210> 295
<211> 491
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT73-327-2

<400> 295

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

```
Lys Gly Ala Lys Val Asp Cys Ile Val Ser Asp Thr Ile Leu Val Trp
        115                 120                 125
Thr Leu Asp Ala Ala Ala Arg Leu Gly Ile Pro Arg Ile Ala Phe Arg
    130                 135                 140
Ser Ser Gly Phe Phe Ser Glu Cys Ile His His Ser Leu Arg Cys His
145                 150                 155                 160
Lys Pro His Lys Lys Val Gly Ser Asp Thr Glu Pro Phe Ile Phe Pro
                165                 170                 175
Gly Leu Pro His Lys Ile Glu Ile Thr Arg Leu Asn Ile Pro Gln Trp
            180                 185                 190
Tyr Ser Glu Glu Gly Tyr Ile Gln His Ile Glu Lys Met Lys Glu Met
        195                 200                 205
Asp Lys Lys Ser Tyr Ala Val Leu Leu Asn Thr Phe Tyr Glu Leu Glu
    210                 215                 220
Ala Asp Tyr Val Glu Tyr Phe Glu Ser Val Ile Gly Leu Lys Thr Trp
225                 230                 235                 240
Ile Val Gly Pro Val Ser Leu Trp Ala Asn Glu Gly Gly Gly Lys Asn
                245                 250                 255
Asp Ser Arg Thr Glu Asn Asn Asn Ala Glu Leu Met Glu Trp Leu Asp
            260                 265                 270
Ser Lys Gln Pro Asn Ser Val Leu Tyr Val Ser Phe Gly Ser Met Thr
        275                 280                 285
Lys Phe Pro Ser Ala Gln Val Leu Glu Ile Ala His Gly Leu Glu Asp
    290                 295                 300
Ser Gly Cys His Phe Ile Trp Val Val Arg Lys Met Asn Glu Ser Glu
305                 310                 315                 320
Ala Ala Asp Glu Glu Phe Pro Glu Gly Phe Glu Glu Arg Val Arg Glu
                325                 330                 335
Ser Lys Arg Gly Leu Ile Ile Arg Asp Trp Ala Pro Gln Glu Leu Ile
            340                 345                 350
Leu Asn His Ala Ala Val Gly Gly Phe Val Thr His Cys Gly Trp Asn
        355                 360                 365
Ser Ile Leu Glu Ser Val Cys Ala Gly Arg Pro Ile Ile Ala Trp Pro
    370                 375                 380
Leu Ser Ala Glu Gln Phe Phe Asn Glu Lys Phe Val Thr Arg Val Leu
385                 390                 395                 400
Lys Val Gly Val Ser Ile Gly Val Arg Lys Trp Trp Gly Ser Thr Ser
                405                 410                 415
Ser Glu Thr Leu Asp Val Val Lys Arg Asp Arg Ile Ala Glu Ala Val
            420                 425                 430
Ala Arg Leu Met Gly Asp Asp Arg Glu Val Val Glu Met Arg Asp Gly
        435                 440                 445
Val Arg Glu Leu Ser His Ala Ala Lys Arg Ala Ile Lys Glu Gly Gly
    450                 455                 460
Ser Ser His Ser Thr Leu Leu Ser Leu Ile His Glu Leu Lys Thr Met
465                 470                 475                 480
Lys Phe Lys Arg Gln Ser Ser Asn Val Asp Gly
                485                 490
```

<210> 296
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT74-345-2

<400> 296
Met Asp Glu Thr Thr Val Asn Gly Gly Arg Arg Ala Ser Asp Val Val
 1               5                  10                  15
Val Phe Ala Phe Pro Arg His Gly His Met Ser Pro Met Leu Gln Phe
            20                  25                  30
Ser Lys Arg Leu Val Ser Lys Gly Leu Arg Val Thr Phe Leu Ile Thr
        35                  40                  45
Thr Ser Ala Thr Glu Ser Leu Arg Leu Asn Leu Pro Pro Ser Ser Ser
    50                  55                  60
Leu Asp Leu Gln Val Ile Ser Asp Val Pro Glu Ser Asn Asp Ile Ala
65                  70                  75                  80
Thr Leu Glu Gly Tyr Leu Arg Ser Phe Lys Ala Thr Val Ser Lys Thr
                85                  90                  95
Leu Ala Asp Phe Ile Asp Gly Ile Gly Asn Pro Pro Lys Phe Ile Val
            100                 105                 110
Tyr Asp Ser Val Met Pro Trp Val Gln Glu Val Ala Arg Gly Arg Gly
        115                 120                 125
Leu Asp Ala Ala Pro Phe Phe Thr Gln Ser Ser Ala Val Asn His Ile
    130                 135                 140
Leu Asn His Val Tyr Gly Gly Ser Leu Ser Ile Pro Ala Pro Glu Asn
145                 150                 155                 160
Thr Ala Val Ser Leu Pro Ser Met Pro Val Leu Gln Ala Glu Asp Leu
                165                 170                 175
Pro Ala Phe Pro Asp Asp Pro Glu Val Val Met Asn Phe Met Thr Ser
            180                 185                 190
Gln Phe Ser Asn Phe Gln Asp Ala Lys Trp Ile Phe Phe Asn Thr Phe
        195                 200                 205
Asp Gln Leu Glu Cys Lys Val Val Asn Trp Met Ala Asp Arg Trp Pro
    210                 215                 220
Ile Lys Thr Val Gly Pro Thr Ile Pro Ser Ala Tyr Leu Asp Asp Gly
225                 230                 235                 240
Arg Leu Glu Asp Asp Arg Ala Phe Gly Leu Asn Leu Leu Lys Pro Glu
                245                 250                 255
Asp Gly Lys Asn Thr Arg Gln Trp Gln Trp Leu Asp Ser Lys Asp Thr
            260                 265                 270
Ala Ser Val Leu Tyr Ile Ser Phe Gly Ser Leu Ala Ile Leu Gln Glu
        275                 280                 285
Glu Gln Val Lys Glu Leu Ala Tyr Phe Leu Lys Asp Thr Asn Leu Ser
    290                 295                 300
Phe Leu Trp Val Leu Arg Asp Ser Glu Leu Gln Lys Leu Pro His Asn
305                 310                 315                 320
Phe Val Gln Glu Thr Ser His Arg Gly Leu Val Val Asn Trp Cys Ser
                325                 330                 335
Gln Leu Gln Val Leu Ser His Arg Ala Val Ser Cys Phe Val Thr His
            340                 345                 350
Cys Gly Trp Asn Ser Thr Leu Glu Ala Leu Ser Leu Gly Val Pro Met
        355                 360                 365
Val Ala Ile Pro Gln Trp Val Asp Gln Thr Thr Asn Ala Lys Phe Val
    370                 375                 380
Ala Asp Val Trp Arg Val Gly Val Arg Val Lys Lys Lys Asp Glu Arg

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

<210> 297
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT75-281-2

<400> 297
Met Met Arg Asn His His Phe Leu Leu Val Cys Phe Pro Ser Gln Gly
1 5 10 15
Tyr Ile Asn Pro Ser Leu Gln Leu Ala Arg Arg Leu Ile Ser Leu Gly
20 25 30
Val Asn Val Thr Phe Ala Thr Thr Val Leu Ala Gly Arg Arg Met Lys
35 40 45
Asn Lys Thr His Gln Thr Ala Thr Thr Pro Gly Leu Ser Phe Ala Thr
50 55 60
Phe Ser Asp Gly Phe Asp Asp Glu Thr Leu Lys Pro Asn Gly Asp Leu
65 70 75 80
Thr His Tyr Phe Ser Glu Leu Arg Arg Cys Gly Ser Glu Ser Leu Thr
85 90 95
His Leu Ile Thr Ser Ala Ala Asn Glu Gly Arg Pro Ile Thr Phe Val
100 105 110
Ile Tyr Ser Leu Leu Leu Ser Trp Ala Ala Asp Ile Ala Ser Thr Tyr
115 120 125
Asp Ile Pro Ser Ala Leu Phe Phe Ala Gln Pro Ala Thr Val Leu Ala
130 135 140
Leu Tyr Phe Tyr Tyr Phe His Gly Tyr Gly Asp Thr Ile Cys Ser Lys
145 150 155 160
Leu Gln Asp Pro Ser Ser Tyr Ile Glu Leu Pro Gly Leu Pro Leu Leu
165 170 175
Thr Ser Gln Asp Met Pro Ser Phe Phe Ser Pro Ser Gly Pro His Ala
180 185 190
Phe Ile Leu Pro Pro Met Arg Glu Gln Ala Glu Phe Leu Gly Arg Gln
195 200 205
Ser Gln Pro Lys Val Leu Val Asn Thr Phe Asp Ala Leu Glu Ala Asp
210 215 220
Ala Leu Arg Ala Ile Asp Lys Leu Lys Met Leu Ala Ile Gly Pro Leu
225 230 235 240
Ile Pro Ser Ala Leu Leu Gly Gly Asn Asp Ser Ser Asp Ala Ser Phe
245 250 255
Cys Gly Asp Leu Phe Gln Val Ser Ser Glu Asp Tyr Ile Glu Trp Leu
260 265 270

```
Asn Ser Lys Pro Asp Ser Ser Val Val Tyr Ile Ser Val Gly Ser Ile
        275                 280                 285
Cys Val Leu Ser Asp Glu Gln Glu Asp Glu Leu Val His Ala Leu Leu
    290                 295                 300
Asn Ser Gly His Thr Phe Leu Trp Val Lys Arg Ser Lys Glu Asn Asn
305                 310                 315                 320
Glu Gly Val Lys Gln Glu Thr Asp Glu Glu Lys Leu Lys Lys Leu Glu
                325                 330                 335
Glu Gln Gly Lys Met Val Ser Trp Cys Arg Gln Val Glu Val Leu Lys
            340                 345                 350
His Pro Ala Leu Gly Cys Phe Leu Thr His Cys Gly Trp Asn Ser Thr
        355                 360                 365
Ile Glu Ser Leu Val Ser Gly Leu Pro Val Val Ala Phe Pro Gln Gln
    370                 375                 380
Ile Asp Gln Ala Thr Asn Ala Lys Leu Ile Glu Asp Val Trp Lys Thr
385                 390                 395                 400
Gly Val Arg Val Lys Ala Asn Thr Glu Gly Ile Val Glu Arg Glu Glu
                405                 410                 415
Ile Arg Arg Cys Leu Asp Leu Val Met Gly Ser Arg Asp Gly Gln Lys
            420                 425                 430
Glu Glu Ile Glu Arg Asn Ala Lys Lys Trp Lys Glu Leu Ala Arg Gln
        435                 440                 445
Ala Ile Gly Glu Gly Gly Ser Ser Asp Ser Asn Leu Lys Thr Phe Leu
    450                 455                 460
Trp Glu Ile Asp Leu Glu Ile
465                 470
```

<210> 298
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT75-281-2

```
<400> 298
Met Met Arg Asn His His Phe Leu Leu Val Cys Phe Pro Ser Gln Gly
 1               5                  10                  15
Tyr Ile Asn Pro Ser Leu Gln Leu Ala Arg Arg Leu Ile Ser Leu Gly
            20                  25                  30
Val Asn Val Thr Phe Ala Thr Thr Val Leu Ala Gly Arg Arg Met Lys
        35                  40                  45
Asn Lys Thr His Gln Thr Ala Thr Thr Pro Gly Leu Ser Phe Ala Thr
    50                  55                  60
Phe Ser Asp Gly Phe Asp Asp Glu Thr Leu Lys Pro Asn Gly Asp Leu
65                  70                  75                  80
Thr His Tyr Phe Ser Glu Leu Arg Arg Cys Gly Ser Glu Ser Leu Thr
                85                  90                  95
His Leu Ile Thr Ser Ala Ala Asn Glu Gly Arg Pro Ile Thr Phe Val
            100                 105                 110
Ile Tyr Ser Leu Leu Leu Ser Trp Ala Ala Asp Ile Ala Ser Thr Tyr
        115                 120                 125
Asp Ile Pro Ser Ala Leu Phe Phe Ala Gln Pro Ala Thr Val Leu Ala
```

```
    130                 135                 140
Leu Tyr Phe Tyr Tyr Phe His Gly Tyr Gly Asp Thr Ile Cys Ser Lys
145                 150                 155                 160
Leu Gln Asp Pro Ser Ser Tyr Ile Glu Leu Pro Gly Leu Pro Leu Leu
                165                 170                 175
Thr Ser Gln Asp Met Pro Ser Phe Phe Ser Pro Ser Gly Pro His Ala
            180                 185                 190
Phe Ile Leu Pro Pro Met Arg Glu Gln Ala Glu Phe Leu Gly Arg Gln
        195                 200                 205
Ser Gln Pro Lys Val Leu Val Asn Thr Phe Asp Ala Leu Glu Ala Asp
    210                 215                 220
Ala Leu Arg Ala Ile Asp Lys Leu Lys Met Leu Ala Ile Gly Pro Leu
225                 230                 235                 240
Ile Pro Ser Ala Leu Leu Gly Gly Asn Asp Ser Ser Asp Ala Ser Phe
                245                 250                 255
Cys Gly Asp Leu Phe Gln Val Ser Ser Glu Asp Tyr Ile Glu Trp Leu
            260                 265                 270
Asn Ser Lys Pro Asp Ser Ser Val Val Tyr Ile Ser Val Gly Ser Ile
        275                 280                 285
Cys Val Leu Ser Asp Glu Gln Glu Asp Glu Leu Val His Ala Leu Leu
    290                 295                 300
Asn Ser Gly His Thr Phe Leu Trp Val Lys Arg Ser Lys Glu Asn Asn
305                 310                 315                 320
Glu Gly Val Lys Gln Glu Thr Asp Glu Glu Lys Leu Lys Lys Leu Glu
                325                 330                 335
Glu Gln Gly Lys Met Val Ser Trp Cys Arg Gln Val Glu Val Leu Lys
            340                 345                 350
His Pro Ala Leu Gly Cys Phe Leu Thr His Cys Gly Trp Asn Ser Thr
        355                 360                 365
Ile Glu Ser Leu Val Ser Gly Leu Pro Val Val Ala Phe Pro Gln Gln
    370                 375                 380
Ile Asp Gln Ala Thr Asn Ala Lys Leu Ile Glu Asp Val Trp Lys Thr
385                 390                 395                 400
Gly Val Arg Val Lys Ala Asn Thr Glu Gly Ile Val Glu Arg Glu Glu
                405                 410                 415
Ile Arg Arg Cys Leu Asp Leu Val Met Gly Ser Arg Asp Gly Gln Lys
            420                 425                 430
Glu Glu Ile Glu Arg Asn Ala Lys Lys Trp Lys Glu Leu Ala Arg Gln
        435                 440                 445
Ala Ile Gly Glu Gly Gly Ser Ser Asp Ser Asn Leu Lys Thr Phe Leu
    450                 455                 460
Trp Glu Ile Asp Leu Glu Ile
465                 470
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<210> 299
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85-269-4

<400> 299

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

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Gln Lys Thr Ile Ala Glu Leu Ala Lys Gln Ala Lys Tyr Lys Val Ser
        435                 440                 445
Lys Asp Gly Thr Ser Tyr Gln Asn Leu Glu Cys Leu Ile Gln Asp Ile
    450                 455                 460
Lys Lys Leu Asn Gln Ile Glu Gly Phe Ile Asn Asn Pro Asn Phe Ser
465                 470                 475                 480
Asp Leu Leu Arg Val
                485
```

<210> 300
<211> 419
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT85-269-1

<400> 300

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

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

<210> 301
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT94-289-1

<400> 301

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

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

<210> 302
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT94-289-2

<400> 302
Met Asp Ala Gln Gln Gly His Thr Thr Thr Ile Leu Met Leu Pro Trp
 1               5                  10                  15
Val Gly Tyr Gly His Leu Leu Pro Phe Leu Glu Leu Ala Lys Ser Leu
            20                  25                  30
Ser Arg Arg Lys Leu Phe His Ile Tyr Phe Cys Ser Thr Ser Val Ser
        35                  40                  45
Leu Asp Ala Ile Lys Pro Lys Leu Pro Pro Ser Ile Ser Ser Asp Asp
    50                  55                  60
Ser Ile Gln Leu Val Glu Leu Arg Leu Pro Ser Ser Pro Glu Leu Pro

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

<210> 303
<211> 452
<212> PRT

<213> Artificial Sequence

<220>
<223> UGT94-289-3

<400> 303
Met Asp Ala Ala Gln Gln Gly Asp Thr Thr Thr Ile Leu Met Leu Pro
 1               5                  10                  15
Trp Leu Gly Tyr Gly His Leu Ser Ala Phe Leu Glu Leu Ala Lys Ser
            20                  25                  30
Leu Ser Arg Arg Asn Phe His Ile Tyr Phe Cys Ser Thr Ser Val Asn
        35                  40                  45
Leu Asp Ala Ile Lys Pro Lys Leu Pro Ser Ser Phe Ser Asp Ser Ile
    50                  55                  60
Gln Phe Val Glu Leu His Leu Pro Ser Ser Pro Glu Phe Pro Pro His
65                  70                  75                  80
Leu His Thr Thr Asn Gly Leu Pro Pro Thr Leu Met Pro Ala Leu His
                85                  90                  95
Gln Ala Phe Ser Met Ala Ala Gln His Phe Glu Ser Ile Leu Gln Thr
            100                 105                 110
Leu Ala Pro His Leu Leu Ile Tyr Asp Ser Leu Gln Pro Trp Ala Pro
        115                 120                 125
Arg Val Ala Ser Ser Leu Lys Ile Pro Ala Ile Asn Phe Asn Thr Thr
    130                 135                 140
Gly Val Phe Val Ile Ser Gln Gly Leu His Pro Ile His Tyr Pro His
145                 150                 155                 160
Ser Lys Phe Pro Phe Ser Glu Phe Val Leu His Asn His Trp Lys Ala
                165                 170                 175
Met Tyr Ser Thr Ala Asp Gly Ala Ser Thr Glu Arg Thr Arg Lys Arg
            180                 185                 190
Gly Glu Ala Phe Leu Tyr Cys Leu His Ala Ser Cys Ser Val Ile Leu
        195                 200                 205
Ile Asn Ser Phe Arg Glu Leu Glu Gly Lys Tyr Met Asp Tyr Leu Ser
    210                 215                 220
Val Leu Leu Asn Lys Lys Val Val Pro Val Gly Pro Leu Val Tyr Glu
225                 230                 235                 240
Pro Asn Gln Asp Gly Glu Asp Glu Gly Tyr Ser Ser Ile Lys Asn Trp
                245                 250                 255
Leu Asp Lys Lys Glu Pro Ser Ser Thr Val Phe Val Ser Phe Gly Ser
            260                 265                 270
Glu Tyr Phe Pro Ser Lys Glu Glu Met Glu Glu Ile Ala His Gly Leu
        275                 280                 285
Glu Ala Ser Glu Val Asn Phe Ile Trp Val Val Arg Phe Pro Gln Gly
    290                 295                 300
Asp Asn Thr Ser Gly Ile Glu Asp Ala Leu Pro Lys Gly Phe Leu Glu
305                 310                 315                 320
Arg Ala Gly Glu Arg Gly Met Val Val Lys Gly Trp Ala Pro Gln Ala
                325                 330                 335
Lys Ile Leu Lys His Trp Ser Thr Gly Gly Phe Val Ser His Cys Gly
            340                 345                 350
Trp Asn Ser Val Met Glu Ser Met Met Phe Gly Val Pro Ile Ile Gly
        355                 360                 365
Val Pro Met His Val Asp Gln Pro Phe Asn Ala Gly Leu Val Glu Glu
    370                 375                 380

Ala Gly Val Gly Val Glu Ala Lys Arg Asp Pro Asp Gly Lys Ile Gln
385 390 395 400
Arg Asp Glu Val Ala Lys Leu Ile Lys Glu Val Val Val Glu Lys Thr
405 410 415
Arg Glu Asp Val Arg Lys Lys Ala Arg Glu Met Ser Glu Ile Leu Arg
420 425 430
Ser Lys Gly Glu Glu Lys Phe Asp Glu Met Val Ala Glu Ile Ser Leu
435 440 445
Leu Leu Lys Ile
450

<210> 304
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> 330

<400> 304
Met Asp Thr Arg Lys Arg Ser Ile Arg Ile Leu Met Phe Pro Trp Leu
1 5 10 15
Ala His Gly His Ile Ser Ala Phe Leu Glu Leu Ala Lys Ser Leu Ala
20 25 30
Lys Arg Asn Phe Val Ile Tyr Ile Cys Ser Ser Gln Val Asn Leu Asn
35 40 45
Ser Ile Ser Lys Asn Met Ser Ser Lys Asp Ser Ile Ser Val Lys Leu
50 55 60
Val Glu Leu His Ile Pro Thr Thr Ile Leu Pro Pro Pro Tyr His Thr
65 70 75 80
Thr Asn Gly Leu Pro Pro His Leu Met Ser Thr Leu Lys Arg Ala Leu
85 90 95
Asp Ser Ala Arg Pro Ala Phe Ser Thr Leu Leu Gln Thr Leu Lys Pro
100 105 110
Asp Leu Val Leu Tyr Asp Phe Leu Gln Ser Trp Ala Ser Glu Glu Ala
115 120 125
Glu Ser Gln Asn Ile Pro Ala Met Val Phe Leu Ser Thr Gly Ala Ala
130 135 140
Ala Ile Ser Phe Ile Met Tyr His Trp Phe Glu Thr Arg Pro Glu Glu
145 150 155 160
Tyr Pro Phe Pro Ala Ile Tyr Phe Arg Glu His Glu Tyr Asp Asn Phe
165 170 175
Cys Arg Phe Lys Ser Ser Asp Ser Gly Thr Ser Asp Gln Leu Arg Val
180 185 190
Ser Asp Cys Val Lys Arg Ser His Asp Leu Val Leu Ile Lys Thr Phe
195 200 205
Arg Glu Leu Glu Gly Gln Tyr Val Asp Phe Leu Ser Asp Leu Thr Arg
210 215 220
Lys Arg Phe Val Pro Val Gly Pro Leu Val Gln Glu Val Gly Cys Asp
225 230 235 240
Met Glu Asn Glu Gly Asn Asp Ile Ile Glu Trp Leu Asp Gly Lys Asp
245 250 255
Arg Arg Ser Thr Val Phe Ser Ser Phe Gly Ser Glu Tyr Phe Leu Ser

```
            260                 265                 270
Ala Asn Glu Ile Glu Glu Ile Ala Tyr Gly Leu Glu Leu Ser Gly Leu
        275                 280                 285
Asn Phe Ile Trp Val Val Arg Phe Pro His Gly Asp Glu Lys Ile Lys
    290                 295                 300
Ile Glu Glu Lys Leu Pro Glu Gly Phe Leu Glu Arg Val Glu Gly Arg
305                 310                 315                 320
Gly Leu Val Val Glu Gly Trp Ala Gln Gln Arg Arg Ile Leu Ser His
                325                 330                 335
Pro Ser Val Gly Gly Phe Leu Ser His Cys Gly Trp Ser Ser Val Met
            340                 345                 350
Glu Gly Val Tyr Ser Gly Val Pro Ile Ile Ala Val Pro Met His Leu
        355                 360                 365
Asp Gln Pro Phe Asn Ala Arg Leu Val Glu Ala Val Gly Phe Gly Glu
    370                 375                 380
Glu Val Val Arg Ser Arg Gln Gly Asn Leu Asp Arg Gly Glu Val Ala
385                 390                 395                 400
Arg Val Val Lys Lys Leu Val Met Gly Lys Ser Gly Glu Gly Leu Arg
                405                 410                 415
Arg Arg Val Glu Glu Leu Ser Glu Lys Met Arg Glu Lys Gly Glu Glu
            420                 425                 430
Glu Ile Asp Ser Leu Val Glu Glu Leu Val Thr Val Val Arg Arg Arg
        435                 440                 445
Glu Arg Ser Asn Leu Lys Ser Glu Asn Ser Met Lys Lys Leu Asn Val
    450                 455                 460
Met Asp Asp Gly Glu
465
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<210> 305
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> 330

<400> 305
atggatacaa gaaagagaag catcaggatt ctaatgttcc catggcttgc tcatggccat 60
atctcagcat tcctcgagct ggcgaagtca cttgccaaaa gaaacttcgt catttacatt 120
tgttcttcac aagtaaatct aaattccatc agcaagaaca tgtcatcaaa agactccatt 180
tccgtaaaac ttgttgagct tcacattccc accaccatac ttccccctcc ttaccacacc 240
accaatggcc tcccacccca cctcatgtcc accctcaaga gagccctcga cagtgcccgg 300
cccgccttct ccaccctcct ccaaaccctc aagcccgact tggttttata cgatttcctc 360
cagtcgtggg cctcggagga ggccgagtcg cagaatatac cagccatggt gtttctgagt 420
accggagctg cagcgatttc ttttattatg taccattggt ttgagaccag accggaggag 480
tacccttttc cggctatata cttccgggaa cacgagtatg ataacttctg ccgttttaag 540
tcttccgaca gcggtactag tgatcaattg agagtcagcg attgcgttaa acggtcgcac 600
gatttggttc tgatcaagac attccgtgaa ctggaaggac aatacgtaga ttttctctcc 660
gacttgactc ggaagagatt cgtaccagtt ggccccttg ttcaggaggt aggttgtgat 720
atggagaatg aaggaaatga catcatcgaa tggctcgacg ggaaagaccg tcgttcgacg 780
gttttctcct cattcgggag cgagtacttc ttgtctgcca atgagatcga agagatagct 840
tatgggctgg agctaagcgg gcttaacttc atctgggttg ttaggtttcc tcatggcgac 900
gagaaaatca agattgagga gaaactgccg gaagggtttc ttgagagagt ggaaggaaga 960
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gggttggtgg tggagggatg ggcacagcag aggagaatat tgtcacatcc gagtgttgga 1020
gggtttttga gccactgtgg gtggagttct gtgatggaag gggtgtattc cggtgtgccg 1080
attattgccg tgccgatgca tcttgaccag ccgttcaatg ctaggttggt ggaggcggtg 1140
gggtttgggg aggaggtggt gaggagtaga caaggaaatc ttgacagagg agaggtggcg 1200
agggtggtga agaagctggt tatggggaaa agtggggagg ggttacggcg gagggtggag 1260
gagttgagtg agaagatgag agagaaaggg gaggaggaga ttgattcact ggtggaggaa 1320
ttggtgacgg tggttaggag gagagagaga tcgaatctca agtctgagaa ttctatgaag 1380
aaattgaatg tgatggatga tggagaatag 1410

<210> 306
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT98 Native host S. grosvenorii

<400> 306
Met Asp Ala Gln Arg Gly His Thr Thr Thr Ile Leu Met Phe Pro Trp
 1               5                  10                  15
Leu Gly Tyr Gly His Leu Ser Ala Phe Leu Glu Leu Ala Lys Ser Leu
            20                  25                  30
Ser Arg Arg Asn Phe His Ile Tyr Phe Cys Ser Thr Ser Val Asn Leu
        35                  40                  45
Asp Ala Ile Lys Pro Lys Leu Pro Ser Ser Ser Ser Ser Asp Ser Ile
    50                  55                  60
Gln Leu Val Glu Leu Cys Leu Pro Ser Ser Pro Asp Gln Leu Pro Pro
65                  70                  75                  80
His Leu His Thr Thr Asn Ala Leu Pro Pro His Leu Met Pro Thr Leu
                85                  90                  95
His Gln Ala Phe Ser Met Ala Ala Gln His Phe Ala Ala Ile Leu His
            100                 105                 110
Thr Leu Ala Pro His Leu Leu Ile Tyr Asp Ser Phe Gln Pro Trp Ala
        115                 120                 125
Pro Gln Leu Ala Ser Ser Leu Asn Ile Pro Ala Ile Asn Phe Asn Thr
    130                 135                 140
Thr Gly Ala Ser Val Leu Thr Arg Met Leu His Ala Thr His Tyr Pro
145                 150                 155                 160
Ser Ser Lys Phe Pro Ile Ser Glu Phe Val Leu His Asp Tyr Trp Lys
                165                 170                 175
Ala Met Tyr Ser Ala Ala Gly Gly Ala Val Thr Lys Lys Asp His Lys
            180                 185                 190
Ile Gly Glu Thr Leu Ala Asn Cys Leu His Ala Ser Cys Ser Val Ile
        195                 200                 205
Leu Ile Asn Ser Phe Arg Glu Leu Glu Glu Lys Tyr Met Asp Tyr Leu
    210                 215                 220
Ser Val Leu Leu Asn Lys Lys Val Val Pro Val Gly Pro Leu Val Tyr
225                 230                 235                 240
Glu Pro Asn Gln Asp Gly Glu Asp Glu Gly Tyr Ser Ser Ile Lys Asn
                245                 250                 255
Trp Leu Asp Lys Lys Glu Pro Ser Ser Thr Val Phe Val Ser Phe Gly
            260                 265                 270
Ser Glu Tyr Phe Pro Ser Lys Glu Glu Met Glu Glu Ile Ala His Gly
        275                 280                 285

```
Leu Glu Ala Ser Glu Val His Phe Ile Trp Val Val Arg Phe Pro Gln
    290                 295                 300
Gly Asp Asn Thr Ser Ala Ile Glu Asp Ala Leu Pro Lys Gly Phe Leu
305                 310                 315                 320
Glu Arg Val Gly Glu Arg Gly Met Val Val Lys Gly Trp Ala Pro Gln
                325                 330                 335
Ala Lys Ile Leu Lys His Trp Ser Thr Gly Gly Phe Val Ser His Cys
            340                 345                 350
Gly Trp Asn Ser Val Met Glu Ser Met Met Phe Gly Val Pro Ile Ile
        355                 360                 365
Gly Val Pro Met His Leu Asp Gln Pro Phe Asn Ala Gly Leu Ala Glu
    370                 375                 380
Glu Ala Gly Val Gly Val Glu Ala Lys Arg Asp Ser Asp Gly Lys Ile
385                 390                 395                 400
Gln Arg Glu Glu Val Ala Lys Ser Ile Lys Glu Val Val Ile Glu Lys
                405                 410                 415
Thr Arg Glu Asp Val Arg Lys Lys Ala Arg Glu Met Gly Glu Ile Leu
            420                 425                 430
Arg Ser Lys Gly Asp Glu Lys Ile Asp Glu Leu Val Ala Glu Ile Ser
        435                 440                 445
Leu Leu Arg Lys Lys Ala Pro Cys Ser Ile Ala Ala Ala Leu Glu His
    450                 455                 460
His His His His His
465
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<210> 307
<211> 1419
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT98 Native host S. grosvenorii

<400> 307

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ctcgaattca tggatgccca gcgaggtcac accacaacca ttttgatgtt tccatggctc 60
ggctatggcc atctttcggc tttcctagag ttggccaaaa gcctctcaag gaggaacttc 120
catatctact tctgttcaac ctctgttaac ctcgacgcca ttaaaccaaa gcttccttct 180
tcttcctctt ctgattccat ccaacttgtg gaactttgtc ttccatcttc tcctgatcag 240
ctccctcctc atcttcacac aaccaacgcc ctccccccctc acctcatgcc cactctccac 300
caagccttct ccatggctgc ccaacacttt gctgccattt tacacacact tgctccgcat 360
ctcctcattt acgactcttt ccaaccttgg gctcctcaac tagcttcatc cctcaacatt 420
ccagccatca acttcaatac tacgggagct tcagtcctga cccgaatgct tcacgctact 480
cactacccaa gttctaaatt cccaatttca gagtttgttc tccacgatta ttggaaagcc 540
atgtacagcg ccgccggtgg ggctgttaca aaaaaagacc acaaaattgg agaaacactt 600
gcgaattgct tgcatgcttc ttgtagtgta attctaatca atagtttcag agagctcgag 660
gagaaatata tggattatct ctccgttctc ttgaacaaga aagttgttcc ggttggtcct 720
ttggtttacg aaccgaatca agacggggaa gatgaaggtt attcaagcat caaaaattgg 780
cttgacaaaa aggaaccgtc ctccaccgtc ttcgtttcat ttggaagcga atacttcccg 840
tcaaaggaag aaatggaaga gatagcccat gggttagagg cgagcgaggt tcatttcatc 900
tgggtcgtta ggtttcctca aggagacaac accagcgcca ttgaagatgc cttgccgaag 960
gggtttctgg agagggtggg agagagaggg atggtggtga agggttgggc tccccaggcg 1020
aagatactga agcattggag cacaggggga ttcgtgagcc actgtggatg gaactcggtg 1080
atggaaagca tgatgtttgg cgttcccata atagggggttc cgatgcatct ggaccagccc 1140
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tttaacgccg gactcgcgga agaagctggc gtcggcgtgg aagccaagcg agattcggac 1200
ggcaaaattc aaagagaaga agttgcaaag tcgatcaaag aagtggtgat tgagaaaacc 1260
agggaagacg tgaggaagaa agcaagagaa atgggtgaga ttttgaggag taaaggagat 1320
gagaaaattg atgagttggt ggctgaaatt tctcttttgc gcaaaaaggc cccatgttca 1380
attgcggccg cactcgagca ccaccaccac caccactga 1419

<210> 308
<211> 520
<212> PRT
<213> Artificial Sequence

<220>
<223> CYP 1798

<400> 308
Met Glu Met Ser Ser Ser Val Ala Ala Thr Ile Ser Ile Trp Met Val
 1               5                  10                  15
Val Val Cys Ile Val Gly Val Gly Trp Arg Val Val Asn Trp Val Trp
            20                  25                  30
Leu Arg Pro Lys Lys Leu Glu Lys Arg Leu Arg Glu Gln Gly Leu Ala
        35                  40                  45
Gly Asn Ser Tyr Arg Leu Leu Phe Gly Asp Leu Lys Glu Arg Ala Ala
    50                  55                  60
Met Glu Glu Gln Ala Asn Ser Lys Pro Ile Asn Phe Ser His Asp Ile
65                  70                  75                  80
Gly Pro Arg Val Phe Pro Ser Met Tyr Lys Thr Ile Gln Asn Tyr Gly
                85                  90                  95
Lys Asn Ser Tyr Met Trp Leu Gly Pro Tyr Pro Arg Val His Ile Met
            100                 105                 110
Asp Pro Gln Gln Leu Lys Thr Val Phe Thr Leu Val Tyr Asp Ile Gln
        115                 120                 125
Lys Pro Asn Leu Asn Pro Leu Ile Lys Phe Leu Leu Asp Gly Ile Val
    130                 135                 140
Thr His Glu Gly Glu Lys Trp Ala Lys His Arg Lys Ile Ile Asn Pro
145                 150                 155                 160
Ala Phe His Leu Glu Lys Leu Lys Asp Met Ile Pro Ala Phe Phe His
                165                 170                 175
Ser Cys Asn Glu Ile Val Asn Glu Trp Glu Arg Leu Ile Ser Lys Glu
            180                 185                 190
Gly Ser Cys Glu Leu Asp Val Met Pro Tyr Leu Gln Asn Leu Ala Ala
        195                 200                 205
Asp Ala Ile Ser Arg Thr Ala Phe Gly Ser Ser Tyr Glu Glu Gly Lys
    210                 215                 220
Met Ile Phe Gln Leu Leu Lys Glu Leu Thr Asp Leu Val Val Lys Val
225                 230                 235                 240
Ala Phe Gly Val Tyr Ile Pro Gly Trp Arg Phe Leu Pro Thr Lys Ser
                245                 250                 255
Asn Asn Lys Met Lys Glu Ile Asn Arg Lys Ile Lys Ser Leu Leu Leu
            260                 265                 270
Gly Ile Ile Asn Lys Arg Gln Lys Ala Asn Met Glu Glu Gly Glu Ala
        275                 280                 285
Gly Gln Ser Asp Leu Leu Gly Ile Leu Met Glu Ser Asn Ser Asn Glu
    290                 295                 300
Ile Gln Gly Glu Gly Asn Asn Lys Glu Asp Gly Met Ser Ile Glu Asp

305 310 315 320
Val Ile Glu Glu Cys Lys Val Phe Tyr Ile Gly Gly Gln Glu Thr Thr
325 330 335
Ala Arg Leu Leu Ile Trp Thr Met Ile Leu Leu Ser Ser His Thr Glu
340 345 350
Trp Gln Glu Arg Ala Arg Thr Glu Val Leu Lys Val Phe Gly Asn Lys
355 360 365
Lys Pro Asp Phe Asp Gly Leu Ser Arg Leu Lys Val Val Thr Met Ile
370 375 380
Leu Asn Glu Val Leu Arg Leu Tyr Pro Pro Ala Ser Met Leu Thr Arg
385 390 395 400
Ile Ile Gln Lys Glu Thr Arg Val Gly Lys Leu Thr Leu Pro Ala Gly
405 410 415
Val Ile Leu Ile Met Pro Ile Ile Leu Ile His Arg Asp His Asp Leu
420 425 430
Trp Gly Glu Asp Ala Asn Glu Phe Lys Pro Glu Arg Phe Ser Lys Gly
435 440 445
Val Ser Lys Ala Ala Lys Val Gln Pro Ala Phe Phe Pro Phe Gly Trp
450 455 460
Gly Arg Ile Cys Met Gly Gln Asn Phe Ala Met Ile Glu Ala Lys Met
465 470 475 480
Ala Leu Ser Leu Ile Leu Gln Arg Phe Ser Phe Glu Leu Ser Ser Ser
485 490 495
Tyr Val His Ala Pro Thr Val Val Phe Thr Thr Gln Pro Gln His Gly
500 505 510
Ala His Ile Val Leu Arg Lys Leu
515 520

<210> 309
<211> 316
<212> PRT
<213> Artificial Sequence

<220>
<223> Epoxide hydrolase

<400> 309
Met Asp Ala Ile Glu His Arg Thr Val Ser Val Asn Gly Ile Asn Ser
1 5 10 15
His Val Ala Glu Lys Gly Glu Gly Pro Val Val Leu Leu Leu His Gly
20 25 30
Phe Pro Glu Leu Trp Tyr Ser Trp Arg His Gln Ile Leu Ala Leu Ser
35 40 45
Ser Leu Gly Tyr Arg Ala Val Ala Pro Asp Leu Arg Gly Tyr Gly Asp
50 55 60
Thr Asp Ala Pro Gly Ser Ile Ser Ser Tyr Thr Cys Phe His Ile Val
65 70 75 80
Gly Asp Leu Val Ala Leu Val Glu Ser Leu Gly Met Asp Arg Val Phe
85 90 95
Val Val Ala His Asp Trp Gly Ala Met Ile Ala Trp Cys Leu Cys Leu
100 105 110
Phe Arg Pro Glu Met Val Lys Ala Phe Val Cys Leu Ser Val Pro Phe
115 120 125

```
Arg Gln Arg Asn Pro Lys Met Lys Pro Val Gln Ser Met Arg Ala Phe
    130                 135                 140
Phe Gly Asp Asp Tyr Tyr Ile Cys Arg Phe Gln Asn Pro Gly Glu Ile
145                 150                 155                 160
Glu Glu Glu Met Ala Gln Val Gly Ala Arg Glu Val Leu Arg Gly Ile
                165                 170                 175
Leu Thr Ser Arg Arg Pro Gly Pro Pro Ile Leu Pro Lys Gly Gln Ala
            180                 185                 190
Phe Arg Ala Arg Pro Gly Ala Ser Thr Ala Leu Pro Ser Trp Leu Ser
        195                 200                 205
Glu Lys Asp Leu Ser Phe Phe Ala Ser Lys Tyr Asp Gln Lys Gly Phe
    210                 215                 220
Thr Gly Pro Leu Asn Tyr Tyr Arg Ala Met Asp Leu Asn Trp Glu Leu
225                 230                 235                 240
Thr Ala Ser Trp Thr Gly Val Gln Val Lys Val Pro Val Lys Tyr Ile
                245                 250                 255
Val Gly Asp Val Asp Met Val Phe Thr Thr Pro Gly Val Lys Glu Tyr
            260                 265                 270
Val Asn Gly Gly Gly Phe Lys Lys Asp Val Pro Phe Leu Gln Glu Val
        275                 280                 285
Val Ile Met Glu Gly Val Gly His Phe Ile Asn Gln Glu Lys Gln Glu
    290                 295                 300
Ile Ser Ser His Ile Met Asp Phe Ile Ser Lys Phe
305                 310                 315
```

<210> 310
<211> 316
<212> PRT
<213> Artificial Sequence

<220>
<223> Epoxide hydrolase

<400> 310

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

145 150 155 160
Glu Glu Asp Phe Ala Ser Ile Asp Thr Ala Gln Leu Phe Lys Thr Ser
165 170 175
Leu Cys Asn Arg Ser Ser Ala Pro Pro Cys Leu Pro Lys Glu Ile Gly
180 185 190
Phe Arg Ala Ile Pro Pro Pro Glu Asn Leu Pro Ser Trp Leu Thr Glu
195 200 205
Glu Asp Ile Asn Phe Tyr Ala Ala Lys Phe Lys Gln Thr Gly Phe Thr
210 215 220
Gly Ala Leu Asn Tyr Tyr Arg Ala Phe Asp Leu Thr Trp Glu Leu Thr
225 230 235 240
Ala Pro Trp Thr Gly Ala Gln Ile Gln Val Pro Val Lys Phe Ile Val
245 250 255
Gly Asp Ser Asp Leu Thr Tyr His Phe Pro Gly Ala Lys Glu Tyr Ile
260 265 270
His Asn Gly Gly Phe Lys Arg Asp Val Pro Leu Leu Glu Glu Val Val
275 280 285
Val Val Lys Asp Ala Cys His Phe Phe Asn Gln Glu Arg Pro Gln Glu
290 295 300
Ile Asn Ala His Ile His Asp Phe Ile Asn Lys Phe
305 310 315

<210> 311
<211> 316
<212> PRT
<213> Artificial Sequence

<220>
<223> Epoxide hydrolase

<400> 311
Met Glu Asn Ile Glu His Thr Thr Val Gln Thr Asn Gly Ile Lys Met
1 5 10 15
His Val Ala Ala Ile Gly Thr Gly Pro Pro Val Leu Leu Leu His Gly
20 25 30
Phe Pro Glu Leu Trp Tyr Ser Trp Arg His Gln Leu Leu Tyr Leu Ser
35 40 45
Ser Ala Gly Tyr Arg Ala Ile Ala Pro Asp Leu Arg Gly Tyr Gly Asp
50 55 60
Thr Asp Ala Pro Pro Ser Pro Ser Ser Tyr Thr Ala Leu His Ile Val
65 70 75 80
Gly Asp Leu Val Gly Leu Leu Asp Val Leu Gly Ile Glu Lys Val Phe
85 90 95
Leu Ile Gly His Asp Trp Gly Ala Ile Ile Ala Trp Tyr Phe Cys Leu
100 105 110
Phe Arg Pro Asp Arg Ile Lys Ala Leu Val Asn Leu Ser Val Gln Phe
115 120 125
Phe Pro Arg Asn Pro Thr Thr Pro Phe Val Lys Gly Phe Arg Ala Val
130 135 140
Leu Gly Asp Gln Phe Tyr Met Val Arg Phe Gln Glu Pro Gly Lys Ala
145 150 155 160
Glu Glu Glu Phe Ala Ser Val Asp Ile Arg Glu Phe Phe Lys Asn Val
165 170 175

```
Leu Ser Asn Arg Asp Pro Gln Ala Pro Tyr Leu Pro Asn Glu Val Lys
            180                 185                 190
Phe Glu Gly Val Pro Pro Pro Ala Leu Ala Pro Trp Leu Thr Pro Glu
        195                 200                 205
Asp Ile Asp Val Tyr Ala Asp Lys Phe Ala Glu Thr Gly Phe Thr Gly
    210                 215                 220
Gly Leu Asn Tyr Tyr Arg Ala Phe Asp Arg Thr Trp Glu Leu Thr Ala
225                 230                 235                 240
Pro Trp Thr Gly Ala Arg Ile Gly Val Pro Val Lys Phe Ile Val Gly
                245                 250                 255
Asp Leu Asp Leu Thr Tyr His Phe Pro Gly Ala Gln Lys Tyr Ile His
            260                 265                 270
Gly Glu Gly Phe Lys Lys Ala Val Pro Gly Leu Glu Glu Val Val Val
        275                 280                 285
Met Glu Asp Thr Ser His Phe Ile Asn Gln Glu Arg Pro His Glu Ile
    290                 295                 300
Asn Ser His Ile His Asp Phe Phe Ser Lys Phe Cys
305                 310                 315


<210> 312
<211> 316
<212> PRT
<213> Artificial Sequence

<220>
<223> Epoxide hydrolase

<400> 312
Met Asp Gln Ile Glu His Ile Thr Ile Asn Thr Asn Gly Ile Lys Met
 1               5                  10                  15
His Ile Ala Ser Val Gly Thr Gly Pro Val Val Leu Leu Leu His Gly
            20                  25                  30
Phe Pro Glu Leu Trp Tyr Ser Trp Arg His Gln Leu Leu Tyr Leu Ser
        35                  40                  45
Ser Val Gly Tyr Arg Ala Ile Ala Pro Asp Leu Arg Gly Tyr Gly Asp
    50                  55                  60
Thr Asp Ser Pro Ala Ser Pro Thr Ser Tyr Thr Ala Leu His Ile Val
65                  70                  75                  80
Gly Asp Leu Val Gly Ala Leu Asp Glu Leu Gly Ile Glu Lys Val Phe
                85                  90                  95
Leu Val Gly His Asp Trp Ala Ala Ile Ile Ala Trp Tyr Phe Cys Leu
            100                 105                 110
Phe Arg Pro Asp Arg Ile Lys Ala Leu Val Asn Leu Ser Val Gln Phe
        115                 120                 125
Ile Pro Arg Asn Pro Ala Ile Pro Phe Ile Glu Gly Phe Arg Thr Ala
    130                 135                 140
Phe Gly Asp Asp Phe Tyr Met Cys Arg Phe Gln Val Pro Gly Glu Ala
145                 150                 155                 160
Glu Glu Asp Phe Ala Ser Ile Asp Thr Ala Gln Leu Phe Lys Thr Ser
                165                 170                 175
Leu Cys Asn Arg Ser Ser Ala Pro Pro Cys Leu Pro Lys Glu Ile Gly
            180                 185                 190
Phe Arg Ala Ile Pro Pro Pro Glu Asn Leu Pro Ser Trp Leu Thr Glu
```

```
        195                 200                 205
Glu Asp Ile Asn Tyr Tyr Ala Ala Lys Phe Lys Gln Thr Gly Phe Thr
    210                 215                 220
Gly Ala Leu Asn Tyr Tyr Arg Ala Phe Asp Leu Thr Trp Glu Leu Thr
225                 230                 235                 240
Ala Pro Trp Thr Gly Ala Gln Ile Gln Val Pro Val Lys Phe Ile Val
                245                 250                 255
Gly Asp Ser Asp Leu Thr Tyr His Phe Pro Gly Ala Lys Glu Tyr Ile
            260                 265                 270
His Asn Gly Gly Phe Lys Lys Asp Val Pro Leu Leu Glu Glu Val Val
        275                 280                 285
Val Val Lys Asp Ala Cys His Phe Ile Asn Gln Glu Arg Pro Gln Glu
    290                 295                 300
Ile Asn Ala His Ile His Asp Phe Ile Asn Lys Phe
305                 310                 315


<210> 313
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> Epoxide hydrolase

<400> 313
Met Glu Lys Ile Glu His Ser Thr Ile Ala Thr Asn Gly Ile Asn Met
 1               5                  10                  15
His Val Ala Ser Ala Gly Ser Gly Pro Ala Val Leu Phe Leu His Gly
            20                  25                  30
Phe Pro Glu Leu Trp Tyr Ser Trp Arg His Gln Leu Leu Tyr Leu Ser
        35                  40                  45
Ser Leu Gly Tyr Arg Ala Ile Ala Pro Asp Leu Arg Gly Phe Gly Asp
    50                  55                  60
Thr Asp Ala Pro Pro Ser Pro Ser Ser Tyr Thr Ala His His Ile Val
65                  70                  75                  80
Gly Asp Leu Val Gly Leu Leu Asp Gln Leu Gly Val Asp Gln Val Phe
                85                  90                  95
Leu Val Gly His Asp Trp Gly Ala Met Met Ala Trp Tyr Phe Cys Leu
            100                 105                 110
Phe Arg Pro Asp Arg Val Lys Ala Leu Val Asn Leu Ser Val His Phe
        115                 120                 125
Thr Pro Arg Asn Pro Ala Ile Ser Pro Leu Asp Gly Phe Arg Leu Met
    130                 135                 140
Leu Gly Asp Asp Phe Tyr Val Cys Lys Phe Gln Glu Pro Gly Val Ala
145                 150                 155                 160
Glu Ala Asp Phe Gly Ser Val Asp Thr Ala Thr Met Phe Lys Lys Phe
                165                 170                 175
Leu Thr Met Arg Asp Pro Arg Pro Pro Ile Ile Pro Asn Gly Phe Arg
            180                 185                 190
Ser Leu Ala Thr Pro Glu Ala Leu Pro Ser Trp Leu Thr Glu Glu Asp
        195                 200                 205
Ile Asp Tyr Phe Ala Ala Lys Phe Ala Lys Thr Gly Phe Thr Gly Gly
    210                 215                 220
```

Phe Asn Tyr Tyr Arg Ala Ile Asp Leu Thr Trp Glu Leu Thr Ala Pro
225 230 235 240
Trp Ser Gly Ser Glu Ile Lys Val Pro Thr Lys Phe Ile Val Gly Asp
245 250 255
Leu Asp Leu Val Tyr His Phe Pro Gly Val Lys Glu Tyr Ile His Gly
260 265 270
Gly Gly Phe Lys Lys Asp Val Pro Phe Leu Glu Glu Val Val Val Met
275 280 285
Glu Gly Ala Ala His Phe Ile Asn Gln Glu Lys Ala Asp Glu Ile Asn
290 295 300
Ser Leu Ile Tyr Asp Phe Ile Lys Gln Phe
305 310

<210> 314
<211> 316
<212> PRT
<213> Artificial Sequence

<220>
<223> Epoxide hydrolase

<400> 314
Met Glu Lys Ile Glu His Thr Thr Ile Ser Thr Asn Gly Ile Asn Met
1 5 10 15
His Val Ala Ser Ile Gly Ser Gly Pro Ala Val Leu Phe Leu His Gly
20 25 30
Phe Pro Glu Leu Trp Tyr Ser Trp Arg His Gln Leu Leu Phe Leu Ser
35 40 45
Ser Met Gly Tyr Arg Ala Ile Ala Pro Asp Leu Arg Gly Phe Gly Asp
50 55 60
Thr Asp Ala Pro Pro Ser Pro Ser Ser Tyr Thr Ala His His Ile Val
65 70 75 80
Gly Asp Leu Val Gly Leu Leu Asp Gln Leu Gly Ile Asp Gln Val Phe
85 90 95
Leu Val Gly His Asp Trp Gly Ala Met Met Ala Trp Tyr Phe Cys Leu
100 105 110
Phe Arg Pro Asp Arg Val Lys Ala Leu Val Asn Leu Ser Val His Phe
115 120 125
Leu Arg Arg His Pro Ser Ile Lys Phe Val Asp Gly Phe Arg Ala Leu
130 135 140
Leu Gly Asp Asp Phe Tyr Phe Cys Gln Phe Gln Glu Pro Gly Val Ala
145 150 155 160
Glu Ala Asp Phe Gly Ser Val Asp Val Ala Thr Met Leu Lys Lys Phe
165 170 175
Leu Thr Met Arg Asp Pro Arg Pro Pro Met Ile Pro Lys Glu Lys Gly
180 185 190
Phe Arg Ala Leu Glu Thr Pro Asp Pro Leu Pro Ala Trp Leu Thr Glu
195 200 205
Glu Asp Ile Asp Tyr Phe Ala Gly Lys Phe Arg Lys Thr Gly Phe Thr
210 215 220
Gly Gly Phe Asn Tyr Tyr Arg Ala Phe Asn Leu Thr Trp Glu Leu Thr
225 230 235 240
Ala Pro Trp Ser Gly Ser Glu Ile Lys Val Ala Ala Lys Phe Ile Val

```
                245                 250                 255
Gly Asp Leu Asp Leu Val Tyr His Phe Pro Gly Ala Lys Glu Tyr Ile
            260                 265                 270
His Gly Gly Gly Phe Lys Lys Asp Val Pro Leu Leu Glu Glu Val Val
        275                 280                 285
Val Val Asp Gly Ala Ala His Phe Ile Asn Gln Glu Arg Pro Ala Glu
    290                 295                 300
Ile Ser Ser Leu Ile Tyr Asp Phe Ile Lys Lys Phe
305                 310                 315


<210> 315
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> CYP87D18

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

```
Ile Gln Leu Leu Phe Ser Ile Ser Phe Ala Ser Phe Glu Ser Ile Ser
        275                 280                 285
Thr Thr Leu Thr Leu Ile Leu Lys Leu Leu Asp Glu His Pro Glu Val
    290                 295                 300
Val Lys Glu Leu Glu Ala Glu His Glu Ala Ile Arg Lys Ala Arg Ala
305                 310                 315                 320
Asp Pro Asp Gly Pro Ile Thr Trp Glu Glu Tyr Lys Ser Met Thr Phe
                325                 330                 335
Thr Leu Gln Val Ile Asn Glu Thr Leu Arg Leu Gly Ser Val Thr Pro
            340                 345                 350
Ala Leu Leu Arg Lys Thr Val Lys Asp Leu Gln Val Lys Gly Tyr Ile
        355                 360                 365
Ile Pro Glu Gly Trp Thr Ile Met Leu Val Thr Ala Ser Arg His Arg
    370                 375                 380
Asp Pro Lys Val Tyr Lys Asp Pro His Ile Phe Asn Pro Trp Arg Trp
385                 390                 395                 400
Lys Asp Leu Asp Ser Ile Thr Ile Gln Lys Asn Phe Met Pro Phe Gly
                405                 410                 415
Gly Gly Leu Arg His Cys Ala Gly Ala Glu Tyr Ser Lys Val Tyr Leu
            420                 425                 430
Cys Thr Phe Leu His Ile Leu Cys Thr Lys Tyr Arg Trp Thr Lys Leu
        435                 440                 445
Gly Gly Gly Arg Ile Ala Arg Ala His Ile Leu Ser Phe Glu Asp Gly
    450                 455                 460
Leu His Val Lys Phe Thr Pro Lys Glu
465                 470
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<210> 316
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> CYP87D18

<400> 316
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atgtggactg tcgtgctcgg tttggcgacg ctgtttgtcg cctactacat ccattggatt 60
aacaaatgga gagattccaa gttcaacgga gttctgccgc cgggcaccat gggtttgccg 120
ctcatcggag agacgattca actgagtcga cccagtgact ccctcgacgt tcacccttc 180
atccagaaaa aagttgaaag atacgggccg atcttcaaaa catgtctggc cggaaggccg 240
gtggtggtgt cggcggacgc agagttcaac aactacataa tgctgcagga aggaagagca 300
gtggaaatgt ggtatttgga tacgctctcc aaatttttcg gcctcgacac cgagtggctc 360
aaagctctgg gcctcatcca caagtacatc agaagcatta ctctcaatca cttcggcgcc 420
gaggccctgc gggagagatt tcttcctttt attgaagcat cctccatgga agcccttcac 480
tcctggtcta ctcaacctag cgtcgaagtc aaaaatgcct ccgctctcat ggtttttagg 540
acctcggtga ataagatgtt cggtgaggat gcgaagaagc tatcgggaaa tatccctggg 600
aagttcacga agcttctagg aggatttctc agtttaccac tgaattttcc cggcaccacc 660
taccacaaat gcttgaagga tatgaaggaa atccagaaga agctaagaga ggttgtagac 720
gatagattgg ctaatgtggg ccctgatgtg gaagatttct tggggcaagc ccttaaagat 780
aaggaatcag agaagttcat ttcagaggag ttcatcatcc aactgttgtt ttctatcagt 840
tttgctagct ttgagtccat ctccaccact cttactttga ttctcaagct ccttgatgaa 900
cacccagaag tagtgaaaga gttggaagct gaacacgagg cgattcgaaa agctagagca 960
gatccagatg gaccaattac ttgggaagaa tacaaatcca tgacttttac attacaagtc 1020
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atcaatgaaa ccctaaggtt ggggagtgtc acacctgcct tgttgaggaa aacagttaaa 1080
gatcttcaag taaaaggata cataatcccg gaaggatgga caataatgct tgtcaccgct 1140
tcacgtcaca gagacccaaa agtctataag gaccctcata tcttcaatcc atggcgttgg 1200
aaggacttgg actcaattac catccaaaag aacttcatgc cttttggggg aggcttaagg 1260
cattgtgctg gtgctgagta ctctaaagtc tacttgtgca ccttcttgca catcctctgt 1320
accaaatacc gatggaccaa acttgggggа ggaaggattg caagagctca tatattgagt 1380
tttgaagatg ggttacatgt gaagttcaca cccaaggaat ga 1422

<210> 317
<211> 688
<212> PRT
<213> Artificial Sequence

<220>
<223> AtCPR

<400> 317
Met Thr Ser Ala Leu Tyr Ala Ser Asp Leu Phe Lys Gln Leu Lys Ser
 1               5                  10                  15
Ile Met Gly Thr Asp Ser Leu Ser Asp Asp Val Val Leu Val Ile Ala
            20                  25                  30
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 Asp Asp Tyr Ala Ala Asp Asp Asp Gln Tyr Glu
        115                 120                 125
Glu Lys Leu Lys Lys Glu Thr Leu Ala Phe Phe Cys Val Ala Thr Tyr
    130                 135                 140
Gly Asp Gly Glu Pro Thr Asp Asn Ala Ala Arg Phe Tyr Lys Trp Phe
145                 150                 155                 160
Thr Glu Glu Asn Glu Arg Asp Ile Lys Leu Gln Gln Leu Ala Tyr Gly
                165                 170                 175
Val Phe Ala Leu Gly Asn Arg Gln Tyr Glu His Phe Asn Lys Ile Gly
            180                 185                 190
Ile Val Leu Asp Glu Glu Leu Cys Lys Lys Gly Ala Lys Arg Leu Ile
        195                 200                 205
Glu Val Gly Leu Gly Asp Asp Asp Gln Ser Ile Glu Asp Asp Phe Asn
    210                 215                 220
Ala Trp Lys Glu Ser Leu Trp Ser Glu Leu Asp Lys Leu Leu Lys Asp
225                 230                 235                 240
Glu Asp Asp Lys Ser Val Ala Thr Pro Tyr Thr Ala Val Ile Pro Glu
                245                 250                 255
Tyr Arg Val Val Thr His Asp Pro Arg Phe Thr Thr Gln Lys Ser Met
            260                 265                 270
Glu Ser Asn Val Ala Asn Gly Asn Thr Thr Ile Asp Ile His His Pro
        275                 280                 285
Cys Arg Val Asp Val Ala Val Gln Lys Glu Leu His Thr His Glu Ser

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    290                 295                 300
Asp Arg Ser Cys Ile His Leu Glu Phe Asp Ile Ser Arg Thr Gly Ile
305                 310                 315                 320
Thr Tyr Glu Thr Gly Asp His Val Gly Val Tyr Ala Glu Asn His Val
                325                 330                 335
Glu Ile Val Glu Glu Ala Gly Lys Leu Leu Gly His Ser Leu Asp Leu
            340                 345                 350
Val Phe Ser Ile His Ala Asp Lys Glu Asp Gly Ser Pro Leu Glu Ser
        355                 360                 365
Ala Val Pro Pro Pro Phe Pro Gly Pro Cys Thr Leu Gly Thr Gly Leu
    370                 375                 380
Ala Arg Tyr Ala Asp Leu Leu Asn Pro Pro Arg Lys Ser Ala Leu Val
385                 390                 395                 400
Ala Leu Ala Ala Tyr Ala Thr Glu Pro Ser Glu Ala Glu Lys Leu Lys
                405                 410                 415
His Leu Thr Ser Pro Asp Gly Lys Asp Glu Tyr Ser Gln Trp Ile Val
            420                 425                 430
Ala Ser Gln Arg Ser Leu Leu Glu Val Met Ala Ala Phe Pro Ser Ala
        435                 440                 445
Lys Pro Pro Leu Gly Val Phe Phe Ala Ala Ile Ala Pro Arg Leu Gln
    450                 455                 460
Pro Arg Tyr Tyr Ser Ile Ser Ser Ser Pro Arg Leu Ala Pro Ser Arg
465                 470                 475                 480
Val His Val Thr Ser Ala Leu Val Tyr Gly Pro Thr Pro Thr Gly Arg
                485                 490                 495
Ile His Lys Gly Val Cys Ser Thr Trp Met Lys Asn Ala Val Pro Ala
            500                 505                 510
Glu Lys Ser His Glu Cys Ser Gly Ala Pro Ile Phe Ile Arg Ala Ser
        515                 520                 525
Asn Phe Lys Leu Pro Ser Asn Pro Ser Thr Pro Ile Val Met Val Gly
    530                 535                 540
Pro Gly Thr Gly Leu Ala Pro Phe Arg Gly Phe Leu Gln Glu Arg Met
545                 550                 555                 560
Ala Leu Lys Glu Asp Gly Glu Glu Leu Gly Ser Ser Leu Leu Phe Phe
                565                 570                 575
Gly Cys Arg Asn Arg Gln Met Asp Phe Ile Tyr Glu Asp Glu Leu Asn
            580                 585                 590
Asn Phe Val Asp Gln Gly Val Ile Ser Glu Leu Ile Met Ala Phe Ser
        595                 600                 605
Arg Glu Gly Ala Gln Lys Glu Tyr Val Gln His Lys Met Met Glu Lys
    610                 615                 620
Ala Ala Gln Val Trp Asp Leu Ile Lys Glu Glu Gly Tyr Leu Tyr Val
625                 630                 635                 640
Cys Gly Asp Ala Lys Gly Met Ala Arg Asp Val His Arg Thr Leu His
                645                 650                 655
Thr Ile Val Gln Glu Gln Glu Gly Val Ser Ser Ser Glu Ala Glu Ala
            660                 665                 670
Ile Val Lys Lys Leu Gln Thr Glu Gly Arg Tyr Leu Arg Asp Val Trp
        675                 680                 685
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<210> 318
<211> 2067
<212> DNA

<213> Artificial Sequence

<220>
<223> AtCPR

<400> 318
atgacttctg ctttgtatgc ttccgatttg tttaagcagc tcaagtcaat tatggggaca 60
gattcgttat ccgacgatgt tgtacttgtg attgcaacga cgtctttggc actagtagct 120
ggatttgtgg tgttgttatg gaagaaaacg acggcggatc ggagcgggga gctgaagcct 180
ttgatgatcc ctaagtctct tatggctaag gacgaggatg atgatttgga tttgggatcc 240
gggaagacta gagtctctat cttcttcggt acgcagactg gaacagctga gggatttgct 300
aaggcattat ccgaagaaat caaagcgaga tatgaaaaag cagcagtcaa agatgactat 360
gctgccgatg atgaccagta tgaagagaaa ttgaagaagg aaactttggc atttttctgt 420
gttgctactt atggagatgg agagcctact gacaatgctg ccagatttta caaatggttt 480
acggaggaaa atgaacggga tataaagctt caacaactag catatggtgt gtttgctctt 540
ggtaatcgcc aatatgaaca ttttaataag atcgggatag ttcttgatga agagttatgt 600
aagaaaggtg caaagcgtct tattgaagtc ggtctaggag atgatgatca gagcattgag 660
gatgatttta atgcctggaa agaatcacta tggtctgagc tagacaagct cctcaaagac 720
gaggatgata aaagtgtggc aactccttat acagctgtta ttcctgaata ccgggtggtg 780
actcatgatc ctcggtttac aactcaaaaa tcaatggaat caaatgtggc caatggaaat 840
actactattg acattcatca tccctgcaga gttgatgttg ctgtgcagaa ggagcttcac 900
acacatgaat ctgatcggtc ttgcattcat ctcgagttcg acatatccag gacgggtatt 960
acatatgaaa caggtgacca tgtaggtgta tatgctgaaa atcatgttga aatagttgaa 1020
gaagctggaa aattgcttgg ccactcttta gatttagtat tttccataca tgctgacaag 1080
gaagatggct ccccattgga aagcgcagtg ccgcctcctt tccctggtcc atgcacactt 1140
gggactggtt tggcaagata cgcagacctt ttgaaccctc ctcgaaagtc tgcgttagtt 1200
gccttggcgg cctatgccac tgaaccaagt gaagccgaga aacttaagca cctgacatca 1260
cctgatggaa aggatgagta ctcacaatgg attgttgcaa gtcagagaag tcttttagag 1320
gtgatggctg cttttccatc tgcaaaaccc ccactaggtg tatttttgc tgcaatagct 1380
cctcgtctac aacctcgtta ctactccatc tcatcctcgc caagattggc gccaagtaga 1440
gttcatgtta catccgcact agtatatggt ccaactccta ctggtagaat ccacaagggt 1500
gtgtgttcta cgtggatgaa gaatgcagtt cctgcggaga aaagtcatga atgtagtgga 1560
gccccaatct ttattcgagc atctaatttc aagttaccat ccaacccttc aactccaatc 1620
gttatggtgg gacctgggac tgggctggca ccttttagag gttttctgca ggaaaggatg 1680
gcactaaaag aagatggaga agaactaggt tcatctttgc tcttctttgg gtgtagaaat 1740
cgacagatgg actttatata cgaggatgag ctcaataatt ttgttgatca aggcgtaata 1800
tctgagctca tcatggcatt ctcccgtgaa ggagctcaga aggagtatgt tcaacataag 1860
atgatggaga aggcagcaca agtttgggat ctaataaagg aagaaggata tctctatgta 1920
tgcggtgatg ctaagggcat ggcgagggac gtccaccgaa ctctacacac cattgttcag 1980
gagcaggaag gtgtgagttc gtcagaggca gaggctatag ttaagaaact tcaaaccgaa 2040
ggaagatacc tcagagatgt ctggtga 2067

<210> 319
<211> 759
<212> PRT
<213> Artificial Sequence

<220>
<223> Cucurbitadienol synthase Native host S.
grosvernorii Seq 59 SgCbQ

<400> 319
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1 5 10 15

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Lys Trp Leu Lys Ser Ile Ser Asn His Leu Gly Arg Gln Val Trp Glu
            20                  25                  30
Phe Cys Pro Asp Ala Gly Thr Gln Gln Gln Leu Leu Gln Val His Lys
        35                  40                  45
Ala Arg Lys Ala Phe His Asp Asp Arg Phe His Arg Lys Gln Ser Ser
    50                  55                  60
Asp Leu Phe Ile Thr Ile Gln Tyr Gly Lys Glu Val Glu Asn Gly Gly
65                  70                  75                  80
Lys Thr Ala Gly Val Lys Leu Lys Glu Gly Glu Glu Val Arg Lys Glu
                85                  90                  95
Ala Val Glu Ser Ser Leu Glu Arg Ala Leu Ser Phe Tyr Ser Ser Ile
            100                 105                 110
Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro Met Phe
        115                 120                 125
Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val Thr Gly Val Leu Asn
    130                 135                 140
Ser Val Leu Ser Lys His His Arg Gln Glu Met Cys Arg Tyr Val Tyr
145                 150                 155                 160
Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly Pro
                165                 170                 175
Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu Leu
            180                 185                 190
Gly Glu Asp Ala Asn Ala Gly Ala Met Pro Lys Ala Arg Ala Trp Ile
        195                 200                 205
Leu Asp His Gly Gly Ala Thr Gly Ile Thr Ser Trp Gly Lys Leu Trp
    210                 215                 220
Leu Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn Pro Leu Pro
225                 230                 235                 240
Pro Glu Phe Trp Leu Phe Pro Tyr Phe Leu Pro Phe His Pro Gly Arg
                245                 250                 255
Met Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr
            260                 265                 270
Gly Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu Ser Leu Arg
        275                 280                 285
Lys Glu Leu Tyr Ala Val Pro Tyr His Glu Ile Asp Trp Asn Lys Ser
    290                 295                 300
Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met
305                 310                 315                 320
Gln Asp Ile Leu Trp Gly Ser Leu His His Val Tyr Glu Pro Leu Phe
                325                 330                 335
Thr Arg Trp Pro Ala Lys Arg Leu Arg Glu Lys Ala Leu Gln Thr Ala
            340                 345                 350
Met Gln His Ile His Tyr Glu Asp Glu Asn Thr Arg Tyr Ile Cys Leu
        355                 360                 365
Gly Pro Val Asn Lys Val Leu Asn Leu Leu Cys Cys Trp Val Glu Asp
    370                 375                 380
Pro Tyr Ser Asp Ala Phe Lys Leu His Leu Gln Arg Val His Asp Tyr
385                 390                 395                 400
Leu Trp Val Ala Glu Asp Gly Met Lys Met Gln Gly Tyr Asn Gly Ser
                405                 410                 415
Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Val Ser Thr Lys
            420                 425                 430
Leu Val Asp Asn Tyr Gly Pro Thr Leu Arg Lys Ala His Asp Phe Val
        435                 440                 445
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Lys Ser Ser Gln Ile Gln Gln Asp Cys Pro Gly Asp Pro Asn Val Trp
    450                 455                 460
Tyr Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His
465                 470                 475                 480
Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ala Leu
                485                 490                 495
Met Leu Ser Lys Leu Pro Ser Glu Thr Val Gly Glu Ser Leu Glu Arg
            500                 505                 510
Asn Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Asp
        515                 520                 525
Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu
    530                 535                 540
Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr
545                 550                 555                 560
Pro Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Thr Leu Phe
                565                 570                 575
Lys Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Thr Ala Ile
            580                 585                 590
Val Arg Ala Ala Asn Phe Leu Glu Asn Met Gln Arg Thr Asp Gly Ser
        595                 600                 605
Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly
    610                 615                 620
Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Leu Ala
625                 630                 635                 640
Ile Arg Lys Ala Cys Asp Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly
                645                 650                 655
Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn
            660                 665                 670
Leu Glu Gly Asn Arg Pro His Leu Val Asn Thr Ala Trp Val Leu Met
        675                 680                 685
Ala Leu Ile Glu Ala Gly Gln Ala Glu Arg Asp Pro Thr Pro Leu His
    690                 695                 700
Arg Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Asn Gly Asp Phe
705                 710                 715                 720
Pro Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr
                725                 730                 735
Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr
            740                 745                 750
Cys His Arg Val Leu Thr Glu
        755
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<210> 320
<211> 2280
<212> DNA
<213> Artificial Sequence

<220>
<223> Cucurbitadienol synthase SgCbQ

<400> 320
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agcataagca atcacttggg acgccaggtg tgggagttct gtccggatgc cggcacccaa 120
caacagctct tgcaagtcca caaagctcgt aaagctttcc acgatgaccg tttccaccga 180

aagcaatctt ccgatctctt tatcactatt cagtatggaa aggaagtaga aaatggtgga 240
aagacagcgg gagtgaaatt gaaagaaggg gaagaggtga ggaaagaggc agtagagagt 300
agcttagaga gggcattaag tttctactca agcatccaga caagcgatgg gaactgggct 360
tcggatcttg gggggcccat gtttttactt ccgggtctgg tgattgccct ctacgttaca 420
ggcgtcttga attctgtttt atccaagcac caccggcaag agatgtgcag atatgtttac 480
aatcaccaga atgaagatgg ggggtggggt ctccacatcg agggcccaag caccatgttt 540
ggttccgcac tgaattatgt tgcactcagg ctgcttggag aagacgccaa cgccggggca 600
atgccaaaag cacgtgcttg gatcttggac cacggtggcg ccaccggaat cacttcctgg 660
ggcaaattgt ggctttctgt acttggagtc tacgaatgga gtggcaataa tcctcttcca 720
cccgaatttt ggttatttcc ttacttccta ccatttcatc caggaagaat gtggtgccat 780
tgtcgaatgg tttatctacc aatgtcatac ttatatggaa agagatttgt tgggccaatc 840
acacccatag ttctgtctct cagaaaagaa ctctacgcag ttccatatca tgaaatagac 900
tggaataaat ctcgcaatac atgtgcaaag gaggatctgt actatccaca tcccaagatg 960
caagatattc tgtggggatc tctccaccac gtgtatgagc ccttgtttac tcgttggcct 1020
gccaaacgcc tgagagaaaa ggctttgcag actgcaatgc aacatattca ctatgaagat 1080
gagaataccc gatatatatg ccttggccct gtcaacaagg tactcaatct gctttgttgt 1140
tgggttgaag atccctactc cgacgccttc aaacttcatc ttcaacgagt ccatgactat 1200
ctctgggttg ctgaagatgg catgaaaatg cagggttata atgggagcca gttgtgggac 1260
actgctttct ccatccaagc aatcgtatcc accaaacttg tagacaacta tggcccaacc 1320
ttaagaaagg cacacgactt cgttaaaagt tctcagattc agcaggactg tcctggggat 1380
cctaatgttt ggtaccgtca cattcataaa ggtgcatggc cattttcaac tcgagatcat 1440
ggatggctca tctctgactg tacagcagag ggattaaagg ctgctttgat gttatccaaa 1500
cttccatccg aaacagttgg ggaatcatta gaacggaatc gcctttgcga tgctgtaaac 1560
gttctccttt ctttgcaaaa cgataatggt ggctttgcat catatgagtt gacaagatca 1620
taccttggt tggagttgat caaccccgca gaaacgtttg gagatattgt cattgattat 1680
ccgtatgtgg agtgcacctc agccacaatg gaagcactga cgttgtttaa gaaattacat 1740
cccggccata ggaccaaaga aattgatact gctattgtca gggcggccaa cttccttgaa 1800
aatatgcaaa ggacggatgg ctcttggtat ggatgttggg gggtttgctt cacgtatgcg 1860
gggtggtttg gcataaaggg attggtggct gcaggaagga catataataa ttgccttgcc 1920
attcgcaagg cttgcgattt tttactatct aaagagctgc ccggcggtgg atggggagag 1980
agttaccttt catgtcagaa taaggtatac acaaatcttg aaggaaacag accgcacctg 2040
gttaacacgg cctgggtttt aatggccctc atagaagctg gccaggctga gagagaccca 2100
acaccattgc atcgtgcagc aaggttgtta atcaattccc agttggagaa tggtgatttc 2160
ccccaacagg agatcatggg agtctttaat aaaaattgca tgatcacata tgctgcatac 2220
cgaaacattt ttcccatttg ggctcttgga gagtattgcc atcgggtttt gactgaataa 2280

<210> 321
<211> 766
<212> PRT
<213> Artificial Sequence

<220>
<223> Cucurbitadienol synthase Cpep2

<400> 321
Met Trp Arg Leu Lys Val Gly Ala Glu Ser Val Gly Glu Lys Asp Glu
 1               5                  10                  15
Lys Trp Val Lys Ser Val Ser Asn His Leu Gly Arg Gln Val Trp Glu
            20                  25                  30
Phe Cys Ala Ala Asp Ala Ala Ala Val Thr Pro His Gln Leu Leu Gln
        35                  40                  45
Ile Gln Asn Ala Arg Asn His Phe His Arg Asn Arg Phe His Arg Lys
    50                  55                  60

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Gln Ser Ser Asp Leu Phe Leu Ala Ile Gln Tyr Glu Lys Glu Ile Ala
65                  70                  75                  80
Lys Gly Gly Lys Gly Lys Glu Ala Val Lys Val Lys Glu Gly Glu Glu
                85                  90                  95
Val Gly Lys Glu Ala Val Lys Ser Thr Leu Glu Arg Ala Leu Ser Phe
            100                 105                 110
Tyr Thr Ala Val Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu Gly
        115                 120                 125
Gly Pro Met Phe Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val Thr
    130                 135                 140
Gly Val Leu Asn Ser Val Leu Ser Lys His His Arg Val Glu Met Cys
145                 150                 155                 160
Arg Tyr Ile Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His
                165                 170                 175
Ile Glu Gly Thr Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala
            180                 185                 190
Leu Arg Leu Leu Gly Glu Asp Ala Asp Gly Gly Asp Asp Gly Ala Met
        195                 200                 205
Thr Lys Ala Arg Ala Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile
    210                 215                 220
Thr Ser Trp Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp
225                 230                 235                 240
Ser Gly Asn Asn Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr Ser
                245                 250                 255
Leu Pro Phe His Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr
            260                 265                 270
Leu Pro Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr
        275                 280                 285
Pro Lys Val Leu Ser Leu Arg Gln Glu Leu Tyr Thr Val Pro Tyr His
    290                 295                 300
Glu Ile Asp Trp Asn Lys Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu
305                 310                 315                 320
Tyr Tyr Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr
                325                 330                 335
His Val Tyr Glu Pro Leu Phe Thr Arg Trp Pro Gly Lys Arg Leu Arg
            340                 345                 350
Glu Lys Ala Leu Gln Thr Ala Met Lys His Ile His Tyr Glu Asp Glu
        355                 360                 365
Asn Ser Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met
    370                 375                 380
Leu Cys Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Leu His
385                 390                 395                 400
Leu Gln Arg Val His Asp Tyr Leu Trp Val Ala Glu Asp Gly Met Arg
                405                 410                 415
Met Gln Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile
            420                 425                 430
Gln Ala Ile Val Ala Thr Lys Leu Val Asp Ser Tyr Ala Pro Thr Leu
        435                 440                 445
Arg Lys Ala His Asp Phe Val Lys Asp Ser Gln Ile Gln Glu Asp Cys
    450                 455                 460
Pro Gly Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp
465                 470                 475                 480
Pro Phe Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala
                485                 490                 495
```

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

<210> 322
<211> 2301
<212> DNA
<213> Artificial Sequence

<220>
<223> Cucurbitadienol synthase Cpep2

<400> 322
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agcgtaagca atcacttggg ccgccaagtt tgggagttct gtgccgccga cgccgccgcc 120
gtcactcctc accagttact acaaattcag aatgctcgca accacttcca tcgcaatcgt 180
ttccaccgga agcagtcttc cgatctcttt ctcgctattc agtatgaaaa ggaaatagcg 240
aagggcggaa aagggaaaga ggcggtgaaa gtgaaagaag gggaggaggt ggggaaagag 300
gcggtgaaga gtacgttaga gagggcacta agtttctaca cagccgtgca gacgagcgat 360
gggaattggg cctcggatct tggagggccc atgtttttac ttccgggtct cgtgattgcc 420
ctttatgtca caggcgtgtt gaattcagtt ttgtccaagc accaccgcgt agagatgtgc 480
agatatattt acaatcacca gaatgaagat ggagggtggg gtctacatat tgagggcaca 540

agcaccatgt ttggttcggc actcaattat gttgcactta ggctgcttgg agaagacgcc 600
gatggcggag acgatggtgc aatgacaaaa gcacgtgctt ggatcttgga gcgcggcggc 660
gccactgcga tcacttcgtg gggaaaattg tggctgtccg tgcttggagt gtacgaatgg 720
agtggcaaca accctcttcc gcctgagttt tggcttctcc cttacagcct accatttcat 780
ccaggacgaa tgtggtgcca ttgtcgaatg gtttatcttc ccatgtctta cttatatggg 840
aagagatttg ttggcccaat cactcccaaa gttctttctc taagacaaga gctctacacg 900
gttccttatc atgaaataga ctggaataaa tcccgcaata catgtgcaaa ggaggatcta 960
tactatccac atcccaagat gcaagacata ctatggggat ctatctacca tgtatatgag 1020
ccattgttca ctcgttggcc tgggaaacgc ctgagggaaa aggctttaca aactgcaatg 1080
aaacatattc actatgaaga tgaaaatagt cgctatatat gtcttggccc agtcaacaag 1140
gtactcaaca tgctttgttg ttgggttgaa gatccctact cagacgcctt caaacttcac 1200
cttcaacgcg tccatgacta tctctgggtt gctgaagatg gcatgagaat gcagggttac 1260
aatggcagcc agttgtggga cactgctttc tccatccaag ccattgtagc taccaaactt 1320
gtagacagct atgccccaac tttaagaaaa gcacatgact ttgttaagga ttctcagatc 1380
caggaggact gtcctgggga tcctaatgtt tggttccgtc atattcataa aggtgcttgg 1440
ccattttcga ctcgagatca tggatggctc atctctgact gcacggctga gggattgaag 1500
gcttctttga tgttatccaa acttccatcc acaatggttg gggagccatt agaaaagaat 1560
cgcctttgtg atgctgttaa tgttctcctt tctttgcaaa atgataacgg tggatttgca 1620
tcatacgagt tgacgagatc ataccttgg ttggagttga tcaacccagc agaaacattc 1680
ggagacattg tcatcgacta tccgtatgtg gagtgcaccg cagcaacaat ggaagcactg 1740
acgttattta agaagctaca tccaggccat aggaccaaag agattgacac agctattggc 1800
aaggcagcca acttccttga gaaaatgcaa agggcggatg gctcttggta tgggtgttgg 1860
ggggtttgtt tcacgtatgc ggggtggttt ggcatcaagg gattggtggc tgcaggaaga 1920
acatataata gctgccttgc catccgcaag gcttgtgagt ttctgctatc taaagagctg 1980
cccggcggtg gatgggggga gagttacctt tcatgtcaga ataaggtgta caccaatctt 2040
gagggaaaca agccacactt ggttaacact gcctgggttt taatggctct cattgaagcc 2100
ggccagggtg agagagaccc agcaccattg caccgtggag caaggttggt aatgaattct 2160
caactggaga atggtgattt cgtgcaacag gagatcatgg gagtgttcaa taagaactgc 2220
atgatcacat atgctgcata ccgaaacatc ttccccattt gggcgcttgg agagtattgc 2280
catcgggttc ttactgaatg a 2301

<210> 323
<211> 766
<212> PRT
<213> Artificial Sequence

<220>
<223> Cucurbitadienol synthase Cpep4

<400> 323
Met Trp Arg Leu Lys Val Gly Ala Glu Ser Val Gly Glu Lys Asp Glu
 1               5                  10                  15
Lys Trp Val Lys Ser Val Ser Asn His Leu Gly Arg Gln Val Trp Glu
            20                  25                  30
Phe Cys Ala Ala Asp Ala Ala Ala Val Thr Pro His Gln Leu Leu Gln
        35                  40                  45
Ile Gln Asn Ala Arg Asn His Phe His Arg Asn Arg Phe His Arg Lys
    50                  55                  60
Gln Ser Ser Asp Leu Phe Leu Ala Ile Gln Tyr Glu Lys Glu Ile Ala
65                  70                  75                  80
Lys Gly Gly Lys Gly Lys Glu Ala Val Lys Val Lys Glu Gly Glu Glu
                85                  90                  95
Val Gly Lys Glu Ala Val Lys Ser Thr Leu Glu Arg Ala Leu Ser Phe
            100                 105                 110

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Tyr Thr Ala Val Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu Gly
        115                 120                 125
Gly Pro Met Phe Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val Thr
    130                 135                 140
Gly Val Leu Asn Ser Val Leu Ser Lys His His Arg Val Glu Met Cys
145                 150                 155                 160
Arg Tyr Ile Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His
                165                 170                 175
Ile Glu Gly Thr Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala
            180                 185                 190
Leu Arg Leu Leu Gly Glu Asp Ala Asp Gly Gly Asp Asp Gly Ala Met
        195                 200                 205
Thr Lys Ala Arg Ala Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile
    210                 215                 220
Thr Ser Trp Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp
225                 230                 235                 240
Ser Gly Asn Asn Pro Leu Pro Pro Glu Phe Leu Leu Leu Pro Tyr Ser
                245                 250                 255
Leu Pro Phe His Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr
            260                 265                 270
Leu Pro Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr
        275                 280                 285
Pro Lys Val Leu Ser Leu Arg Gln Glu Leu Tyr Thr Val Pro Tyr His
    290                 295                 300
Glu Ile Asp Trp Asn Lys Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu
305                 310                 315                 320
Tyr Tyr Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr
                325                 330                 335
His Val Tyr Glu Pro Leu Phe Thr Arg Trp Pro Gly Lys Arg Leu Arg
            340                 345                 350
Glu Lys Ala Leu Gln Thr Ala Met Lys His Ile His Tyr Glu Asp Glu
        355                 360                 365
Asn Ser Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met
    370                 375                 380
Leu Cys Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Leu His
385                 390                 395                 400
Leu Gln Arg Val His Asp Tyr Leu Trp Val Ala Glu Asp Gly Met Arg
                405                 410                 415
Met Gln Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile
            420                 425                 430
Gln Ala Ile Val Ala Thr Lys Leu Val Asp Ser Tyr Ala Pro Thr Leu
        435                 440                 445
Arg Lys Ala His Asp Phe Val Lys Asp Ser Gln Ile Gln Glu Asp Cys
    450                 455                 460
Pro Gly Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp
465                 470                 475                 480
Pro Phe Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala
                485                 490                 495
Glu Gly Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Thr Met
            500                 505                 510
Val Gly Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val
        515                 520                 525
Leu Leu Ser Leu Gln Asn Asp Asn Gly Gly Phe Ala Ser Tyr Glu Leu
    530                 535                 540
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Thr Arg Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe
545 550 555 560
Gly Asp Ile Val Ile Asp Tyr Ser Tyr Val Glu Cys Thr Ala Ala Thr
565 570 575
Met Glu Ala Leu Thr Leu Phe Lys Lys Leu His Pro Gly His Arg Thr
580 585 590
Lys Glu Ile Asp Thr Ala Ile Gly Lys Ala Ala Asn Phe Leu Glu Lys
595 600 605
Met Gln Arg Ala Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe
610 615 620
Thr Tyr Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg
625 630 635 640
Thr Tyr Asn Ser Cys Leu Ala Ile Arg Lys Ala Cys Glu Phe Leu Leu
645 650 655
Ser Lys Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys
660 665 670
Gln Asn Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val
675 680 685
Asn Thr Ala Trp Val Leu Met Ala Leu Ile Glu Ala Gly Gln Gly Glu
690 695 700
Arg Asp Pro Ala Pro Leu His Arg Ala Ala Arg Leu Val Met Asn Ser
705 710 715 720
Gln Leu Glu Asn Gly Asp Phe Val Gln Gln Glu Ile Met Gly Val Phe
725 730 735
Asn Lys Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro
740 745 750
Ile Trp Ala Leu Gly Glu Tyr Cys His Arg Val Leu Thr Glu
755 760 765

<210> 324
<211> 2301
<212> DNA
<213> Artificial Sequence

<220>
<223> Cucurbitadienol synthase Cpep4

<400> 324
atgtggaggc tgaaggtggg agcagagagc gttggggaga aggatgagaa atgggtgaag 60
agcgtaagca atcacttggg ccgccaagtt tgggagttct gtgccgccga cgccgccgcc 120
gtcactcctc accagttact acaaattcag aatgctcgca accacttcca tcgcaatcgt 180
ttccaccgga agcagtcttc cgatctcttt ctcgctattc agtatgaaaa ggaaatagcg 240
aagggcggaa aagggaaaga ggcggtgaaa gtgaaagaag gggaggaggt ggggaaagag 300
gcggtgaaga gtacgttaga gagggcacta agtttctaca cagccgtgca gacgagcgat 360
gggaattggg cctcggatct tggagggccc atgtttttac ttccgggtct cgtgattgcc 420
ctttatgtca caggcgtgtt gaattcagtt ttgtccaagc accaccgcgt agagatgtgc 480
agatatattt acaatcacca gaatgaagat ggagggtggg gtctacatat tgagggcaca 540
agcaccatgt ttggttcggc actcaattat gttgcactta ggctgcttgg agaagacgcc 600
gatggcggag acgatggtgc aatgacaaaa gcacgtgctt ggatcttgga gcgcggcggc 660
gccactgcga tcacttcgtg gggaaaattg tggctgtccg tgcttggagt gtacgaatgg 720
agtggcaaca accctcttcc gcctgagttt ttgcttctcc cttacagcct accatttcat 780
ccaggacgaa tgtggtgcca ttgtcgaatg gtttatcttc ccatgtctta cttatatggg 840
aagagatctg ttcgcccaat cactcccaaa gttctttctc taagacaaga gctctacacg 900

gttccttatc atgaaataga ctggaataaa tcccgcaata catgtgcaaa ggaggatcta 960
tactatccac atcccaagat gcaagacata ctatggggat ctatctacca tgtatatgag 1020
ccattgttca ctcgttggcc tgggaaacgc ctgagggaaa aggctttaca aactgcaatg 1080
aaacatattc actatgaaga tgaaaatagt cgctatatat gtcttggccc agtcaacaag 1140
gtactcaaca tgctttgttg ttgggttgaa gatccctact cagacgcctt caaacttcac 1200
cttcaacgcg tccatgacta tctctgggtt gctgaagatg gcatgagaat gcagggttac 1260
aatggcagcc agttgtggga cactgctttc tccatccaag ccattgtagc taccaaactt 1320
gtagacagct atgccccaac tttaagaaaa gcacatgact ttgttaagga ttctcagatc 1380
caggaggact gtcctgggga tcctaatgtt tggttccgtc atattcataa aggtgcttgg 1440
ccattttcga ctcgagatca tggatggctc atctctgact gcacggctga gggattgaag 1500
gcttctttga tgttatccaa acttccatcc acaatggttg gggagccatt agaaaagaat 1560
cgcctttgtg atgctgttaa tgttctcctt tctttgcaaa atgataacgg cggatttgca 1620
tcatacgagt tgacgagatc ataccttgg ttggagttga tcaacccagc agaaacattc 1680
ggagacattg tcatcgacta ttcgtatgtg gagtgcaccg cagcaacaat ggaagcactg 1740
acgttattta agaagctaca tccaggccat aggaccaaag agattgacac agctattggc 1800
aaggcagcca acttccttga gaaaatgcaa agggcggatg gctcttggta tgggtgttgg 1860
ggggtttgtt tcacgtatgc ggggtggttt ggcataaagg gattggtggc tgcaggaaga 1920
acatataata gctgtcttgc catccgcaag gcttgtgagt ttctgctatc taaagagctg 1980
cccggcggtg gatgggggga gagttacctt tcatgtcaga ataaggtgta caccaatctt 2040
gagggaaaca agccacactt ggttaacact gcctgggttt taatggctct cattgaagct 2100
ggccagggtg agagagaccc agcaccattg caccgtgcag caaggttggt aatgaattct 2160
caactggaga atggcgattt cgtgcaacag gagatcatgg gagtgttcaa taagaactgc 2220
atgatcacat atgctgcata ccgaaacatc ttccccattt gggcgcttgg agagtattgc 2280
catcgggttc ttactgaatg a 2301

<210> 325
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Cucurbitadienol synthase Cmax1

<400> 325
Met Trp Arg Leu Lys Val Gly Ala Glu Ser Val Gly Glu Lys Asp Glu
 1               5                  10                  15
Lys Trp Val Lys Ser Val Ser Asn His Leu Gly Arg Gln Val Trp Glu
            20                  25                  30
Phe Cys Ala Asp Ala Ala Ala Asp Thr Pro His Gln Leu Leu Gln Ile
        35                  40                  45
Gln Asn Ala Arg Asn His Phe His His Asn Arg Phe His Arg Lys Gln
    50                  55                  60
Ser Ser Asp Leu Phe Leu Ala Ile Gln Tyr Glu Lys Glu Ile Ala Lys
65                  70                  75                  80
Gly Ala Lys Gly Gly Ala Val Lys Val Lys Glu Gly Glu Glu Val Gly
                85                  90                  95
Lys Glu Ala Val Lys Ser Thr Leu Glu Ser Ala Leu Gly Phe Tyr Ser
            100                 105                 110
Ala Val Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro
        115                 120                 125
Met Phe Leu Leu Pro Gly Leu Val Ile Ala Leu His Val Thr Gly Val
    130                 135                 140
Leu Asn Ser Val Leu Ser Lys His His Arg Val Glu Met Cys Arg Tyr
145                 150                 155                 160

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Leu Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile Glu
                165                 170                 175
Gly Thr Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg
            180                 185                 190
Leu Leu Gly Glu Asp Ala Asp Gly Gly Asp Gly Gly Ala Met Thr Lys
        195                 200                 205
Ala Arg Ala Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser
    210                 215                 220
Trp Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp Ser Gly
225                 230                 235                 240
Asn Asn Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro
                245                 250                 255
Phe His Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr Leu Pro
            260                 265                 270
Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr Pro Lys
        275                 280                 285
Val Leu Ser Leu Arg Gln Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile
    290                 295                 300
Asp Trp Asn Lys Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr
305                 310                 315                 320
Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His Val
                325                 330                 335
Tyr Glu Pro Leu Phe Thr Arg Trp Pro Gly Lys Arg Leu Arg Glu Lys
            340                 345                 350
Ala Leu Gln Ala Ala Met Lys His Ile His Tyr Glu Asp Glu Asn Ser
        355                 360                 365
Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu Cys
    370                 375                 380
Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Leu His Leu Gln
385                 390                 395                 400
Arg Val His Asp Tyr Leu Trp Val Ala Glu Asp Gly Met Arg Met Gln
                405                 410                 415
Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala
            420                 425                 430
Ile Val Ala Thr Lys Leu Val Asp Ser Tyr Ala Pro Thr Leu Arg Lys
        435                 440                 445
Ala His Asp Phe Val Lys Asp Ser Gln Ile Gln Glu Asp Cys Pro Gly
    450                 455                 460
Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp Pro Phe
465                 470                 475                 480
Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly
                485                 490                 495
Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Ala Met Val Gly
            500                 505                 510
Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val Leu Leu
        515                 520                 525
Ser Leu Gln Asn Asp Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg
    530                 535                 540
Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp
545                 550                 555                 560
Ile Val Ile Asp Tyr Pro Tyr Val Glu Cys Thr Ala Ala Thr Met Glu
                565                 570                 575
Ala Leu Thr Leu Phe Lys Lys Leu His Pro Gly His Arg Thr Lys Glu
            580                 585                 590
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Ile Asp Thr Ala Ile Gly Lys Ala Ala Asn Phe Leu Glu Lys Met Gln
595 600 605
Arg Ala Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr
610 615 620
Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr
625 630 635 640
Asn Ser Cys Leu Ala Ile Arg Lys Ala Cys Glu Phe Leu Leu Ser Lys
645 650 655
Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn
660 665 670
Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val Asn Thr
675 680 685
Ala Trp Val Leu Met Ala Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp
690 695 700
Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu Met Asn Ser Gln Leu
705 710 715 720
Glu Asn Gly Asp Phe Val Gln Gln Glu Ile Met Gly Val Phe Asn Lys
725 730 735
Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp
740 745 750
Ala Leu Gly Glu Tyr Cys His Arg Val Leu Thr Glu
755 760

<210> 326
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Cucurbitadienol synthase

<400> 326
atgtggaggc tgaaggtggg agcagagagc gttggggagg aggatgagaa atgggtgaag 60
agcgtaagca atcacttggg ccgccaagtt tgggagttct gtgccgacgc cgccgccgac 120
actcctcacc agttactaca aattcagaat gctcgcaacc acttccatca caatcgtttc 180
caccggaagc agtcttccga tctctttctg gctattcaat atgaaaagga aatagcaaag 240
ggcgcaaaag gtggagcggt gaaagtgaaa gaaggggagg aggtggggaa agaggcggtg 300
aagagtacgt tagaaagggc actcggtttc tactcggccg tgcagacaag agatgggaat 360
tgggcctcgg atcttggagg gcccttgttt ttacttccgg gtctcgtgat tgcccttcat 420
gtcacaggcg tcttgaattc agttttgtcc aagcaccacc gcgtagagat gtgcagatat 480
ctttacaatc accagaatga agatggaggg tggggtctac atattgaggg cacaagcacc 540
atgtttggtt cggcactgaa ttacgttgca ctaaggctgc ttggagaaga cgccgatggc 600
ggagacggtg gcgcaatgac aaaagcacgt gcttggatct tggagcgcgg cggcgccact 660
gcgatcactt cgtggggaaa attgtggctg tccgtacttg gagtgtacga atggagtggc 720
aacaaccctc ttccgcctga gttttggctt ctcccttaca gcctaccatt tcatccagga 780
agaatgtggt gccattgtcg aatggtttat cttccaatgt cttacttata tgggaagaga 840
tttgttgggc caatcactcc caaagttctt tctctaaggc aagagctcta cacaattcct 900
tatcatgaaa tagactggaa taaatcccgc aatacatgtg caaaggagga tctgtactat 960
ccacatccca agatgcaaga cattctatgg ggatccatct accatgtata tgagccattg 1020
ttcactcgtt ggcctgggaa acgcctgagg gaaaaggctt tacaagctgc aatgaaacat 1080
attcactatg aagatgaaaa tagtcgatat atatgtcttg gcccagtcaa caaggtactc 1140
aacatgcttt gttgttgggt tgaagatccc tactcagacg ccttcaaact tcaccttcaa 1200
cgcgtccatg actatctctg ggttgctgaa gatggcatga gaatgcaggg ctacaatggc 1260

agccagttgt gggacactgc tttctccatc caagccatcg tagccaccaa acttgtagac 1320
agctatgccc caactttaag aaaagcacat gactttgtta aggattctca gatccaggag 1380
gactgtcctg gggatcctaa tgtttggttc cgtcatattc ataaaggtgc ttggccactt 1440
tcgacacgag atcatggatg gctcatctcc gactgtacag ctgagggatt gaaggcttct 1500
ttgatgttat ccaaacttcc atccacaatg gttggggagc cattagaaaa gaatcgcctt 1560
tgtgatgctg ttaatgttct cctttctttg caaaatgata atggtggatt tgcatcatac 1620
gagttgacga gatcataccc ttggttggag ttgatcaacc cagctgaaac attcggagac 1680
attgtcattg actatccgta tgtggagtgc accgcagcaa caatggaagc actgacgtta 1740
tttaagaagc tacatccagg ccataggacc aaagagattg acacagctat tggcaaggca 1800
gccaacttcc ttgagaaaat gcagagggcg gatggctctt ggtacgggtg ttgggggttt 1860
tgttttacgt atgcgggttg gtttggcata aagggattgg tggctgcagg aagaacatat 1920
aatagctgcc ttgccattcg caaggcttgt gagtttctgc tatctaaaga gctgcccggc 1980
ggtggatggg gggagagtta cctttcatgt cagaataagg tgtacaccaa tcttgagggg 2040
aacaagccac acttggttaa cactgcctgg gttttaatgg ctctcattga agctggccag 2100
ggtgagagag acccagcacc attgcaccgt gcagcaaggt tgctaatgaa ttcccaattg 2160
gagaatggcg atttcgtgca acaggagatc atgggagtgt tcaataagaa ctgcatgatc 2220
acatatgctg cataccgaaa catcttcccc atttgggcgc ttggagagta ttgccatcgg 2280
gttcttactg aatga 2295

<210> 327
<211> 765
<212> PRT
<213> Artificial Sequence

<220>
<223> Cucurbitadienol synthase Cmos1

<400> 327
Met Trp Arg Leu Lys Val Gly Ala Glu Ser Val Gly Glu Lys Asp Glu
 1               5                  10                  15
Lys Trp Val Lys Ser Val Ser Asn His Leu Gly Arg Gln Val Trp Glu
            20                  25                  30
Phe Cys Ala Asp Ala Ala Ala Ala Ala Thr Pro Arg Gln Leu Leu Gln
        35                  40                  45
Ile Gln Asn Ala Arg Asn His Phe His Arg Asn Arg Phe His Arg Lys
    50                  55                  60
Gln Ser Ser Asp Leu Phe Leu Ala Ile Gln Tyr Glu Lys Glu Ile Ala
65                  70                  75                  80
Glu Gly Gly Lys Gly Gly Ala Val Lys Val Lys Glu Glu Glu Glu Val
                85                  90                  95
Gly Lys Glu Ala Val Lys Ser Thr Leu Glu Arg Ala Leu Ser Phe Tyr
            100                 105                 110
Ser Ala Val Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu Gly Gly
        115                 120                 125
Pro Met Phe Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val Thr Gly
    130                 135                 140
Val Leu Asn Ser Val Leu Ser Lys His His Arg Val Glu Met Cys Arg
145                 150                 155                 160
Tyr Leu Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile
                165                 170                 175
Glu Gly Thr Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu
            180                 185                 190
Arg Leu Leu Gly Glu Asp Ala Asp Gly Gly Asp Asp Gly Ala Met Thr
        195                 200                 205

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Lys Ala Arg Ala Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile Thr
    210                 215                 220
Ser Trp Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp Ser
225                 230                 235                 240
Gly Asn Asn Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr Ser Leu
                245                 250                 255
Pro Phe His Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr Leu
            260                 265                 270
Pro Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr Pro
        275                 280                 285
Lys Val Leu Ser Leu Arg Gln Glu Leu Tyr Thr Val Pro Tyr His Glu
    290                 295                 300
Ile Asp Trp Asn Lys Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr
305                 310                 315                 320
Tyr Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His
                325                 330                 335
Val Tyr Glu Pro Leu Phe Thr Arg Trp Pro Gly Lys Arg Leu Arg Glu
            340                 345                 350
Lys Ala Leu Gln Thr Ala Met Lys His Ile His Tyr Glu Asp Glu Asn
        355                 360                 365
Ser Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu
    370                 375                 380
Cys Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Leu His Leu
385                 390                 395                 400
Gln Arg Val His Asp Tyr Leu Trp Val Ala Glu Asp Gly Met Arg Met
                405                 410                 415
Gln Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln
            420                 425                 430
Ala Ile Val Ala Thr Lys Leu Val Asp Ser Tyr Ala Pro Thr Leu Arg
        435                 440                 445
Lys Ala His Asp Phe Val Lys Asp Ser Gln Ile Gln Glu Asp Cys Pro
    450                 455                 460
Gly Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp Pro
465                 470                 475                 480
Phe Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu
                485                 490                 495
Gly Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Ala Met Val
            500                 505                 510
Gly Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val Leu
        515                 520                 525
Leu Ser Leu Gln Asn Asp Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr
    530                 535                 540
Arg Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly
545                 550                 555                 560
Asp Ile Val Ile Asp Tyr Pro Tyr Val Glu Cys Thr Ala Ala Thr Met
                565                 570                 575
Glu Ala Leu Thr Leu Phe Lys Lys Leu His Pro Gly His Arg Thr Lys
            580                 585                 590
Glu Ile Asp Thr Ala Ile Gly Lys Ala Ala Asn Phe Leu Glu Lys Met
        595                 600                 605
Gln Arg Ala Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr
    610                 615                 620
Tyr Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr
625                 630                 635                 640
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Tyr Asn Ser Cys Leu Ala Ile Arg Lys Ala Cys Glu Phe Leu Leu Ser
                645                 650                 655
Lys Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln
            660                 665                 670
Asn Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val Asn
        675                 680                 685
Thr Ala Trp Val Leu Met Ala Leu Ile Glu Ala Gly Gln Gly Glu Arg
    690                 695                 700
Asp Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu Met Asn Ser Gln
705                 710                 715                 720
Leu Glu Asn Gly Asp Phe Val Gln Gln Glu Ile Met Gly Val Phe Asn
                725                 730                 735
Lys Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile
            740                 745                 750
Trp Ala Leu Gly Glu Tyr Cys His Arg Val Leu Thr Glu
        755                 760                 765
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<210> 328
<211> 2296
<212> DNA
<213> Artificial Sequence

<220>
<223> Cucurbitadienol synthase Cmos1

<400> 328
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agcgtaagca atcacttggg ccgccaagtt tgggagttct gtgccgacgc cgccgccgcc 120
gccactcctc gccagttact acaaattcag aatgctcgca accacttcca tcgcaatcgt 180
ttccaccgga agcagtcttc cgatctcttt ctcgctattc agtatgaaaa ggaaatagca 240
gagggcggaa aaggtggagc ggtgaaagtg aaagaagagg aggaggtggg gaaagaggcg 300
gtgaagagta cgttagaaag ggcactaagt ttctactcag ccgtgcagac aagcgatggg 360
aattgggcct cggatcttgg agggcccatg tttttacttc cgggtctcgt gattgccctt 420
tatgtcacag gcgtgttgaa ttcagttttg tccaagcacc accgcgtaga gatgtgcaga 480
tatctttaca atcaccagaa tgaagatgga gggtggggtc tacatattga gggcacaagc 540
accatgtttg gttcggcact caattacgtt gcactaaggc tgcttggaga agacgcggat 600
ggcggagacg atggcgcaat gacaaaagca cgtgcttgga tcttggagcg cggcggcgcc 660
actgcgatca cttcgtgggg aaagttgtgg ctgtccgtgc ttggagtgta cgaatggagt 720
ggcaacaacc ctcttccgcc tgagttttgg cttctccctt acagcctacc atttcatcca 780
ggaagaatgt ggtgccattg tcgaatggtt tatcttccca tgtcttactt atatgggaag 840
agatttgttg ggccaatcac tcccaaagtt ctatcgctaa gacaagagct ttacacggtt 900
ccttatcatg aaatagactg gaacaaatcc cgcaatacat gtgcaaagga ggatctatac 960
tatccacatc ccaagatgca agacattcta tggggatcca tctaccatgt gtatgagcca 1020
ttgttcactc gttggcctgg gaaacgcctg agggaaaagg ctttacaaac tgcaatgaaa 1080
catattcact atgaagatga aaatagtcga tatatatgtc ttggcccagt caacaaggta 1140
ctcaacatgc tttgttgttg ggttgaagat ccctactcag acgccttcaa acttcacctt 1200
caacgcgtcc atgactatct ctgggttgct gaagatggca tgagaatgca gggctacaat 1260
ggcagccagt tgtgggacac tgctttctcc atccaagcca tcgtagccac caaacttgta 1320
gacagctatg ccccaacttt aagaaaagca catgactttg ttaaggattc tcagatccag 1380
gaggactgtc ctggggatcc taatgtttgg ttccgtcata ttcataaagg tgcttggcca 1440
ttttcgactc gagatcatgg atggctcatc tccgactgta cagctgaggg attgaaggct 1500
tctttgatgt tatccaaact tccatccgca atggttgggg agccattaga aaagaatcgc 1560
ctttgtgatg ctgttaatgt tctcctttct ttgcaaaatg ataatggtgg atttgcatca 1620
```

tacgagttga cgagatcata cccttggttg gagttgatca acccagcaga aacattcgga 1680
gacattgtca tcgactatcc gtatgtggag tgcaccgcag caacaatgga agcactgacg 1740
ttatttaaga agctacatcc aggccatagg accaaagaga ttgacacagc tattggcaag 1800
gcagccaact tccttgagaa aatgcagagg gcggatggct cttggtatgg gtgttggggg 1860
gtttgtttca cgtatgcggg gtggtttggc ataaagggat tggtggctgc aggaagaaca 1920
tataatagct gccttgccat ccgcaaggct tgtgagtttc tgctatctaa agagctgccc 1980
ggcggtggat ggggggagag ttacctttca tgtcagaata aggtgtacac caatcttgag 2040
ggaaacaagc cacacttggt taacactgcc tgggttttaa tggctctcat tgaagctggc 2100
cagggtgaga gagacccagc accattgcac cgtgcagcaa ggttgctaat gaattcccaa 2160
ttggagaatg gcgatttcgt gcaacaggag atcatgggag tgttcaataa gaactgcatg 2220
atcacatatg ctgcataccg aaacatcttc cccatttggg cgcttggaga gtattgccat 2280
cgggttctga ctgaat 2296

<210> 329
<211> 774
<212> PRT
<213> Artificial Sequence

<220>
<223> Cucurbitadienol synthase cucumis melo

<400> 329
Met Trp Arg Leu Lys Val Gly Lys Glu Ser Val Gly Glu Lys Glu Glu
 1               5                  10                  15
Lys Trp Ile Lys Ser Ile Ser Asn His Leu Gly Arg Gln Val Trp Glu
            20                  25                  30
Phe Cys Ser Gly Glu Asn Glu Asn Asp Asp Asp Glu Ala Ile Ala Val
        35                  40                  45
Ala Asn Asn Ser Ala Ser Lys Phe Glu Asn Ala Arg Asn His Phe Arg
    50                  55                  60
Asn Asn Arg Phe His Arg Lys Gln Ser Ser Asp Leu Phe Leu Ala Ile
65                  70                  75                  80
Gln Cys Glu Lys Glu Ile Ile Arg Asn Gly Ala Lys Asn Glu Gly Thr
                85                  90                  95
Thr Lys Val Lys Glu Gly Glu Asp Val Lys Lys Glu Ala Val Lys Asn
            100                 105                 110
Thr Leu Glu Arg Ala Leu Ser Phe Tyr Ser Ala Val Gln Thr Ser Asp
        115                 120                 125
Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro Met Phe Leu Leu Pro Gly
    130                 135                 140
Leu Val Ile Ala Leu Tyr Val Thr Gly Val Leu Asn Ser Val Leu Ser
145                 150                 155                 160
Lys His His Arg Gln Glu Met Cys Arg Tyr Ile Tyr Asn His Gln Asn
                165                 170                 175
Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly Ser Ser Thr Met Phe
            180                 185                 190
Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu Leu Gly Glu Ala Ala
        195                 200                 205
Asp Gly Gly Glu His Gly Ala Met Thr Lys Ala Arg Ser Trp Ile Leu
    210                 215                 220
Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser Trp Gly Lys Leu Trp Leu
225                 230                 235                 240
Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn Pro Leu Pro Pro
                245                 250                 255

```
Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro Phe His Pro Gly Arg Met
            260                 265                 270
Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly
        275                 280                 285
Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu Ser Leu Arg Lys
    290                 295                 300
Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile Asp Trp Asn Arg Ser Arg
305                 310                 315                 320
Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met Gln
                325                 330                 335
Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu Pro Leu Phe Ser
            340                 345                 350
Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met Lys Ile Ala Met
        355                 360                 365
Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile Cys Leu Gly
    370                 375                 380
Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro
385                 390                 395                 400
Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile Pro Asp Tyr Leu
                405                 410                 415
Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn Gly Ser Gln
            420                 425                 430
Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile Ser Thr Lys Leu
        435                 440                 445
Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His His Phe Val Lys
    450                 455                 460
His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro Asn Val Trp Phe
465                 470                 475                 480
Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His Gly
                485                 490                 495
Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ser Leu Met
            500                 505                 510
Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro Leu Glu Lys Asn
        515                 520                 525
Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Glu Asn
    530                 535                 540
Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu Glu
545                 550                 555                 560
Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr Ser
                565                 570                 575
Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Ala Leu Phe Lys
            580                 585                 590
Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Ala Ala Ile Ala
        595                 600                 605
Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys Thr Asp Gly Ser Trp
    610                 615                 620
Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly Ile
625                 630                 635                 640
Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Val Ala Ile
                645                 650                 655
Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly Gly
            660                 665                 670
Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu
        675                 680                 685
```

Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp Val Met Met Ala
    690                 695                 700
Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala Pro Leu His Arg
705                 710                 715                 720
Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser Gly Asp Phe Pro
                725                 730                 735
Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr
            740                 745                 750
Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Ser
        755                 760                 765
His Arg Val Leu Asp Met
    770

<210> 330
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Cucurbitadienol synthase Citrullus colocynthis

<400> 330
Met Trp Arg Leu Lys Val Gly Ala Glu Ser Val Gly Glu Lys Glu Glu
 1               5                  10                  15
Lys Trp Leu Lys Ser Ile Ser Asn His Leu Gly Arg Gln Val Trp Glu
            20                  25                  30
Phe Cys Ala Asp Gln Pro Thr Ala Ser Pro Asn His Leu Gln Gln Ile
        35                  40                  45
Asp Asn Ala Arg Lys His Phe Arg Asn Asn Arg Phe His Arg Lys Gln
    50                  55                  60
Ser Ser Asp Leu Phe Leu Ala Ile Gln Asn Glu Lys Glu Ile Ala Asn
65                  70                  75                  80
Gly Thr Lys Gly Gly Gly Ile Lys Val Lys Glu Glu Glu Asp Val Arg
                85                  90                  95
Lys Glu Thr Val Lys Asn Thr Val Glu Arg Ala Leu Ser Phe Tyr Ser
            100                 105                 110
Ala Ile Gln Thr Asn Asp Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro
        115                 120                 125
Met Phe Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val Thr Gly Val
    130                 135                 140
Leu Asn Ser Val Leu Ser Lys His His Arg Gln Glu Met Cys Arg Tyr
145                 150                 155                 160
Leu Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile Glu
                165                 170                 175
Gly Thr Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg
            180                 185                 190
Leu Leu Gly Glu Asp Ala Asp Gly Gly Glu Gly Gly Ala Met Thr Lys
        195                 200                 205
Ala Arg Gly Trp Ile Leu Asp Arg Gly Gly Ala Thr Ala Ile Thr Ser
    210                 215                 220
Trp Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp Ser Gly
225                 230                 235                 240
Asn Asn Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr Cys Leu Pro

```
                245                 250                 255
Phe His Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr Leu Pro
            260                 265                 270
Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr Pro Ile
        275                 280                 285
Val Leu Ser Leu Arg Lys Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile
    290                 295                 300
Asp Trp Asn Lys Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr
305                 310                 315                 320
Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His Leu
                325                 330                 335
Tyr Glu Pro Leu Phe Thr Arg Trp Pro Gly Lys Arg Leu Arg Glu Lys
            340                 345                 350
Ala Leu Gln Met Ala Met Lys His Ile His Tyr Glu Asp Glu Asn Ser
        355                 360                 365
Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu Cys
    370                 375                 380
Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Phe His Leu Gln
385                 390                 395                 400
Arg Val Pro Asp Tyr Leu Trp Ile Ala Glu Asp Gly Met Arg Met Gln
                405                 410                 415
Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Val Gln Ala
            420                 425                 430
Ile Ile Ser Thr Lys Leu Ile Asp Ser Phe Gly Thr Thr Leu Lys Lys
        435                 440                 445
Ala His Asp Phe Val Lys Asp Ser Gln Ile Gln Gln Asp Phe Pro Gly
    450                 455                 460
Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp Pro Phe
465                 470                 475                 480
Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly
                485                 490                 495
Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Lys Ile Val Gly
            500                 505                 510
Glu Pro Leu Glu Lys Ser Arg Leu Cys Asp Ala Val Asn Val Leu Leu
        515                 520                 525
Ser Leu Gln Asn Glu Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg
    530                 535                 540
Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp
545                 550                 555                 560
Ile Val Ile Asp Tyr Pro Tyr Val Glu Cys Thr Ser Ala Thr Met Glu
                565                 570                 575
Ala Leu Thr Leu Phe Lys Lys Leu His Pro Gly His Arg Thr Lys Glu
            580                 585                 590
Ile Asp Thr Ala Val Ala Lys Ala Ala Asn Phe Leu Glu Asn Met Gln
        595                 600                 605
Arg Thr Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr
    610                 615                 620
Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr
625                 630                 635                 640
Ser Thr Cys Val Ala Ile Arg Lys Ala Cys Asp Phe Leu Leu Ser Lys
                645                 650                 655
Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn
            660                 665                 670
Lys Val Tyr Thr Asn Leu Glu Gly Asn Arg Pro His Leu Val Asn Thr
```

```
        675                 680                 685
Ala Trp Val Leu Met Ala Leu Ile Glu Ala Gly Gln Ala Glu Arg Asp
    690                 695                 700
Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu
705                 710                 715                 720
Glu Asn Gly Asp Phe Pro Gln Glu Glu Ile Met Gly Val Phe Asn Lys
                725                 730                 735
Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp
            740                 745                 750
Ala Leu Gly Glu Tyr Phe His Arg Val Leu Thr Glu
        755                 760


<210> 331
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Cucurbitadienol synthase Cucurbita pepo

<400> 331
Met Trp Arg Leu Lys Val Gly Ala Glu Ser Val Gly Glu Glu Asp Glu
 1               5                  10                  15
Lys Trp Val Lys Ser Val Ser Asn His Leu Gly Arg Gln Val Trp Glu
            20                  25                  30
Phe Cys Ala Asp Ala Ala Ala Asp Thr Pro His Gln Leu Leu Gln Ile
        35                  40                  45
Gln Asn Ala Arg Asn His Phe His His Asn Arg Phe His Arg Lys Gln
    50                  55                  60
Ser Ser Asp Leu Phe Leu Ala Ile Gln Tyr Glu Lys Glu Ile Ala Lys
65                  70                  75                  80
Gly Ala Lys Gly Gly Ala Val Lys Val Lys Glu Gly Glu Glu Val Gly
                85                  90                  95
Lys Glu Ala Val Lys Ser Thr Leu Glu Arg Ala Leu Gly Phe Tyr Ser
            100                 105                 110
Ala Val Gln Thr Arg Asp Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro
        115                 120                 125
Leu Phe Leu Leu Pro Gly Leu Val Ile Ala Leu His Val Thr Gly Val
    130                 135                 140
Leu Asn Ser Val Leu Ser Lys His His Arg Val Glu Met Cys Arg Tyr
145                 150                 155                 160
Leu Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile Glu
                165                 170                 175
Gly Thr Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg
            180                 185                 190
Leu Leu Gly Glu Asp Ala Asp Gly Gly Asp Gly Gly Ala Met Thr Lys
        195                 200                 205
Ala Arg Ala Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser
    210                 215                 220
Trp Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp Ser Gly
225                 230                 235                 240
Asn Asn Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro
                245                 250                 255
```

```
Phe His Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr Leu Pro
            260                 265                 270
Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr Pro Lys
        275                 280                 285
Val Leu Ser Leu Arg Gln Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile
    290                 295                 300
Asp Trp Asn Lys Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr
305                 310                 315                 320
Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His Val
                325                 330                 335
Tyr Glu Pro Leu Phe Thr Arg Trp Pro Gly Lys Arg Leu Arg Glu Lys
            340                 345                 350
Ala Leu Gln Ala Ala Met Lys His Ile His Tyr Glu Asp Glu Asn Ser
        355                 360                 365
Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu Cys
    370                 375                 380
Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Leu His Leu Gln
385                 390                 395                 400
Arg Val His Asp Tyr Leu Trp Val Ala Glu Asp Gly Met Arg Met Gln
                405                 410                 415
Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala
            420                 425                 430
Ile Val Ala Thr Lys Leu Val Asp Ser Tyr Ala Pro Thr Leu Arg Lys
        435                 440                 445
Ala His Asp Phe Val Lys Asp Ser Gln Ile Gln Glu Asp Cys Pro Gly
    450                 455                 460
Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp Pro Leu
465                 470                 475                 480
Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly
                485                 490                 495
Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Thr Met Val Gly
            500                 505                 510
Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val Leu Leu
        515                 520                 525
Ser Leu Gln Asn Asp Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg
    530                 535                 540
Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp
545                 550                 555                 560
Ile Val Ile Asp Tyr Pro Tyr Val Glu Cys Thr Ala Ala Thr Met Glu
                565                 570                 575
Ala Leu Thr Leu Phe Lys Lys Leu His Pro Gly His Arg Thr Lys Glu
            580                 585                 590
Ile Asp Thr Ala Ile Gly Lys Ala Ala Asn Phe Leu Glu Lys Met Gln
        595                 600                 605
Arg Ala Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr
    610                 615                 620
Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr
625                 630                 635                 640
Asn Ser Cys Leu Ala Ile Arg Lys Ala Cys Glu Phe Leu Leu Ser Lys
                645                 650                 655
Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn
            660                 665                 670
Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val Asn Thr
        675                 680                 685
```

```
Ala Trp Val Leu Met Ala Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp
    690                 695                 700
Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu Met Asn Ser Gln Leu
705                 710                 715                 720
Glu Asn Gly Asp Phe Val Gln Gln Glu Ile Met Gly Val Phe Asn Lys
                725                 730                 735
Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp
            740                 745                 750
Ala Leu Gly Glu Tyr Cys His Arg Val Leu Thr Glu
        755                 760
```

<210> 332
<211> 785
<212> PRT
<213> Artificial Sequence

<220>
<223> Cucurbitadienol synthase Cucumis sativa

<400> 332

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

```
            260                 265                 270
Pro Tyr Ser Leu Pro Phe His Pro Gly Arg Met Trp Cys His Cys Arg
        275                 280                 285
Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly
    290                 295                 300
Pro Ile Thr His Met Val Leu Ser Leu Arg Lys Glu Leu Tyr Thr Ile
305                 310                 315                 320
Pro Tyr His Glu Ile Asp Trp Asn Arg Ser Arg Asn Thr Cys Ala Gln
                325                 330                 335
Glu Asp Leu Tyr Tyr Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly
            340                 345                 350
Ser Ile Tyr His Val Tyr Glu Pro Leu Phe Asn Gly Trp Pro Gly Arg
        355                 360                 365
Arg Leu Arg Glu Lys Ala Met Lys Ile Ala Met Glu His Ile His Tyr
    370                 375                 380
Glu Asp Glu Asn Ser Arg Tyr Ile Tyr Leu Gly Pro Val Asn Lys Val
385                 390                 395                 400
Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe
                405                 410                 415
Lys Phe His Leu Gln Arg Ile Pro Asp Tyr Leu Trp Leu Ala Glu Asp
            420                 425                 430
Gly Met Arg Met Gln Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala
        435                 440                 445
Phe Ser Ile Gln Ala Ile Leu Ser Thr Lys Leu Ile Asp Thr Phe Gly
    450                 455                 460
Ser Thr Leu Arg Lys Ala His His Phe Val Lys His Ser Gln Ile Gln
465                 470                 475                 480
Glu Asp Cys Pro Gly Asp Pro Asn Val Trp Phe Arg His Ile His Lys
                485                 490                 495
Gly Ala Trp Pro Phe Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp
            500                 505                 510
Cys Thr Ala Glu Gly Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro
        515                 520                 525
Ser Lys Ile Val Gly Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala
    530                 535                 540
Val Asn Val Leu Leu Ser Leu Gln Asn Glu Asn Gly Gly Phe Ala Ser
545                 550                 555                 560
Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala
                565                 570                 575
Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr Ser Tyr Val Glu Cys Thr
            580                 585                 590
Ser Ala Thr Met Glu Ala Leu Ala Leu Phe Lys Lys Leu His Pro Gly
        595                 600                 605
His Arg Thr Lys Glu Ile Asp Ala Ala Leu Ala Lys Ala Ala Asn Phe
    610                 615                 620
Leu Glu Asn Met Gln Arg Thr Asp Gly Ser Trp Tyr Gly Cys Trp Gly
625                 630                 635                 640
Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala
                645                 650                 655
Ala Gly Arg Thr Tyr Asn Asn Cys Val Ala Ile Arg Lys Ala Cys His
            660                 665                 670
Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr
        675                 680                 685
Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu Glu Gly Asn Arg Pro
```

```
    690                 695                 700
His Leu Val Asn Thr Ala Trp Val Leu Met Ala Leu Ile Glu Ala Gly
705                 710                 715                 720
Gln Gly Glu Arg Asp Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu
                725                 730                 735
Ile Asn Ser Gln Leu Glu Asn Gly Asp Phe Pro Gln Gln Glu Ile Met
            740                 745                 750
Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn
        755                 760                 765
Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Ser His Arg Val Leu Thr
    770                 775                 780
Glu
785
```

<210> 333
<211> 647
<212> PRT
<213> Artificial Sequence

<220>
<223> Cucurbitadienol synthase Citrullus lanatus

<400> 333

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

```
Met Lys His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile Cys Leu
                245                 250                 255
Gly Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp
            260                 265                 270
Pro Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Val Pro Asp Tyr
        275                 280                 285
Leu Trp Val Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn Gly Ser
    290                 295                 300
Gln Leu Trp Asp Thr Ala Phe Ser Val Gln Ala Ile Ile Ser Thr Lys
305                 310                 315                 320
Leu Ile Asp Ser Phe Gly Thr Thr Leu Lys Lys Ala His Asp Phe Val
                325                 330                 335
Lys Asp Ser Gln Ile Gln Gln Asp Cys Pro Gly Asp Pro Asn Val Trp
            340                 345                 350
Phe Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His
        355                 360                 365
Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ser Leu
    370                 375                 380
Met Leu Ser Lys Leu Pro Ser Glu Ile Val Gly Glu Pro Leu Glu Lys
385                 390                 395                 400
Ser Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Glu
                405                 410                 415
Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu
            420                 425                 430
Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr
        435                 440                 445
Pro Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Thr Leu Phe
    450                 455                 460
Lys Lys Leu His Pro Gly Arg Arg Thr Lys Glu Ile Asp Ile Ala Val
465                 470                 475                 480
Ala Arg Ala Ala Asn Phe Leu Glu Asn Met Gln Arg Thr Asp Gly Ser
                485                 490                 495
Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly
            500                 505                 510
Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Ser Cys Val Ala
        515                 520                 525
Ile Arg Lys Ala Cys Asp Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly
    530                 535                 540
Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn
545                 550                 555                 560
Leu Glu Gly Asn Arg Pro His Leu Val Asn Thr Ala Trp Val Leu Met
                565                 570                 575
Ala Leu Ile Glu Ala Gly Gln Ala Glu Arg Asp Pro Ala Pro Leu His
            580                 585                 590
Arg Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Asn Gly Asp Phe
        595                 600                 605
Pro Gln Glu Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr
    610                 615                 620
Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr
625                 630                 635                 640
Phe His Arg Val Leu Thr Glu
                645
```

<210> 334
<211> 496
<212> PRT
<213> Artificial Sequence

<220>
<223> Squalene epoxidase/squalene monooxidase

<400> 334
Met Ser Ala Val Asn Val Ala Pro Glu Leu Ile Asn Ala Asp Asn Thr
 1               5                  10                  15
Ile Thr Tyr Asp Ala Ile Val Ile Gly Ala Gly Val Ile Gly Pro Cys
            20                  25                  30
Val Ala Thr Gly Leu Ala Arg Lys Gly Lys Lys Val Leu Ile Val Glu
        35                  40                  45
Arg Asp Trp Ala Met Pro Asp Arg Ile Val Gly Glu Leu Met Gln Pro
    50                  55                  60
Gly Gly Val Arg Ala Leu Arg Ser Leu Gly Met Ile Gln Ser Ile Asn
65                  70                  75                  80
Asn Ile Glu Ala Tyr Pro Val Thr Gly Tyr Thr Val Phe Phe Asn Gly
                85                  90                  95
Glu Gln Val Asp Ile Pro Tyr Pro Tyr Lys Ala Asp Ile Pro Lys Val
            100                 105                 110
Glu Lys Leu Lys Asp Leu Val Lys Asp Gly Asn Asp Lys Val Leu Glu
        115                 120                 125
Asp Ser Thr Ile His Ile Lys Asp Tyr Glu Asp Asp Glu Arg Glu Arg
    130                 135                 140
Gly Val Ala Phe Val His Gly Arg Phe Leu Asn Asn Leu Arg Asn Ile
145                 150                 155                 160
Thr Ala Gln Glu Pro Asn Val Thr Arg Val Gln Gly Asn Cys Ile Glu
                165                 170                 175
Ile Leu Lys Asp Glu Lys Asn Glu Val Val Gly Ala Lys Val Asp Ile
            180                 185                 190
Asp Gly Arg Gly Lys Val Glu Phe Lys Ala His Leu Thr Phe Ile Cys
        195                 200                 205
Asp Gly Ile Phe Ser Arg Phe Arg Lys Glu Leu His Pro Asp His Val
    210                 215                 220
Pro Thr Val Gly Ser Ser Phe Val Gly Met Ser Leu Phe Asn Ala Lys
225                 230                 235                 240
Asn Pro Ala Pro Met His Gly His Val Ile Leu Gly Ser Asp His Met
                245                 250                 255
Pro Ile Leu Val Tyr Gln Ile Ser Pro Glu Glu Thr Arg Ile Leu Cys
            260                 265                 270
Ala Tyr Asn Ser Pro Lys Val Pro Ala Asp Ile Lys Ser Trp Met Ile
        275                 280                 285
Lys Asp Val Gln Pro Phe Ile Pro Lys Ser Leu Arg Pro Ser Phe Asp
    290                 295                 300
Glu Ala Val Ser Gln Gly Lys Phe Arg Ala Met Pro Asn Ser Tyr Leu
305                 310                 315                 320
Pro Ala Arg Gln Asn Asp Val Thr Gly Met Cys Val Ile Gly Asp Ala
                325                 330                 335
Leu Asn Met Arg His Pro Leu Thr Gly Gly Gly Met Thr Val Gly Leu
            340                 345                 350
His Asp Val Val Leu Leu Ile Lys Lys Ile Gly Asp Leu Asp Phe Ser

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

<210> 335
<211> 1491
<212> DNA
<213> Artificial Sequence

<220>
<223> Squalene epoxidase/squalene monooxidase

<400> 335
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atgtctgctg ttaacgttgc acctgaattg attaatgccg acaacacaat tacctacgat 60
gcgattgtca tcggtgctgg tgttatcggt ccatgtgttg ctactggtct agcaagaaag 120
ggtaagaaag ttcttatcgt agaacgtgac tgggctatgc ctgatagaat tgttggtgaa 180
ttgatgcaac caggtggtgt tagagcattg agaagtctgg gtatgattca atctatcaac 240
aacatcgaag catatcctgt taccggttat accgtctttt tcaacggcga acaagttgat 300
attccatacc cttacaaggc cgatatccct aaagttgaaa aattgaagga cttggtcaaa 360
gatggtaatg acaaggtctt ggaagacagc actattcaca tcaaggatta cgaagatgat 420
gaaagagaaa ggggtgttgc ttttgttcat ggtagattct tgaacaactt gagaaacatt 480
actgctcaag agccaaatgt tactagagtg caaggtaact gtattgagat attgaaggat 540
gaaaagaatg aggttgttgg tgccaaggtt gacattgatg gccgtggcaa ggtggaattc 600
aaagcccact tgacatttat ctgtgacggt atcttttcac gtttcagaaa ggaattgcac 660
ccagaccatg ttccaactgt cggttcttcg tttgtcggta tgtctttgtt caatgctaag 720
aatcctgctc ctatgcacgg tcacgttatt cttggtagtg atcatatgcc aatcttggtt 780
taccaaatca gtccagaaga aacaagaatc ctttgtgctt acaactctcc aaaggtccca 840
gctgatatca agagttggat gattaaggat gtccaacctt tcattccaaa gagtctacgt 900
ccttcatttg atgaagccgt cagccaaggt aaatttagag ctatgccaaa ctcctacttg 960
ccagctagac aaaacgacgt cactggtatg tgtgttatcg gtgacgctct aaatatgaga 1020
catccattga ctggtggtgg tatgactgtc ggtttgcatg atgttgtctt gttgattaag 1080
aaaataggtg acctagactt cagcgaccgt gaaaaggttt tggatgaatt actagactac 1140
catttcgaaa gaaagagtta cgattccgtt attaacgttt tgtcagtggc tttgtattct 1200
ttgttcgctg ctgacagcga taacttgaag gcattacaaa aaggttgttt caaatatttc 1260
caaagaggtg gcgattgtgt caacaaaccc gttgaatttc tgtctggtgt cttgccaaag 1320
cctttgcaat tgaccagggt tttcttcgct gtcgcttttt acaccattta cttgaacatg 1380
gaagaacgtg gtttcttggg attaccaatg gctttattgg aaggtattat gattttgatc 1440
acagctatta gagtattcac cccatttttg tttggtgagt tgattggtta a          1491
```

<210> 336
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Squalene synthase Erg9

<400> 336
Met Gly Lys Leu Leu Gln Leu Ala Leu His Pro Val Glu Met Lys Ala
 1               5                  10                  15
Ala Leu Lys Leu Lys Phe Cys Arg Thr Pro Leu Phe Ser Ile Tyr Asp
            20                  25                  30
Gln Ser Thr Ser Pro Tyr Leu Leu His Cys Phe Glu Leu Leu Asn Leu
        35                  40                  45
Thr Ser Arg Ser Phe Ala Ala Val Ile Arg Glu Leu His Pro Glu Leu
    50                  55                  60
Arg Asn Cys Val Thr Leu Phe Tyr Leu Ile Leu Arg Ala Leu Asp Thr
65                  70                  75                  80
Ile Glu Asp Asp Met Ser Ile Glu His Asp Leu Lys Ile Asp Leu Leu
                85                  90                  95
Arg His Phe His Glu Lys Leu Leu Leu Thr Lys Trp Ser Phe Asp Gly
            100                 105                 110
Asn Ala Pro Asp Val Lys Asp Arg Ala Val Leu Thr Asp Phe Glu Ser
        115                 120                 125
Ile Leu Ile Glu Phe His Lys Leu Lys Pro Glu Tyr Gln Glu Val Ile
    130                 135                 140
Lys Glu Ile Thr Glu Lys Met Gly Asn Gly Met Ala Asp Tyr Ile Leu
145                 150                 155                 160
Asp Glu Asn Tyr Asn Leu Asn Gly Leu Gln Thr Val His Asp Tyr Asp
                165                 170                 175
Val Tyr Cys His Tyr Val Ala Gly Leu Val Gly Asp Gly Leu Thr Arg
            180                 185                 190
Leu Ile Val Ile Ala Lys Phe Ala Asn Glu Ser Leu Tyr Ser Asn Glu
        195                 200                 205
Gln Leu Tyr Glu Ser Met Gly Leu Phe Leu Gln Lys Thr Asn Ile Ile
    210                 215                 220
Arg Asp Tyr Asn Glu Asp Leu Val Asp Gly Arg Ser Phe Trp Pro Lys
225                 230                 235                 240
Glu Ile Trp Ser Gln Tyr Ala Pro Gln Leu Lys Asp Phe Met Lys Pro
                245                 250                 255
Glu Asn Glu Gln Leu Gly Leu Asp Cys Ile Asn His Leu Val Leu Asn
            260                 265                 270
Ala Leu Ser His Val Ile Asp Val Leu Thr Tyr Leu Ala Gly Ile His
        275                 280                 285
Glu Gln Ser Thr Phe Gln Phe Cys Ala Ile Pro Gln Val Met Ala Ile
    290                 295                 300
Ala Thr Leu Ala Leu Val Phe Asn Asn Arg Glu Val Leu His Gly Asn
305                 310                 315                 320
Val Lys Ile Arg Lys Gly Thr Thr Cys Tyr Leu Ile Leu Lys Ser Arg
                325                 330                 335
Thr Leu Arg Gly Cys Val Glu Ile Phe Asp Tyr Tyr Leu Arg Asp Ile
            340                 345                 350
Lys Ser Lys Leu Ala Val Gln Asp Pro Asn Phe Leu Lys Leu Asn Ile

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

<210> 337
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> Squalene synthase Erg9

<400> 337
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atgggaaagc tattacaatt ggcattgcat ccggtcgaga tgaaggcagc tttgaagctg 60
aagttttgca gaacaccgct attctccatc tatgatcagt ccacgtctcc atatctcttg 120
cactgtttcg aactgttgaa cttgacctcc agatcgtttg ctgctgtgat cagagagctg 180
catccagaat tgagaaactg tgttactctc ttttatttga ttttaagggc tttggatacc 240
atcgaagacg atatgtccat cgaacacgat ttgaaaattg acttgttgcg tcacttccac 300
gagaaattgt tgttaactaa atggagtttc gacggaaatg cccccgatgt gaaggacaga 360
gccgttttga cagatttcga atcgattctt attgaattcc acaaattgaa accagaatat 420
caagaagtca tcaaggagat caccgagaaa atgggtaatg gtatggccga ctacatctta 480
gatgaaaatt acaacttgaa tgggttgcaa accgtccacg actacgacgt gtactgtcac 540
tacgtagctg gtttggtcgg tgatggtttg acccgtttga ttgtcattgc caagtttgcc 600
aacgaatctt tgtattctaa tgagcaattg tatgaaagca tgggtctttt cctacaaaaa 660
accaacatca tcagagatta caatgaagat ttggtcgatg gtagatcctt ctggcccaag 720
gaaatctggt cacaatacgc tcctcagttg aaggacttca tgaaacctga aaacgaacaa 780
ctggggttgg actgtataaa ccacctcgtc ttaaacgcat tgagtcatgt tatcgatgtg 840
ttgacttatt tggccggtat ccacgagcaa tccactttcc aattttgtgc cattccccaa 900
gttatggcca ttgcaacctt ggctttggta ttcaacaacc gtgaagtgct acatggcaat 960
gtaaagattc gtaagggtac tacctgctat ttaattttga aatcaaggac tttgcgtggc 1020
tgtgtcgaga tttttgacta ttacttacgt gatatcaaat ctaaattggc tgtgcaagat 1080
ccaaatttct taaaattgaa cattcaaatc tccaagatcg aacagtttat ggaagaaatg 1140
taccaggata aattacctcc taacgtgaag ccaaatgaaa ctccaatttt cttgaaagtt 1200
aaagaaagat ccagatacga tgatgaattg gttccaaccc aacaagaaga agagtacaag 1260
ttcaatatgg ttttatctat catcttgtcc gttcttcttg ggttttatta tatatacact 1320
ttacacagag cgtga                                                  1335
```

<210> 338
<211> 352
<212> PRT
<213> Artificial Sequence

<220>
<223> Farnesyl PP synthase

<400> 338
Met Ala Ser Glu Lys Glu Ile Arg Arg Glu Arg Phe Leu Asn Val Phe
 1               5                  10                  15
Pro Lys Leu Val Glu Glu Leu Asn Ala Ser Leu Leu Ala Tyr Gly Met
            20                  25                  30
Pro Lys Glu Ala Cys Asp Trp Tyr Ala His Ser Leu Asn Tyr Asn Thr
        35                  40                  45
Pro Gly Gly Lys Leu Asn Arg Gly Leu Ser Val Val Asp Thr Tyr Ala
    50                  55                  60
Ile Leu Ser Asn Lys Thr Val Glu Gln Leu Gly Gln Glu Glu Tyr Glu
65                  70                  75                  80
Lys Val Ala Ile Leu Gly Trp Cys Ile Glu Leu Leu Gln Ala Tyr Phe
                85                  90                  95
Leu Val Ala Asp Asp Met Met Asp Lys Ser Ile Thr Arg Arg Gly Gln
            100                 105                 110
Pro Cys Trp Tyr Lys Val Pro Glu Val Gly Glu Ile Ala Ile Asn Asp
        115                 120                 125
Ala Phe Met Leu Glu Ala Ala Ile Tyr Lys Leu Leu Lys Ser His Phe
    130                 135                 140
Arg Asn Glu Lys Tyr Tyr Ile Asp Ile Thr Glu Leu Phe His Glu Val
145                 150                 155                 160
Thr Phe Gln Thr Glu Leu Gly Gln Leu Met Asp Leu Ile Thr Ala Pro
                165                 170                 175
Glu Asp Lys Val Asp Leu Ser Lys Phe Ser Leu Lys Lys His Ser Phe
            180                 185                 190
Ile Val Thr Phe Lys Thr Ala Tyr Tyr Ser Phe Tyr Leu Pro Val Ala
        195                 200                 205
Leu Ala Met Tyr Val Ala Gly Ile Thr Asp Glu Lys Asp Leu Lys Gln
    210                 215                 220
Ala Arg Asp Val Leu Ile Pro Leu Gly Glu Tyr Phe Gln Ile Gln Asp
225                 230                 235                 240
Asp Tyr Leu Asp Cys Phe Gly Thr Pro Glu Gln Ile Gly Lys Ile Gly
                245                 250                 255
Thr Asp Ile Gln Asp Asn Lys Cys Ser Trp Val Ile Asn Lys Ala Leu
            260                 265                 270
Glu Leu Ala Ser Ala Glu Gln Arg Lys Thr Leu Asp Glu Asn Tyr Gly
        275                 280                 285
Lys Lys Asp Ser Val Ala Glu Ala Lys Cys Lys Lys Ile Phe Asn Asp
    290                 295                 300
Leu Lys Ile Glu Gln Leu Tyr His Glu Tyr Glu Glu Ser Ile Ala Lys
305                 310                 315                 320
Asp Leu Lys Ala Lys Ile Ser Gln Val Asp Glu Ser Arg Gly Phe Lys
                325                 330                 335
Ala Asp Val Leu Thr Ala Phe Leu Asn Lys Val Tyr Lys Arg Ser Lys
            340                 345                 350

<210> 339
<211> 1059
<212> DNA
<213> Artificial Sequence

<220>
<223> Farnesyl PP synthase

<400> 339
atggcttcag aaaaagaaat taggagagag agattcttga acgttttccc taaattagta 60
gaggaattga acgcatcgct tttggcttac ggtatgccta aggaagcatg tgactggtat 120
gcccactcat tgaactacaa cactccaggc ggtaagctaa atagaggttt gtccgttgtg 180
gacacgtatg ctattctctc caacaagacc gttgaacaat tggggcaaga agaatacgaa 240
aaggttgcca ttctaggttg gtgcattgag ttgttgcagg cttacttctt ggtcgccgat 300
gatatgatgg acaagtccat taccagaaga ggccaaccat gttggtacaa ggttcctgaa 360
gttggggaaa ttgccatcaa tgacgcattc atgttagagg ctgctatcta caagcttttg 420
aaatctcact tcagaaacga aaaatactac atagatatca ccgaattgtt ccatgaggtc 480
accttccaaa ccgaattggg ccaattgatg gacttaatca ctgcacctga agacaaagtc 540
gacttgagta agttctccct aaagaagcac tccttcatag ttactttcaa gactgcttac 600
tattctttct acttgcctgt cgcattggcc atgtacgttg ccggtatcac ggatgaaaag 660
gatttgaaac aagccagaga tgtcttgatt ccattgggtg aatacttcca aattcaagat 720
gactacttag actgcttcgg taccccagaa cagatcggta agatcggtac agatatccaa 780
gataacaaat gttcttgggt aatcaacaag gcattggaac ttgcttccgc agaacaaaga 840
aagactttag acgaaaatta cggtaagaag gactcagtcg cagaagccaa atgcaaaaag 900
attttcaatg acttgaaaat tgaacagcta taccacgaat atgaagagtc tattgccaag 960
gatttgaagg ccaaaatttc tcaggtcgat gagtctcgtg gcttcaaagc tgatgtctta 1020
actgcgttct tgaacaaagt ttacaagaga agcaaatag 1059

<210> 340
<211> 755
<212> PRT
<213> Artificial Sequence

<220>
<223> Cycloartenol synthase

<400> 340
Met Trp Lys Leu Lys Val Ala Glu Gly Gly Thr Pro Trp Leu Arg Thr
 1               5                  10                  15
Leu Asn Asn His Val Gly Arg Gln Val Trp Glu Phe Asp Pro His Ser
            20                  25                  30
Gly Ser Pro Gln Asp Leu Asp Asp Ile Glu Thr Ala Arg Arg Asn Phe
        35                  40                  45
His Asp Asn Arg Phe Thr His Lys His Ser Asp Asp Leu Leu Met Arg
    50                  55                  60
Leu Gln Phe Ala Lys Glu Asn Pro Met Asn Glu Val Leu Pro Lys Val
65                  70                  75                  80
Lys Val Lys Asp Val Glu Asp Val Thr Glu Glu Ala Val Ala Thr Thr
                85                  90                  95
Leu Arg Arg Gly Leu Asn Phe Tyr Ser Thr Ile Gln Ser His Asp Gly
            100                 105                 110
His Trp Pro Gly Asp Tyr Gly Gly Pro Met Phe Leu Met Pro Gly Leu
        115                 120                 125
Val Ile Thr Leu Ser Val Thr Gly Ala Leu Asn Ala Val Leu Thr Asp
    130                 135                 140
Glu His Arg Lys Glu Met Arg Arg Tyr Leu Tyr Asn His Gln Asn Lys
145                 150                 155                 160
Asp Gly Gly Trp Gly Leu His Ile Glu Gly Pro Ser Thr Met Phe Gly
                165                 170                 175
Ser Val Leu Cys Tyr Val Thr Leu Arg Leu Leu Gly Glu Gly Pro Asn
            180                 185                 190

```
Asp Gly Glu Gly Asp Met Glu Arg Gly Arg Asp Trp Ile Leu Glu His
        195                 200                 205
Gly Gly Ala Thr Tyr Ile Thr Ser Trp Gly Lys Met Trp Leu Ser Val
    210                 215                 220
Leu Gly Val Phe Glu Trp Ser Gly Asn Asn Pro Met Pro Pro Glu Trp
225                 230                 235                 240
Leu Leu Pro Tyr Ala Leu Pro Val His Pro Gly Arg Met Trp Cys His
                245                 250                 255
Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly Lys Arg Phe
            260                 265                 270
Val Gly Pro Ile Thr Pro Thr Val Leu Ser Leu Arg Lys Glu Leu Phe
        275                 280                 285
Thr Val Pro Tyr His Asp Ile Asp Trp Asn Gln Ala Arg Asn Leu Cys
    290                 295                 300
Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Leu Val Gln Asp Ile Leu
305                 310                 315                 320
Trp Ala Thr Leu His Lys Phe Val Glu Pro Val Phe Met Asn Trp Pro
                325                 330                 335
Gly Lys Lys Leu Arg Glu Lys Ala Ile Lys Thr Ala Ile Glu His Ile
            340                 345                 350
His Tyr Glu Asp Glu Asn Thr Arg Tyr Ile Cys Ile Gly Pro Val Asn
        355                 360                 365
Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro Asn Ser Glu
    370                 375                 380
Ala Phe Lys Leu His Leu Pro Arg Ile Tyr Asp Tyr Leu Trp Val Ala
385                 390                 395                 400
Glu Asp Gly Met Lys Met Gln Gly Tyr Asn Gly Ser Gln Leu Trp Asp
                405                 410                 415
Thr Ala Phe Ala Ala Gln Ala Ile Ile Ser Thr Asn Leu Ile Asp Glu
            420                 425                 430
Phe Gly Pro Thr Leu Lys Lys Ala His Ala Phe Ile Lys Asn Ser Gln
        435                 440                 445
Val Ser Glu Asp Cys Pro Gly Asp Leu Ser Lys Trp Tyr Arg His Ile
    450                 455                 460
Ser Lys Gly Ala Trp Pro Phe Ser Thr Ala Asp His Gly Trp Pro Ile
465                 470                 475                 480
Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Val Leu Leu Leu Ser Lys
                485                 490                 495
Ile Ala Pro Glu Ile Val Gly Glu Pro Leu Asp Ser Lys Arg Leu Tyr
            500                 505                 510
Asp Ala Val Asn Val Ile Leu Ser Leu Gln Asn Glu Asn Gly Gly Leu
        515                 520                 525
Ala Thr Tyr Glu Leu Thr Arg Ser Tyr Thr Trp Leu Glu Ile Ile Asn
    530                 535                 540
Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Cys Pro Tyr Val Glu
545                 550                 555                 560
Cys Thr Ser Ala Ala Ile Gln Ala Leu Ala Thr Phe Gly Lys Leu Tyr
                565                 570                 575
Pro Gly His Arg Arg Glu Glu Ile Gln Cys Cys Ile Glu Lys Ala Val
            580                 585                 590
Ala Phe Ile Glu Lys Ile Gln Ala Ser Asp Gly Ser Trp Tyr Gly Ser
        595                 600                 605
Trp Gly Val Cys Phe Thr Tyr Gly Thr Trp Phe Gly Ile Lys Gly Leu
    610                 615                 620
```

Ile Ala Ala Gly Lys Asn Phe Ser Asn Cys Leu Ser Ile Arg Lys Ala
625 630 635 640
Cys Glu Phe Leu Leu Ser Lys Gln Leu Pro Ser Gly Gly Trp Ala Glu
645 650 655
Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Ser Asn Leu Glu Gly Asn
660 665 670
Arg Ser His Val Val Asn Thr Gly Trp Ala Met Leu Ala Leu Ile Glu
675 680 685
Ala Glu Gln Ala Lys Arg Asp Pro Thr Pro Leu His Arg Ala Ala Val
690 695 700
Cys Leu Ile Asn Ser Gln Leu Glu Asn Gly Asp Phe Pro Gln Glu Glu
705 710 715 720
Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr Ala Ala Tyr
725 730 735
Arg Cys Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Arg Arg Val Leu
740 745 750
Gln Ala Cys
755

<210> 341
<211> 756
<212> PRT
<213> Artificial Sequence

<220>
<223> Oxidosqualene cylcases

<400> 341
Met Trp Lys Leu Lys Val Ala Glu Gly Gly Thr Pro Trp Leu Arg Thr
1 5 10 15
Leu Asn Asn His Val Gly Arg Gln Val Trp Glu Phe Asp Pro His Ser
20 25 30
Gly Ser Pro Gln Asp Leu Asp Asp Ile Glu Thr Ala Arg Arg Asn Phe
35 40 45
His Asp Asn Arg Phe Thr His Lys His Ser Asp Asp Leu Leu Met Arg
50 55 60
Leu Gln Phe Ala Lys Glu Asn Pro Met Asn Glu Val Leu Pro Lys Val
65 70 75 80
Lys Val Lys Asp Val Glu Asp Val Thr Glu Glu Ala Val Ala Thr Thr
85 90 95
Leu Arg Arg Gly Leu Asn Phe Tyr Ser Thr Ile Gln Ser His Asp Gly
100 105 110
His Trp Pro Gly Asp Leu Gly Gly Pro Met Phe Leu Met Pro Gly Leu
115 120 125
Val Ile Thr Leu Ser Val Thr Gly Ala Leu Asn Ala Val Leu Thr Asp
130 135 140
Glu His Arg Lys Glu Met Arg Arg Tyr Leu Tyr Asn His Gln Asn Lys
145 150 155 160
Asp Gly Gly Trp Gly Leu His Ile Glu Gly Pro Ser Thr Met Phe Gly
165 170 175
Ser Val Leu Cys Tyr Val Thr Leu Arg Leu Leu Gly Glu Gly Pro Asn
180 185 190
Asp Gly Glu Gly Asp Met Glu Arg Gly Arg Asp Trp Ile Leu Glu His

```
        195                 200                 205
Gly Gly Ala Thr Tyr Ile Thr Ser Trp Gly Lys Met Trp Leu Ser Val
    210                 215                 220
Leu Gly Val Phe Glu Trp Ser Gly Asn Asn Pro Met Pro Pro Glu Ile
225                 230                 235                 240
Trp Leu Leu Pro Tyr Ala Leu Pro Val His Pro Gly Arg Met Trp Cys
                245                 250                 255
His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly Lys Arg
            260                 265                 270
Phe Val Gly Pro Ile Thr Pro Thr Val Leu Ser Leu Arg Lys Glu Leu
        275                 280                 285
Phe Thr Val Pro Tyr His Asp Ile Asp Trp Asn Gln Ala Arg Asn Leu
    290                 295                 300
Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Leu Val Gln Asp Ile
305                 310                 315                 320
Leu Trp Ala Thr Leu His Lys Phe Val Glu Pro Val Phe Met Asn Trp
                325                 330                 335
Pro Gly Lys Lys Leu Arg Glu Lys Ala Ile Lys Thr Ala Ile Glu His
            340                 345                 350
Ile His Tyr Glu Asp Glu Asn Thr Arg Tyr Ile Cys Ile Gly Pro Val
        355                 360                 365
Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro Asn Ser
    370                 375                 380
Glu Ala Phe Lys Leu His Leu Pro Arg Ile Tyr Asp Tyr Leu Trp Val
385                 390                 395                 400
Ala Glu Asp Gly Met Lys Met Gln Gly Tyr Asn Gly Ser Gln Leu Trp
                405                 410                 415
Asp Thr Ala Phe Ala Ala Gln Ala Ile Ile Ser Thr Asn Leu Ile Asp
            420                 425                 430
Glu Phe Gly Pro Thr Leu Lys Lys Ala His Ala Phe Ile Lys Asn Ser
        435                 440                 445
Gln Val Ser Glu Asp Cys Pro Gly Asp Leu Ser Lys Trp Tyr Arg His
    450                 455                 460
Ile Ser Lys Gly Ala Trp Pro Phe Ser Thr Ala Asp His Gly Trp Pro
465                 470                 475                 480
Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Val Leu Leu Leu Ser
                485                 490                 495
Lys Ile Ala Pro Glu Ile Val Gly Glu Pro Leu Asp Ser Lys Arg Leu
            500                 505                 510
Tyr Asp Ala Val Asn Val Ile Leu Ser Leu Gln Asn Glu Asn Gly Gly
        515                 520                 525
Leu Ala Thr Tyr Glu Leu Thr Arg Ser Tyr Thr Trp Leu Glu Ile Ile
    530                 535                 540
Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Cys Pro Tyr Val
545                 550                 555                 560
Glu Cys Thr Ser Ala Ala Ile Gln Ala Leu Ala Thr Phe Gly Lys Leu
                565                 570                 575
Tyr Pro Gly His Arg Arg Glu Glu Ile Gln Cys Cys Ile Glu Lys Ala
            580                 585                 590
Val Ala Phe Ile Glu Lys Ile Gln Ala Ser Asp Gly Ser Trp Tyr Gly
        595                 600                 605
Ser Trp Gly Val Cys Phe Thr Tyr Gly Thr Trp Phe Gly Ile Lys Gly
    610                 615                 620
Leu Ile Ala Ala Gly Lys Asn Phe Ser Asn Cys Leu Ser Ile Arg Lys
```

625 630 635 640
Ala Cys Glu Phe Leu Leu Ser Lys Gln Leu Pro Ser Gly Gly Trp Ala
645 650 655
Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Ser Asn Leu Glu Gly
660 665 670
Asn Arg Ser His Val Val Asn Thr Gly Trp Ala Met Leu Ala Leu Ile
675 680 685
Glu Ala Glu Gln Ala Lys Arg Asp Pro Thr Pro Leu His Arg Ala Ala
690 695 700
Val Cys Leu Ile Asn Ser Gln Leu Glu Asn Gly Asp Phe Pro Gln Glu
705 710 715 720
Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr Ala Ala
725 730 735
Tyr Arg Cys Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Arg Arg Val
740 745 750
Leu Gln Ala Cys
755

<210> 342
<211> 2274
<212> DNA
<213> Artificial Sequence

<220>
<223> Oxidosqualene cylcases

<400> 342
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gttgagaggg tgcgtgcgga attcacaaag aacaggttcc agaggaagga gtcacaggac 180
cttcttctac gcttgcagta cgcaaaagac aaccctcttc cggcgaatat tccgacagaa 240
gccaagcttg aaaagagtac agaggtcact cacgagacta tctacgaatc attgatgcga 300
gctttacatc aatattcctc tctacaagca gacgatgggc attggcctgg tgattacagt 360
gggattctct tcattatgcc tatcattata ttctctttat atgttactag atcacttgac 420
acctttttat ctccggaaca tcgtcatgag atatgtcgct acatttacaa tcaacagaat 480
gaagatggtg gttggggaaa aatggttctt ggcccaagta ccatgtttgg atcgtgtatg 540
aattatgcaa ccttaatgat tcttggcgag aagcgaaatg gtgatcataa ggatgcattg 600
gaaaaagggc gttcttggat tttatctcat ggaactgcaa ctgcaatacc acagtgggga 660
aaaatatggt tgtcgataat tggcgtttac gaatggtcag gaaacaatcc tattatacct 720
gaattgtggt tggttccaca ttttcttccg attcacccag gtcgtttttg gtgttttacc 780
cggttgatat acatgtcaat ggcatatctc tatggtaaga aatttgttgg gcctattagt 840
cctacaatat tagctctgcg acaagacctc tatagtatac cttactgcaa cattaattgg 900
gacaaggcgc gtgattattg tgcaaaggag gaccttcatt acccacgctc acgggcacaa 960
gatcttatat ctggttgcct aacgaaaatt gtggagccaa ttttgaattg gtggccagca 1020
aacaagctaa gagatagagc tttaactaac ctcatggagc atatccatta tgacgacgaa 1080
tcaaccaaat atgtgggcat ttgccctatt aacaaggcat tgaacatgat ttgttgttgg 1140
gtagaaaacc caaattcgcc tgaattccaa caacatcttc cacgattcca tgactatttg 1200
tggatggcgg aggatggaat gaaggcacag gtatatgatg gatgtcatag ctgggaacta 1260
gcgttcataa ttcatgccta ttgttccacg gatcttacta gcgagtttat cccgactcta 1320
aaaaaggcgc acgagttcat gaagaactca caggttcttt tcaaccaccc aaatcatgaa 1380
agctattatc gccacagatc aaaaggctca tggacccttt caagtgtaga taatggttgg 1440
tctgtatctg attgtactgc ggaagctgtt aaggcattgc tactattatc aaagatatcc 1500
gctgaccttg ttggcgatcc aataaaacaa gacaggttgt atgatgccat tgattgcatc 1560

ctatctttca tgaatacaga tggaacattt tctacctacg aatgcaaacg gacattcgct 1620
tggttagagg ttctcaaccc ttctgagagt tttcggaaca ttgtcgtgga ctatccatct 1680
gttgaatgca catcatctgt ggttgatgct ctcatattat ttaaagagac gaatccacga 1740
tatcgaagag cagagataga taaatgcatt gaagaagctg ttgtatttat tgagaacagt 1800
caaaataagg atggttcatg gtatggctca tggggtatat gtttcgcata tggatgcatg 1860
tttgcagtaa gggcgttggt tgctacagga aaaacctacg acaattgtgc ttctatcagg 1920
aaatcatgca aatttgtctt atcaaagcaa caaacaacag gtggatgggg tgaagactat 1980
ctttctagtg acaatgggga atatattgat agcggtaggc ctaatgctgt gaccacctca 2040
tgggcaatgt tggctttaat ttatgctgga caggttgaac gtgacccagt accactgtat 2100
aatgctgcaa gacagctaat gaatatgcag ctagaaacag gtgacttccc ccaacaggaa 2160
cacatgggtt gcttcaactc ctccttgaac ttcaactacg ccaactaccg caatctatac 2220
ccgattatgg ctcttgggga acttcgccgt cgacttcttg cgattaagag ctga 2274

<210> 343
<211> 756
<212> PRT
<213> Artificial Sequence

<220>
<223> Cycloartenol synthase

<400> 343
Met Trp Lys Leu Lys Val Ala Glu Gly Gly Thr Pro Trp Leu Arg Thr
 1               5                  10                  15
Leu Asn Asn His Val Gly Arg Gln Val Trp Glu Phe Asp Pro His Ser
            20                  25                  30
Gly Ser Pro Gln Asp Leu Asp Asp Ile Glu Thr Ala Arg Arg Asn Phe
        35                  40                  45
His Asp Asn Arg Phe Thr His Lys His Ser Asp Asp Leu Leu Met Arg
    50                  55                  60
Leu Gln Phe Ala Lys Glu Asn Pro Met Asn Glu Val Leu Pro Lys Val
65                  70                  75                  80
Lys Val Lys Asp Val Glu Asp Val Thr Glu Glu Ala Val Ala Thr Thr
                85                  90                  95
Leu Arg Arg Gly Leu Asn Phe Tyr Ser Thr Ile Gln Ser His Asp Gly
            100                 105                 110
His Trp Pro Gly Asp Leu Gly Gly Pro Met Phe Leu Met Pro Gly Leu
        115                 120                 125
Val Ile Thr Leu Ser Val Thr Gly Ala Leu Asn Ala Val Leu Thr Asp
    130                 135                 140
Glu His Arg Lys Glu Met Arg Arg Tyr Leu Tyr Asn His Gln Asn Lys
145                 150                 155                 160
Asp Gly Gly Trp Gly Leu His Ile Glu Gly Pro Ser Thr Met Phe Gly
                165                 170                 175
Ser Val Leu Cys Tyr Val Thr Leu Arg Leu Leu Gly Glu Gly Pro Asn
            180                 185                 190
Asp Gly Glu Gly Asp Met Glu Arg Gly Arg Asp Trp Ile Leu Glu His
        195                 200                 205
Gly Gly Ala Thr Tyr Ile Thr Ser Trp Gly Lys Met Trp Leu Ser Val
    210                 215                 220
Leu Gly Val Phe Glu Trp Ser Gly Asn Asn Pro Met Pro Pro Glu Ile
225                 230                 235                 240
Trp Leu Leu Pro Tyr Ala Leu Pro Val His Pro Gly Arg Met Trp Cys
                245                 250                 255

```
His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly Lys Arg
            260                 265                 270
Phe Val Gly Pro Ile Thr Pro Thr Val Leu Ser Leu Arg Lys Glu Leu
        275                 280                 285
Phe Thr Val Pro Tyr His Asp Ile Asp Trp Asn Gln Ala Arg Asn Leu
    290                 295                 300
Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Leu Val Gln Asp Ile
305                 310                 315                 320
Leu Trp Ala Thr Leu His Lys Phe Val Glu Pro Val Phe Met Asn Trp
                325                 330                 335
Pro Gly Lys Lys Leu Arg Glu Lys Ala Ile Lys Thr Ala Ile Glu His
            340                 345                 350
Ile His Tyr Glu Asp Glu Asn Thr Arg Tyr Ile Cys Ile Gly Pro Val
        355                 360                 365
Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro Asn Ser
    370                 375                 380
Glu Ala Phe Lys Leu His Leu Pro Arg Ile Tyr Asp Tyr Leu Trp Val
385                 390                 395                 400
Ala Glu Asp Gly Met Lys Met Gln Gly Tyr Asn Gly Ser Gln Leu Trp
                405                 410                 415
Asp Thr Ala Phe Ala Ala Gln Ala Ile Ile Ser Thr Asn Leu Ile Asp
            420                 425                 430
Glu Phe Gly Pro Thr Leu Lys Lys Ala His Ala Phe Ile Lys Asn Ser
        435                 440                 445
Gln Val Ser Glu Asp Cys Pro Gly Asp Leu Ser Lys Trp Tyr Arg His
    450                 455                 460
Ile Ser Lys Gly Ala Trp Pro Phe Ser Thr Ala Asp His Gly Trp Pro
465                 470                 475                 480
Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Val Leu Leu Leu Ser
                485                 490                 495
Lys Ile Ala Pro Glu Ile Val Gly Glu Pro Leu Asp Ser Lys Arg Leu
            500                 505                 510
Tyr Asp Ala Val Asn Val Ile Leu Ser Leu Gln Asn Glu Asn Gly Gly
        515                 520                 525
Leu Ala Thr Tyr Glu Leu Thr Arg Ser Tyr Thr Trp Leu Glu Ile Ile
    530                 535                 540
Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Cys Pro Tyr Val
545                 550                 555                 560
Glu Cys Thr Ser Ala Ala Ile Gln Ala Leu Ala Thr Phe Gly Lys Leu
                565                 570                 575
Tyr Pro Gly His Arg Arg Glu Glu Ile Gln Cys Cys Ile Glu Lys Ala
            580                 585                 590
Val Ala Phe Ile Glu Lys Ile Gln Ala Ser Asp Gly Ser Trp Tyr Gly
        595                 600                 605
Ser Trp Gly Val Cys Phe Thr Tyr Gly Thr Trp Phe Gly Ile Lys Gly
    610                 615                 620
Leu Ile Ala Ala Gly Lys Asn Phe Ser Asn Cys Leu Ser Ile Arg Lys
625                 630                 635                 640
Ala Cys Glu Phe Leu Leu Ser Lys Gln Leu Pro Ser Gly Gly Trp Ala
                645                 650                 655
Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Ser Asn Leu Glu Gly
            660                 665                 670
Asn Arg Ser His Val Val Asn Thr Gly Trp Ala Met Leu Ala Leu Ile
        675                 680                 685
```

```
Glu Ala Glu Gln Ala Lys Arg Asp Pro Thr Pro Leu His Arg Ala Ala
    690                 695                 700
Val Cys Leu Ile Asn Ser Gln Leu Glu Asn Gly Asp Phe Pro Gln Glu
705                 710                 715                 720
Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr Ala Ala
                725                 730                 735
Tyr Arg Cys Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Arg Arg Val
            740                 745                 750
Leu Gln Ala Cys
        755
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<210> 344
<211> 755
<212> PRT
<213> Artificial Sequence

<220>
<223> Beta-amyrin synthase

<400> 344

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

```
            260                 265                 270
Phe Val Gly Pro Ile Ser Pro Thr Ile Leu Ala Leu Arg Gln Asp Leu
        275                 280                 285
Tyr Ser Ile Pro Tyr Cys Asn Ile Asn Trp Asp Lys Ala Arg Asp Tyr
    290                 295                 300
Cys Ala Lys Glu Asp Leu His Tyr Pro Arg Ser Arg Ala Gln Asp Leu
305                 310                 315                 320
Ile Ser Gly Cys Leu Thr Lys Ile Val Glu Pro Ile Leu Asn Trp Trp
                325                 330                 335
Pro Ala Asn Lys Leu Arg Asp Arg Ala Leu Thr Asn Leu Met Glu His
            340                 345                 350
Ile His Tyr Asp Asp Glu Ser Thr Lys Tyr Val Gly Ile Cys Pro Ile
        355                 360                 365
Asn Lys Ala Leu Asn Met Ile Cys Cys Trp Val Glu Asn Pro Asn Ser
    370                 375                 380
Pro Glu Phe Gln Gln His Leu Pro Arg Phe His Asp Tyr Leu Trp Met
385                 390                 395                 400
Ala Glu Asp Gly Met Lys Ala Gln Val Tyr Asp Gly Cys His Ser Trp
                405                 410                 415
Glu Leu Ala Phe Ile Ile His Ala Tyr Cys Ser Thr Asp Leu Thr Ser
            420                 425                 430
Glu Phe Ile Pro Thr Leu Lys Lys Ala His Glu Phe Met Lys Asn Ser
        435                 440                 445
Gln Val Leu Phe Asn His Pro Asn His Glu Ser Tyr Tyr Arg His Arg
    450                 455                 460
Ser Lys Gly Ser Trp Thr Leu Ser Ser Val Asp Asn Gly Trp Ser Val
465                 470                 475                 480
Ser Asp Cys Thr Ala Glu Ala Val Lys Ala Leu Leu Leu Leu Ser Lys
                485                 490                 495
Ile Ser Ala Asp Leu Val Gly Asp Pro Ile Lys Gln Asp Arg Leu Tyr
            500                 505                 510
Asp Ala Ile Asp Cys Ile Leu Ser Phe Met Asn Thr Asp Gly Thr Phe
        515                 520                 525
Ser Thr Tyr Glu Cys Lys Arg Thr Phe Ala Trp Leu Glu Val Leu Asn
    530                 535                 540
Pro Ser Glu Ser Phe Arg Asn Ile Val Val Asp Tyr Pro Ser Val Glu
545                 550                 555                 560
Cys Thr Ser Ser Val Val Asp Ala Leu Ile Leu Phe Lys Glu Thr Asn
                565                 570                 575
Pro Arg Tyr Arg Arg Ala Glu Ile Asp Lys Cys Ile Glu Glu Ala Val
            580                 585                 590
Val Phe Ile Glu Asn Ser Gln Asn Lys Asp Gly Ser Trp Tyr Gly Ser
        595                 600                 605
Trp Gly Ile Cys Phe Ala Tyr Gly Cys Met Phe Ala Val Arg Ala Leu
    610                 615                 620
Val Ala Thr Gly Lys Thr Tyr Asp Asn Cys Ala Ser Ile Arg Lys Ser
625                 630                 635                 640
Cys Lys Phe Val Leu Ser Lys Gln Gln Thr Thr Gly Gly Trp Gly Glu
                645                 650                 655
Asp Tyr Leu Ser Ser Asp Asn Gly Glu Tyr Ile Asp Ser Gly Arg Pro
            660                 665                 670
Asn Ala Val Thr Thr Ser Trp Ala Met Leu Ala Leu Ile Tyr Ala Gly
        675                 680                 685
Gln Val Glu Arg Asp Pro Val Pro Leu Tyr Asn Ala Ala Arg Gln Leu
```

```
    690                 695                 700
Met Asn Met Gln Leu Glu Thr Gly Asp Phe Pro Gln Gln Glu His Met
705                 710                 715                 720
Gly Cys Phe Asn Ser Ser Leu Asn Phe Asn Tyr Ala Asn Tyr Arg Asn
                725                 730                 735
Leu Tyr Pro Ile Met Ala Leu Gly Glu Leu Arg Arg Arg Leu Leu Ala
            740                 745                 750
Ile Lys Ser
        755
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<210> 345
<211> 2273
<212> DNA
<213> Artificial Sequence

<220>
<223> Beta-amyrin synthase

<400> 345

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cttggccgcc aagtgtggga gtacgacgcc gatgccggca cgccggaaga gcgtgccgag 120
gttgagaggg tgcgtgcgga attcacaaag aacaggttcc agaggaagga gtcacaggac 180
cttcttctac gcttgcagta cgcaaaagac aaccctcttc cggcgaatat tccgacagaa 240
gccaagcttg aaaagagtac agaggtcact cacgagacta tctacgaatc attgatgcga 300
gctttacatc aatattcctc tctacaagca gacgatgggc attggcctgg tgattacagt 360
gggattctct tcattatgcc tatcattata ttctctttat atgttactag atcacttgac 420
acctttttat ctccggaaca tcgtcatgag atatgtcgct acatttacaa tcaacagaat 480
gaagatggtg gttggggaaa aatggttctt ggcccaagta ccatgtttgg atcgtgtatg 540
aattatgcaa ccttaatgat tcttggcgag aagcgaaatg gtgatcataa ggatgcattg 600
gaaaaagggc gttcttggat tttatctcat ggaactgcaa ctgcaatacc acagtgggga 660
aaaatatggt tgtcgataat tggcgtttac gaatggtcag gaaacaatcc tattatacct 720
gaattgtggt tggttccaca ttttcttccg attcacccag gtcgtttttg gtgttttacc 780
cggttgatat acatgtcaat ggcatatctc tatggtaaga aatttgttgg gcctattagt 840
cctacaatat tagctctgcg acaagacctc tatagtatac cttactgcaa cattaattgg 900
gacaaggcgc gtgattattg tgcaaaggag gaccttcatt acccacgctc acgggcacaa 960
gatcttatat ctggttgcct aacgaaaatt gtggagccaa ttttgaattg gtggccagca 1020
aacaagctaa gagatagagc tttaactaac ctcatggagc atatccatta tgacgacgaa 1080
tcaaccaaat atgtgggcat ttgccctatt aacaaggcat tgaacatgat ttgttgttgg 1140
gtagaaaacc caaattcgcc tgaattccaa caacatcttc cacgattcca tgactatttg 1200
tggatggcgg aggatggaat gaaggcacag gtatatgatg gatgtcatag ctgggaacta 1260
gcgttcataa ttcatgccta ttgttccacg gatcttacta gcgagtttat cccgactcta 1320
aaaaaggcgc acgagttcat gaagaactca caggttcttt tcaaccaccc aaatcatgaa 1380
agctattatc gccacagatc aaaaggctca tggacccttt caagtgtaga taatggttgg 1440
tctgtatctg attgtactgc ggaagctgtt aaggcattgc tactattatc aaagatatcc 1500
gctgaccttg ttggcgatcc aataaaacaa gacaggttgt atgatgccat tgattgcatc 1560
tatctttcat gaatacagat ggaacatttt ctacctacga atgcaaacgg acattcgctt 1620
ggttagaggt tctcaaccct tctgagagtt ttcggaacat tgtcgtggac tatccatctg 1680
ttgaatgcac atcatctgtg gttgatgctc tcatattatt taaagagacg aatccacgat 1740
atcgaagagc agagatagat aaatgcattg aagaagctgt tgtatttatt gagaacagtc 1800
aaaataagga tggttcatgg tatggctcat ggggtatatg tttcgcatat ggatgcatgt 1860
ttgcagtaag ggcgttggtt gctacaggaa aaacctacga caattgtgct tctatcagga 1920
aatcatgcaa atttgtctta tcaaagcaac aaacaacagg tggatggggt gaagactatc 1980
tttctagtga caatggggaa tatattgata gcggtaggcc taatgctgtg accacctcat 2040
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gggcaatgtt ggctttaatt tatgctggac aggttgaacg tgacccagta ccactgtata 2100
atgctgcaag acagctaatg aatatgcagc tagaaacagg tgacttcccc caacaggaac 2160
acatgggttg cttcaactcc tccttgaact tcaactacgc caactaccgc aatctatacc 2220
cgattatggc tcttggggaa cttcgccgtc gacttcttgc gattaagagc tga 2273

<210> 346
<211> 757
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified sequence of B-amyrin synthase from Avena strigosa (AJ311789) to react preferentially with diepoxysqualene

<400> 346
Met Trp Arg Leu Thr Ile Gly Glu Gly Gly Gly Pro Trp Leu Lys Ser
 1               5                  10                  15
Asn Asn Gly Phe Leu Gly Arg Gln Val Trp Glu Tyr Asp Ala Asp Ala
            20                  25                  30
Gly Thr Pro Glu Glu Arg Ala Glu Val Glu Arg Val Arg Ala Glu Phe
        35                  40                  45
Thr Lys Asn Arg Phe Gln Arg Lys Glu Ser Gln Asp Leu Leu Leu Arg
    50                  55                  60
Leu Gln Tyr Ala Lys Asp Asn Pro Leu Pro Ala Asn Ile Pro Thr Glu
65                  70                  75                  80
Ala Lys Leu Glu Lys Ser Thr Glu Val Thr His Glu Thr Ile Tyr Glu
                85                  90                  95
Ser Leu Met Arg Ala Leu His Gln Tyr Ser Ser Leu Gln Ala Asp Asp
            100                 105                 110
Gly His Trp Pro Gly Asp Tyr Ser Gly Ile Leu Phe Ile Met Pro Ile
        115                 120                 125
Ile Ile Phe Ser Leu Tyr Val Thr Arg Ser Leu Asp Thr Phe Leu Ser
    130                 135                 140
Pro Glu His Arg His Glu Ile Cys Arg Tyr Ile Tyr Asn Gln Gln Asn
145                 150                 155                 160
Glu Asp Gly Gly Trp Gly Lys Met Val Leu Gly Pro Ser Thr Met Phe
                165                 170                 175
Gly Ser Cys Met Asn Tyr Ala Thr Leu Met Ile Leu Gly Glu Lys Arg
            180                 185                 190
Asn Gly Asp His Lys Asp Ala Leu Glu Lys Gly Arg Ser Trp Ile Leu
        195                 200                 205
Ser His Gly Thr Ala Thr Ala Ile Pro Gln Trp Gly Lys Ile Trp Leu
    210                 215                 220
Ser Ile Ile Gly Val Tyr Glu Trp Ser Gly Asn Asn Pro Ile Ile Pro
225                 230                 235                 240
Glu Leu Trp Leu Val Pro His Phe Leu Pro Ile His Pro Gly Arg Phe
                245                 250                 255
Trp Cys Phe Thr Arg Leu Ile Tyr Met Ser Met Ala Tyr Leu Tyr Gly
            260                 265                 270
Lys Lys Phe Val Gly Pro Ile Ser Pro Thr Ile Leu Ala Leu Arg Gln
        275                 280                 285
Asp Leu Tyr Ser Ile Pro Tyr Cys Asn Ile Asn Trp Asp Lys Ala Arg
    290                 295                 300

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Asp Tyr Cys Ala Lys Glu Asp Leu His Tyr Pro Arg Ser Arg Ala Gln
305                 310                 315                 320
Asp Leu Ile Ser Gly Cys Leu Thr Lys Ile Val Glu Pro Ile Leu Asn
                325                 330                 335
Trp Trp Pro Ala Asn Lys Leu Arg Asp Arg Ala Leu Thr Asn Leu Met
            340                 345                 350
Glu His Ile His Tyr Asp Asp Glu Ser Thr Lys Tyr Val Gly Ile Cys
        355                 360                 365
Pro Ile Asn Lys Ala Leu Asn Met Ile Cys Cys Trp Val Glu Asn Pro
    370                 375                 380
Asn Ser Pro Glu Phe Gln Gln His Leu Pro Arg Phe His Asp Tyr Leu
385                 390                 395                 400
Trp Met Ala Glu Asp Gly Met Lys Ala Gln Val Tyr Asp Gly Cys His
                405                 410                 415
Ser Trp Glu Leu Ala Phe Ile Ile His Ala Tyr Cys Ser Thr Asp Leu
            420                 425                 430
Thr Ser Glu Phe Ile Pro Thr Leu Lys Lys Ala His Glu Phe Met Lys
        435                 440                 445
Asn Ser Gln Val Leu Phe Asn His Pro Asn His Glu Ser Tyr Tyr Arg
    450                 455                 460
His Arg Ser Lys Gly Ser Trp Thr Leu Ser Ser Val Asp Asn Gly Trp
465                 470                 475                 480
Ser Val Ser Asp Cys Thr Ala Glu Ala Val Lys Ala Leu Leu Leu Leu
                485                 490                 495
Ser Lys Ile Ser Ala Asp Leu Val Gly Asp Pro Ile Lys Gln Asp Arg
            500                 505                 510
Leu Tyr Asp Ala Ile Asp Cys Ile Leu Ser Phe Met Asn Thr Asp Gly
        515                 520                 525
Thr Phe Ser Thr Tyr Glu Cys Lys Arg Thr Phe Ala Trp Leu Glu Val
    530                 535                 540
Leu Asn Pro Ser Glu Ser Phe Arg Asn Ile Val Val Asp Tyr Pro Ser
545                 550                 555                 560
Val Glu Cys Thr Ser Ser Val Val Asp Ala Leu Ile Leu Phe Lys Glu
                565                 570                 575
Thr Asn Pro Arg Tyr Arg Arg Ala Glu Ile Asp Lys Cys Ile Glu Glu
            580                 585                 590
Ala Val Val Phe Ile Glu Asn Ser Gln Asn Lys Asp Gly Ser Trp Tyr
        595                 600                 605
Gly Ser Trp Gly Ile Cys Phe Ala Tyr Gly Cys Met Phe Ala Val Arg
    610                 615                 620
Ala Leu Val Ala Thr Gly Lys Thr Tyr Asp Asn Cys Ala Ser Ile Arg
625                 630                 635                 640
Lys Ser Cys Lys Phe Val Leu Ser Lys Gln Gln Thr Thr Gly Gly Trp
                645                 650                 655
Gly Glu Asp Tyr Leu Ser Ser Asp Asn Gly Glu Tyr Ile Asp Ser Gly
            660                 665                 670
Arg Pro Asn Ala Val Thr Thr Ser Trp Ala Met Leu Ala Leu Ile Tyr
        675                 680                 685
Ala Gly Gln Val Glu Arg Asp Pro Val Pro Leu Tyr Asn Ala Ala Arg
    690                 695                 700
Gln Leu Met Asn Met Gln Leu Glu Thr Gly Asp Phe Pro Gln Gln Glu
705                 710                 715                 720
His Met Gly Cys Phe Asn Ser Phe Leu Asn Phe Asn Tyr Ala Asn Tyr
                725                 730                 735
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Arg Asn Leu Tyr Pro Ile Met Ala Leu Gly Glu Leu Arg Arg Arg Leu
            740                 745                 750
Leu Ala Ile Lys Ser
        755

<210> 347
<211> 757
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified sequence of from Arabidopsis thaliana
      (AtLup1, Q9C5M3.1) to react preferentially with
      diepoxysqualene

<400> 347
Met Trp Lys Leu Lys Ile Gly Lys Gly Asn Gly Glu Asp Pro His Leu
 1               5                  10                  15
Phe Ser Ser Asn Asn Phe Val Gly Arg Gln Thr Trp Lys Phe Asp His
            20                  25                  30
Lys Ala Gly Ser Pro Glu Glu Arg Ala Ala Val Glu Glu Ala Arg Arg
        35                  40                  45
Gly Phe Leu Asp Asn Arg Phe Arg Val Lys Gly Cys Ser Asp Leu Leu
    50                  55                  60
Trp Arg Met Gln Phe Leu Arg Glu Lys Lys Phe Glu Gln Gly Ile Pro
65                  70                  75                  80
Gln Leu Lys Ala Thr Asn Ile Glu Glu Ile Thr Tyr Glu Thr Thr Thr
                85                  90                  95
Asn Ala Leu Arg Arg Gly Val Arg Tyr Phe Thr Ala Leu Gln Ala Ser
            100                 105                 110
Asp Gly His Trp Pro Gly Glu Ile Thr Gly Pro Leu Phe Phe Leu Pro
        115                 120                 125
Pro Leu Ile Phe Cys Leu Tyr Ile Thr Gly His Leu Glu Glu Val Phe
    130                 135                 140
Asp Ala Glu His Arg Lys Glu Met Leu Arg His Ile Tyr Cys His Gln
145                 150                 155                 160
Asn Glu Asp Gly Gly Trp Gly Leu His Ile Glu Ser Lys Ser Val Met
                165                 170                 175
Phe Cys Thr Val Leu Asn Tyr Ile Cys Leu Arg Met Leu Gly Glu Asn
            180                 185                 190
Pro Glu Gln Asp Ala Cys Lys Arg Ala Arg Gln Trp Ile Leu Asp Arg
        195                 200                 205
Gly Gly Val Ile Phe Ile Pro Ser Trp Gly Lys Phe Trp Leu Ser Ile
    210                 215                 220
Leu Gly Val Tyr Asp Trp Ser Gly Thr Asn Pro Thr Pro Pro Glu Leu
225                 230                 235                 240
Leu Met Leu Pro Ser Phe Leu Pro Ile His Pro Gly Lys Ile Leu Cys
                245                 250                 255
Tyr Ser Arg Met Val Ser Ile Pro Met Ser Tyr Leu Tyr Gly Lys Arg
            260                 265                 270
Phe Val Gly Pro Ile Thr Pro Leu Ile Leu Leu Leu Arg Glu Glu Leu
        275                 280                 285
Tyr Leu Glu Pro Tyr Glu Glu Ile Asn Trp Lys Lys Ser Arg Arg Leu

```
    290                 295                 300
Tyr Ala Lys Glu Asp Met Tyr Tyr Ala His Pro Leu Val Gln Asp Leu
305                 310                 315                 320
Leu Ser Asp Thr Leu Gln Asn Phe Val Glu Pro Leu Leu Thr Arg Trp
                325                 330                 335
Pro Leu Asn Lys Leu Val Arg Glu Lys Ala Leu Gln Leu Thr Met Lys
            340                 345                 350
His Ile His Tyr Glu Asp Glu Asn Ser His Tyr Ile Thr Ile Gly Cys
        355                 360                 365
Val Glu Lys Val Leu Cys Met Leu Ala Cys Trp Val Glu Asn Pro Asn
    370                 375                 380
Gly Asp Tyr Phe Lys Lys His Leu Ala Arg Ile Pro Asp Tyr Met Trp
385                 390                 395                 400
Val Ala Glu Asp Gly Met Lys Met Gln Ser Phe Gly Cys Gln Leu Trp
                405                 410                 415
Asp Thr Gly Phe Ala Ile Gln Ala Leu Leu Ala Ser Asn Leu Pro Asp
            420                 425                 430
Glu Thr Asp Asp Ala Leu Lys Arg Gly His Asn Tyr Ile Lys Ala Ser
        435                 440                 445
Gln Val Arg Glu Asn Pro Ser Gly Asp Phe Arg Ser Met Tyr Arg His
    450                 455                 460
Ile Ser Lys Gly Ala Trp Thr Phe Ser Asp Arg Asp His Gly Trp Gln
465                 470                 475                 480
Val Ser Asp Cys Thr Ala Glu Ala Leu Lys Cys Cys Leu Leu Leu Ser
                485                 490                 495
Met Met Ser Ala Asp Ile Val Gly Gln Lys Ile Asp Asp Glu Gln Leu
            500                 505                 510
Tyr Asp Ser Val Asn Leu Leu Leu Ser Leu Gln Ser Gly Asn Gly Gly
        515                 520                 525
Val Asn Ala Trp Glu Pro Ser Arg Ala Tyr Lys Trp Leu Glu Leu Leu
    530                 535                 540
Asn Pro Thr Glu Phe Met Ala Asn Thr Met Val Glu Arg Glu Phe Val
545                 550                 555                 560
Glu Cys Thr Ser Ser Val Ile Gln Ala Leu Asp Leu Phe Arg Lys Leu
                565                 570                 575
Tyr Pro Asp His Arg Lys Lys Glu Ile Asn Arg Ser Ile Glu Lys Ala
            580                 585                 590
Val Gln Phe Ile Gln Asp Asn Gln Thr Pro Asp Gly Ser Trp Tyr Gly
        595                 600                 605
Asn Trp Gly Val Cys Phe Ile Tyr Ala Thr Trp Phe Ala Leu Gly Gly
    610                 615                 620
Leu Ala Ala Ala Gly Glu Thr Tyr Asn Asp Cys Leu Ala Met Arg Asn
625                 630                 635                 640
Gly Val His Phe Leu Leu Thr Thr Gln Arg Asp Asp Gly Gly Trp Gly
                645                 650                 655
Glu Ser Tyr Leu Ser Cys Ser Glu Gln Arg Tyr Ile Pro Ser Glu Gly
            660                 665                 670
Glu Arg Ser Asn Leu Val Gln Thr Ser Trp Ala Met Met Ala Leu Ile
        675                 680                 685
His Thr Gly Gln Ala Glu Arg Asp Leu Ile Pro Leu His Arg Ala Ala
    690                 695                 700
Lys Leu Ile Ile Asn Ser Gln Leu Glu Asn Gly Asp Phe Pro Gln Gln
705                 710                 715                 720
Glu Ile Val Gly Ala Phe Met Asn Phe Cys Met Leu His Tyr Ala Thr
```

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                725                 730                 735
Tyr Arg Asn Thr Phe Pro Leu Trp Ala Leu Ala Glu Tyr Arg Lys Val
            740                 745                 750
Val Phe Ile Val Asn
        755
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<210> 348

<400> 348
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<210> 349

<400> 349
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<210> 350

<400> 350
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<210> 351

<400> 351
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<210> 352
<211> 601
<212> PRT
<213> Artificial Sequence

<220>
<223> XP_001396506.2

<400> 352

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

```
Phe Asp Glu Ala Gly Asn Pro Val Pro Pro Asn Asn Trp Ala Gln Ile
145                 150                 155                 160
Leu Gly Asp Thr Leu Ser Ala Trp Thr Trp His Ala Glu Thr Gln Glu
                165                 170                 175
Phe Tyr Leu Thr Leu His Thr Ser Ala Gln Ala Glu Leu Asn Trp Glu
            180                 185                 190
Asn Pro Asp Val Val Thr Ala Val Tyr Asp Val Met Glu Phe Trp Leu
        195                 200                 205
Arg Arg Gly Ile Cys Gly Phe Arg Met Asp Val Ile Asn Phe Ile Ser
    210                 215                 220
Lys Asp Gln Ser Phe Pro Asp Ala Pro Ile Ile Asp Pro Ala Ser Lys
225                 230                 235                 240
Tyr Gln Pro Gly Glu Gln Phe Tyr Thr Asn Gly Pro Arg Phe His Glu
                245                 250                 255
Phe Met His Gly Ile Tyr Asp Asn Val Leu Ser Lys Tyr Asp Thr Ile
            260                 265                 270
Thr Val Gly Glu Thr Pro Tyr Val Thr Asp Met Lys Glu Ile Ile Lys
        275                 280                 285
Thr Val Gly Ser Thr Ala Lys Glu Leu Asn Met Ala Phe Asn Phe Asp
    290                 295                 300
His Met Glu Ile Glu Asp Ile Lys Thr Lys Gly Glu Ser Lys Trp Ser
305                 310                 315                 320
Leu Arg Asp Trp Lys Leu Thr Glu Leu Lys Gly Ile Leu Ser Gly Trp
                325                 330                 335
Gln Lys Arg Met Arg Glu Trp Asp Gly Trp Asn Ala Ile Phe Leu Glu
            340                 345                 350
Cys His Asp Gln Ala Arg Ser Val Ser Arg Tyr Thr Asn Asp Ser Asp
        355                 360                 365
Glu Phe Arg Asp Arg Gly Ala Lys Leu Leu Ala Leu Leu Glu Thr Thr
    370                 375                 380
Leu Gly Gly Thr Ile Phe Leu Tyr Gln Gly Gln Glu Ile Gly Met Arg
385                 390                 395                 400
Asn Phe Pro Val Glu Trp Asp Pro Asp Thr Glu Tyr Lys Asp Ile Glu
                405                 410                 415
Ser Val Asn Phe Trp Lys Lys Ser Lys Glu Leu His Pro Val Gly Ser
            420                 425                 430
Glu Gly Leu Ala Gln Ala Arg Thr Leu Leu Gln Lys Lys Ala Arg Asp
        435                 440                 445
His Ala Arg Thr Pro Met Gln Trp Ser Ala Asp Pro His Ala Gly Phe
    450                 455                 460
Thr Val Pro Asp Ala Thr Pro Trp Met Arg Val Asn Asp Asp Tyr Gly
465                 470                 475                 480
Thr Val Asn Val Glu Ala Gln Met Ser Phe Pro Trp Glu Met Lys Gly
                485                 490                 495
Glu Leu Ser Val Trp Gln Tyr Trp Gln Gln Ala Leu Gln Arg Arg Lys
            500                 505                 510
Leu His Lys Gly Ala Phe Val Tyr Gly Asp Phe Glu Asp Leu Asp Tyr
        515                 520                 525
His Asn Glu Leu Val Phe Ala Tyr Ser Arg Thr Ser Ala Asp Gly Lys
    530                 535                 540
Glu Thr Trp Leu Val Ala Met Asn Trp Thr Thr Asp Ala Val Glu Trp
545                 550                 555                 560
Thr Val Pro Ser Gly Ile His Val Thr Arg Trp Val Ser Ser Thr Leu
                565                 570                 575
```

```
Gln Thr Ala Pro Leu Met Ala Gly Gln Ser Thr Val Thr Leu Arg Ala
            580                 585                 590
Leu Glu Gly Val Val Gly Cys Cys Ser
        595                 600
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<210> 353

<400> 353
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<210> 354
<211> 895
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-glucosidase [Trichoderma reesei], GenBank: BAP5915.1

<400> 354

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

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            260                 265                 270
Val Asn Gly Thr Ala Cys Ser Gln His Pro Tyr Leu Met Ser Ala Leu
        275                 280                 285
Leu Lys Asp Glu Met Gly Phe Gln Gly Phe Ile Met Thr Asp Trp Leu
    290                 295                 300
Ala His Met Ser Gly Val Ala Ser Ala Ile Ala Gly Leu Asp Met Asp
305                 310                 315                 320
Met Pro Gly Asp Val Gln Ile Pro Phe Phe Gly Gly Ser Tyr Trp Met
                325                 330                 335
Tyr Glu Leu Thr Arg Ser Ala Leu Asn Gly Ser Val Pro Met Asp Arg
            340                 345                 350
Ile Asn Asp Ala Ala Thr Arg Ile Ala Ala Ala Trp Tyr Lys Met Gly
        355                 360                 365
Gln Asp Lys Gly Phe Pro Ala Thr Asn Phe Asp Thr Asn Ser Arg Ala
    370                 375                 380
Ala Phe Asn Pro Leu Tyr Pro Ala Ala Leu Pro Leu Ser Pro Phe Gly
385                 390                 395                 400
Ile Thr Asn Glu Phe Val Pro Val Gln Asp Asp His Asp Val Ile Ala
                405                 410                 415
Arg Gln Ile Ser Gln Glu Ala Ile Thr Leu Leu Lys Asn Asp Gly Asp
            420                 425                 430
Ile Leu Pro Leu Ser Pro Ser Gln His Leu Lys Val Phe Gly Thr Asp
        435                 440                 445
Ala Gln Lys Asn Pro Asp Gly Ile Asn Ser Cys Thr Asp Arg Asn Cys
    450                 455                 460
Asn Lys Gly Thr Leu Gly Gln Gly Trp Gly Ser Gly Thr Val Asp Tyr
465                 470                 475                 480
Pro Tyr Leu Asp Asp Pro Ile Ser Ala Ile Thr Ala Glu Ala Asp Asn
                485                 490                 495
Val Thr Phe Tyr Asn Thr Asp Lys Phe Pro Ser Val Gly Glu Val Ser
            500                 505                 510
Asp Ser Asp Val Ala Ile Val Phe Val Asn Ser Asp Ala Gly Glu Asn
        515                 520                 525
Thr Tyr Thr Val Glu Gly Asn His Gly Asp Arg Asp Lys Ser Gly Leu
    530                 535                 540
Tyr Ala Trp His Asp Gly Asp Lys Leu Val Gln Asp Ala Ala Ser Lys
545                 550                 555                 560
Phe Ser Asn Val Ile Val Val Ile His Thr Val Gly Pro Leu Ile Leu
                565                 570                 575
Glu Lys Trp Ile Asp Leu Pro Ser Val Lys Ala Val Leu Val Ala His
            580                 585                 590
Leu Pro Gly Gln Glu Ala Gly Lys Ser Leu Thr Asn Val Leu Phe Gly
        595                 600                 605
His Ala Ser Pro Cys Gly His Leu Pro Tyr Ser Ile Thr Lys Glu Glu
    610                 615                 620
Asp Asp Leu Pro Lys Ser Val Thr Thr Leu Ile Asp Ser Glu Phe Leu
625                 630                 635                 640
Asn Gln Pro Gln Asp Thr Tyr Thr Glu Gly Leu Tyr Ile Asp Tyr Arg
                645                 650                 655
Trp Leu Asn Lys Asn Lys Thr Lys Pro Arg Tyr Ala Phe Gly His Gly
            660                 665                 670
Leu Ser Tyr Thr Asn Phe Thr Phe Lys Ala Ala Ser Ile Lys Gln Val
        675                 680                 685
Ala Arg Leu Ser Ala Tyr Pro Pro Ala Arg Pro Ala Lys Gly Ser Thr
```

```
    690                 695                 700
Pro Asp Phe Ala Gln Ser Ile Pro Ser Ala Ser Glu Ala Val Ala Pro
705                 710                 715                 720
Ser Gly Phe Gly Lys Ile Pro Arg Tyr Ile Tyr Ser Trp Leu Ser Gln
                725                 730                 735
Gly Asp Ala Asn Arg Ala Ile Ser Asp Gly Lys Thr Gly Lys Tyr Pro
            740                 745                 750
Tyr Pro Asp Gly Tyr Ser Thr Thr Gln Lys Pro Gly Ala Arg Ala Gly
        755                 760                 765
Gly Gly Glu Gly Gly Asn Pro Ala Leu Trp Asp Val Ala Tyr Ser Leu
    770                 775                 780
Thr Val Thr Val Gln Asn Thr Gly Asp Glu Tyr Ala Gly Lys Ala Ser
785                 790                 795                 800
Val Gln Ala Tyr Leu Gln Phe Pro Asp Asp Ile Asp Tyr Asp Thr Pro
                805                 810                 815
Ile Ile Gln Leu Arg Asp Phe Glu Lys Thr Lys Glu Leu Lys Pro Gly
            820                 825                 830
Glu Thr Thr Thr Val Thr Leu Thr Leu Thr Arg Lys Asp Val Ser Val
        835                 840                 845
Trp Asp Val Val Ala Gln Asp Trp Lys Val Pro Ala Val Asp Gly Gly
    850                 855                 860
Tyr Lys Val Trp Ile Gly Asp Ala Ser Asp Ser Leu Ser Ile Val Cys
865                 870                 875                 880
His Thr Asp Thr Leu Glu Cys Glu Thr Gly Val Val Gly Pro Val
                885                 890                 895


<210> 355
<211> 831
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-glucosidase [Trichodermareesei] 831 aa
      protein BAP59014.1 GI:690966588

<400> 355
Met Met Gly Phe Asp Val Glu Asp Val Leu Ser Gln Leu Ser Gln Asn
 1               5                  10                  15
Glu Lys Ile Ala Leu Leu Ser Gly Ile Asp Phe Trp His Thr Tyr Pro
            20                  25                  30
Ile Pro Lys Tyr Asn Val Pro Ser Val Arg Leu Thr Asp Gly Pro Asn
        35                  40                  45
Gly Ile Arg Gly Thr Lys Phe Phe Ala Gly Ile Pro Ala Ala Cys Leu
    50                  55                  60
Pro Cys Gly Thr Ala Leu Ala Ser Thr Trp Asp Lys Gln Leu Leu Lys
65                  70                  75                  80
Lys Ala Gly Lys Leu Leu Gly Asp Glu Cys Ile Ala Lys Gly Ala His
                85                  90                  95
Cys Trp Leu Gly Pro Thr Ile Asn Thr Pro Arg Ser Pro Leu Gly Gly
            100                 105                 110
Arg Gly Phe Glu Ser Phe Ser Glu Asp Pro Tyr Leu Ser Gly Ile Leu
        115                 120                 125
Ala Ala Ser Met Ile Leu Gly Cys Glu Ser Thr Gly Val Ile Ser Ala
```

```
    130                 135                 140
Val Lys His Phe Val Ala Asn Asp Gln Glu His Glu Arg Arg Ala Val
145                 150                 155                 160
Asp Cys Leu Ile Thr Gln Arg Ala Leu Arg Glu Val Tyr Leu Arg Pro
                165                 170                 175
Phe Gln Ile Val Ala Arg Asp Ala Arg Pro Gly Ala Leu Met Thr Ser
            180                 185                 190
Tyr Asn Lys Val Asn Gly Lys His Val Ala Asp Ser Ala Glu Phe Leu
        195                 200                 205
Gln Gly Ile Leu Arg Thr Glu Trp Asn Trp Asp Pro Leu Ile Val Ser
    210                 215                 220
Asp Trp Tyr Gly Thr Tyr Thr Thr Ile Asp Ala Ile Lys Ala Gly Leu
225                 230                 235                 240
Asp Leu Glu Met Pro Gly Val Ser Arg Tyr Arg Gly Lys Tyr Ile Glu
                245                 250                 255
Ser Ala Leu Gln Ala Arg Leu Leu Lys Gln Ser Thr Ile Asp Glu Arg
            260                 265                 270
Ala Arg Arg Val Leu Arg Phe Ala Gln Lys Ala Ser His Leu Lys Val
        275                 280                 285
Ser Glu Val Glu Gln Gly Arg Asp Phe Pro Glu Asp Arg Val Leu Asn
    290                 295                 300
Arg Gln Ile Cys Gly Ser Ser Ile Val Leu Leu Lys Asn Glu Asn Ser
305                 310                 315                 320
Ile Leu Pro Leu Pro Lys Ser Val Lys Lys Val Ala Leu Val Gly Ser
                325                 330                 335
His Val Arg Leu Pro Ala Ile Ser Gly Gly Gly Ser Ala Ser Leu Val
            340                 345                 350
Pro Tyr Tyr Ala Ile Ser Leu Tyr Asp Ala Val Ser Glu Val Leu Ala
        355                 360                 365
Gly Ala Thr Ile Thr His Glu Val Gly Ala Tyr Ala His Gln Met Leu
    370                 375                 380
Pro Val Ile Asp Ala Met Ile Ser Asn Ala Val Ile His Phe Tyr Asn
385                 390                 395                 400
Asp Pro Ile Asp Val Lys Asp Arg Lys Leu Leu Gly Ser Glu Asn Val
                405                 410                 415
Ser Ser Thr Ser Phe Gln Leu Met Asp Tyr Asn Asn Ile Pro Thr Leu
            420                 425                 430
Asn Lys Ala Met Phe Trp Gly Thr Leu Val Gly Glu Phe Ile Pro Thr
        435                 440                 445
Ala Thr Gly Ile Trp Glu Phe Gly Leu Ser Val Phe Gly Thr Ala Asp
    450                 455                 460
Leu Tyr Ile Asp Asn Glu Leu Val Ile Glu Asn Thr Thr His Gln Thr
465                 470                 475                 480
Arg Gly Thr Ala Phe Phe Gly Lys Gly Thr Thr Glu Lys Val Ala Thr
                485                 490                 495
Arg Arg Met Val Ala Gly Ser Thr Tyr Lys Leu Arg Leu Glu Phe Gly
            500                 505                 510
Ser Ala Asn Thr Thr Lys Met Glu Thr Thr Gly Val Val Asn Phe Gly
        515                 520                 525
Gly Gly Ala Val His Leu Gly Ala Cys Leu Lys Val Asp Pro Gln Glu
    530                 535                 540
Met Ile Ala Arg Ala Val Lys Ala Ala Ala Asp Ala Asp Tyr Thr Ile
545                 550                 555                 560
Ile Cys Thr Gly Leu Ser Gly Glu Trp Glu Ser Glu Gly Phe Asp Arg
```

```
                565                 570                 575
Pro His Met Asp Leu Pro Pro Gly Val Asp Thr Met Ile Ser Gln Val
            580                 585                 590
Leu Asp Ala Ala Pro Asn Ala Val Val Val Asn Gln Ser Gly Thr Pro
        595                 600                 605
Val Thr Met Ser Trp Ala His Lys Ala Lys Ala Ile Val Gln Ala Trp
    610                 615                 620
Tyr Gly Gly Asn Glu Thr Gly His Gly Ile Ser Asp Val Leu Phe Gly
625                 630                 635                 640
Asn Val Asn Pro Ser Gly Lys Leu Ser Leu Ser Trp Pro Val Asp Val
                645                 650                 655
Lys His Asn Pro Ala Tyr Leu Asn Tyr Ala Ser Val Gly Gly Arg Val
            660                 665                 670
Leu Tyr Gly Glu Asp Val Tyr Val Gly Tyr Lys Phe Tyr Asp Lys Thr
        675                 680                 685
Glu Arg Glu Val Leu Phe Pro Phe Gly His Gly Leu Ser Tyr Ala Thr
    690                 695                 700
Phe Lys Leu Pro Asp Ser Thr Val Arg Thr Val Pro Glu Thr Phe His
705                 710                 715                 720
Pro Asp Gln Pro Thr Val Ala Ile Val Lys Ile Lys Asn Thr Ser Ser
                725                 730                 735
Val Pro Gly Ala Gln Val Leu Gln Leu Tyr Ile Ser Ala Pro Asn Ser
            740                 745                 750
Pro Thr His Arg Pro Val Lys Glu Leu His Gly Phe Glu Lys Val Tyr
        755                 760                 765
Leu Glu Ala Gly Glu Glu Lys Glu Val Gln Ile Pro Ile Asp Gln Tyr
    770                 775                 780
Ala Thr Ser Phe Trp Asp Glu Ile Glu Ser Met Trp Lys Ser Glu Arg
785                 790                 795                 800
Gly Ile Tyr Asp Val Leu Val Gly Phe Ser Ser Gln Glu Ile Ser Gly
                805                 810                 815
Lys Gly Lys Leu Ile Val Pro Glu Thr Arg Phe Trp Met Gly Leu
            820                 825                 830


<210> 356
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-glucosidase [Trichoderma reesei] 466 aa
      protein AHK23047.1 GI:588294532

<400> 356
Met Leu Pro Lys Asp Phe Gln Trp Gly Phe Ala Thr Ala Ala Tyr Gln
 1               5                  10                  15
Ile Glu Gly Ala Val Asp Gln Asp Gly Arg Gly Pro Ser Ile Trp Asp
            20                  25                  30
Thr Phe Cys Ala Gln Pro Gly Lys Ile Ala Asp Gly Ser Ser Gly Val
        35                  40                  45
Thr Ala Cys Asp Ser Tyr Asn Arg Thr Ala Glu Asp Ile Ala Leu Leu
    50                  55                  60
Lys Ser Leu Gly Ala Lys Ser Tyr Arg Phe Ser Ile Ser Trp Ser Arg
```

```
65                  70                  75                  80
Ile Ile Pro Glu Gly Gly Arg Gly Asp Ala Val Asn Gln Ala Gly Ile
                85                  90                  95
Asp His Tyr Val Lys Phe Val Asp Asp Leu Leu Asp Ala Gly Ile Thr
            100                 105                 110
Pro Phe Ile Thr Leu Phe His Trp Asp Leu Pro Glu Gly Leu His Gln
        115                 120                 125
Arg Tyr Gly Gly Leu Leu Asn Arg Thr Glu Phe Pro Leu Asp Phe Glu
    130                 135                 140
Asn Tyr Ala Arg Val Met Phe Arg Ala Leu Pro Lys Val Arg Asn Trp
145                 150                 155                 160
Ile Thr Phe Asn Glu Pro Leu Cys Ser Ala Ile Pro Gly Tyr Gly Ser
                165                 170                 175
Gly Thr Phe Ala Pro Gly Arg Gln Ser Thr Ser Glu Pro Trp Thr Val
            180                 185                 190
Gly His Asn Ile Leu Val Ala His Gly Arg Ala Val Lys Ala Tyr Arg
        195                 200                 205
Asp Asp Phe Lys Pro Ala Ser Gly Asp Gly Gln Ile Gly Ile Val Leu
    210                 215                 220
Asn Gly Asp Phe Thr Tyr Pro Trp Asp Ala Ala Asp Pro Ala Asp Lys
225                 230                 235                 240
Glu Ala Ala Glu Arg Arg Leu Glu Phe Phe Thr Ala Trp Phe Ala Asp
                245                 250                 255
Pro Ile Tyr Leu Gly Asp Tyr Pro Ala Ser Met Arg Lys Gln Leu Gly
            260                 265                 270
Asp Arg Leu Pro Thr Phe Thr Pro Glu Glu Arg Ala Leu Val His Gly
        275                 280                 285
Ser Asn Asp Phe Tyr Gly Met Asn His Tyr Thr Ser Asn Tyr Ile Arg
    290                 295                 300
His Arg Ser Ser Pro Ala Ser Ala Asp Asp Thr Val Gly Asn Val Asp
305                 310                 315                 320
Val Leu Phe Thr Asn Lys Gln Gly Asn Cys Ile Gly Pro Glu Thr Gln
                325                 330                 335
Ser Pro Trp Leu Arg Pro Cys Ala Ala Gly Phe Arg Asp Phe Leu Val
            340                 345                 350
Trp Ile Ser Lys Arg Tyr Gly Tyr Pro Pro Ile Tyr Val Thr Glu Asn
        355                 360                 365
Gly Thr Ser Ile Lys Gly Glu Ser Asp Leu Pro Lys Glu Lys Ile Leu
    370                 375                 380
Glu Asp Asp Phe Arg Val Lys Tyr Tyr Asn Glu Tyr Ile Arg Ala Met
385                 390                 395                 400
Val Thr Ala Val Glu Leu Asp Gly Val Asn Val Lys Gly Tyr Phe Ala
                405                 410                 415
Trp Ser Leu Met Asp Asn Phe Glu Trp Ala Asp Gly Tyr Val Thr Arg
            420                 425                 430
Phe Gly Val Thr Tyr Val Asp Tyr Glu Asn Gly Gln Lys Arg Phe Pro
        435                 440                 445
Lys Lys Ser Ala Lys Ser Leu Lys Pro Leu Phe Asp Glu Leu Ile Ala
    450                 455                 460
Ala Ala
465
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<210> 357

<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-glucosidase [Trichoderma reesei] 466 aa
protein BAA74959.1 GI:4249562

<400> 357
Met Leu Pro Lys Asp Phe Gln Trp Gly Phe Ala Thr Ala Ala Tyr Gln
 1               5                  10                  15
Ile Glu Gly Ala Val Asp Gln Asp Gly Arg Gly Pro Ser Ile Trp Asp
            20                  25                  30
Thr Phe Cys Ala Gln Pro Gly Lys Ile Ala Asp Gly Ser Ser Gly Val
        35                  40                  45
Thr Ala Cys Asp Ser Tyr Asn Arg Thr Ala Glu Asp Ile Ala Leu Leu
    50                  55                  60
Lys Ser Leu Gly Ala Lys Ser Tyr Arg Phe Ser Ile Ser Trp Ser Arg
65                  70                  75                  80
Ile Ile Pro Glu Gly Gly Arg Gly Asp Ala Val Asn Gln Ala Gly Ile
                85                  90                  95
Asp His Tyr Val Lys Phe Val Asp Asp Leu Leu Asp Ala Gly Ile Thr
            100                 105                 110
Pro Phe Ile Thr Leu Phe His Trp Asp Leu Pro Glu Gly Leu His Gln
        115                 120                 125
Arg Tyr Gly Gly Leu Leu Asn Arg Thr Glu Phe Pro Leu Asp Phe Glu
    130                 135                 140
Asn Tyr Ala Arg Val Met Phe Arg Ala Leu Pro Lys Val Arg Asn Trp
145                 150                 155                 160
Ile Thr Phe Asn Glu Pro Leu Cys Ser Ala Ile Pro Gly Tyr Gly Ser
                165                 170                 175
Gly Thr Phe Ala Pro Gly Arg Gln Ser Thr Ser Glu Pro Trp Thr Val
            180                 185                 190
Gly His Asn Ile Leu Val Ala His Gly Arg Ala Val Lys Ala Tyr Arg
        195                 200                 205
Asp Asp Phe Lys Pro Ala Ser Gly Asp Gly Gln Ile Gly Ile Val Leu
    210                 215                 220
Asn Gly Asp Phe Thr Tyr Pro Trp Asp Ala Ala Asp Pro Ala Asp Lys
225                 230                 235                 240
Glu Ala Ala Glu Arg Arg Leu Glu Phe Phe Thr Ala Trp Phe Ala Asp
                245                 250                 255
Pro Ile Tyr Leu Gly Asp Tyr Pro Ala Ser Met Arg Lys Gln Leu Gly
            260                 265                 270
Asp Arg Leu Pro Thr Phe Thr Pro Glu Glu Arg Ala Leu Val His Gly
        275                 280                 285
Ser Asn Asp Phe Tyr Gly Met Asn His Tyr Thr Ser Asn Tyr Ile Arg
    290                 295                 300
His Arg Ser Ser Pro Ala Ser Ala Asp Asp Thr Val Gly Asn Val Asp
305                 310                 315                 320
Val Leu Phe Thr Asn Lys Gln Gly Asn Cys Ile Gly Pro Glu Thr Gln
                325                 330                 335
Ser Pro Trp Leu Arg Pro Cys Ala Ala Gly Phe Arg Asp Phe Leu Val
            340                 345                 350
Trp Ile Ser Lys Arg Tyr Gly Tyr Pro Pro Ile Tyr Val Thr Glu Asn

```
        355                 360                 365
Gly Thr Ser Ile Lys Gly Glu Ser Asp Leu Pro Lys Glu Lys Ile Leu
    370                 375                 380
Glu Asp Asp Phe Arg Val Lys Tyr Tyr Asn Glu Tyr Ile Arg Ala Met
385                 390                 395                 400
Val Thr Ala Val Glu Leu Asp Gly Val Asn Val Lys Gly Tyr Phe Ala
                405                 410                 415
Trp Ser Leu Met Asp Asn Phe Glu Trp Ala Asp Gly Tyr Val Thr Arg
            420                 425                 430
Phe Gly Val Thr Tyr Val Asp Tyr Glu Asn Gly Gln Lys Arg Phe Pro
        435                 440                 445
Lys Lys Ser Ala Lys Ser Leu Lys Pro Leu Phe Asp Glu Leu Ile Ala
    450                 455                 460
Ala Ala
465
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<210> 358
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-glucosidase [Trichoderma reesei RUT C-3] 466
aa protein ETS5552.1 GI:572282538

<400> 358

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

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


<210> 359
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain D, Crystal Structure Of Beta-Glucosidase 2
      From  Fungus Trichoderma Reesei In Complex With
      Tris 473 aa protein 3AHY_D GI:303324838

<400> 359
Met His His His His His His Met Leu Pro Lys Asp Phe Gln Trp Gly
 1               5                  10                  15
Phe Ala Thr Ala Ala Tyr Gln Ile Glu Gly Ala Val Asp Gln Asp Gly
            20                  25                  30
Arg Gly Pro Ser Ile Trp Asp Thr Phe Cys Ala Gln Pro Gly Lys Ile
        35                  40                  45
Ala Asp Gly Ser Ser Gly Val Thr Ala Cys Asp Ser Tyr Asn Arg Thr
    50                  55                  60
```

```
Ala Glu Asp Ile Ala Leu Leu Lys Ser Leu Gly Ala Lys Ser Tyr Arg
65                  70                  75                  80
Phe Ser Ile Ser Trp Ser Arg Ile Ile Pro Glu Gly Gly Arg Gly Asp
                85                  90                  95
Ala Val Asn Gln Ala Gly Ile Asp His Tyr Val Lys Phe Val Asp Asp
            100                 105                 110
Leu Leu Asp Ala Gly Ile Thr Pro Phe Ile Thr Leu Phe His Trp Asp
        115                 120                 125
Leu Pro Glu Gly Leu His Gln Arg Tyr Gly Gly Leu Leu Asn Arg Thr
    130                 135                 140
Glu Phe Pro Leu Asp Phe Glu Asn Tyr Ala Arg Val Met Phe Arg Ala
145                 150                 155                 160
Leu Pro Lys Val Arg Asn Trp Ile Thr Phe Asn Glu Pro Leu Cys Ser
                165                 170                 175
Ala Ile Pro Gly Tyr Gly Ser Gly Thr Phe Ala Pro Gly Arg Gln Ser
            180                 185                 190
Thr Ser Glu Pro Trp Thr Val Gly His Asn Ile Leu Val Ala His Gly
        195                 200                 205
Arg Ala Val Lys Ala Tyr Arg Asp Asp Phe Lys Pro Ala Ser Gly Asp
    210                 215                 220
Gly Gln Ile Gly Ile Val Leu Asn Gly Asp Phe Thr Tyr Pro Trp Asp
225                 230                 235                 240
Ala Ala Asp Pro Ala Asp Lys Glu Ala Ala Glu Arg Arg Leu Glu Phe
                245                 250                 255
Phe Thr Ala Trp Phe Ala Asp Pro Ile Tyr Leu Gly Asp Tyr Pro Ala
            260                 265                 270
Ser Met Arg Lys Gln Leu Gly Asp Arg Leu Pro Thr Phe Thr Pro Glu
        275                 280                 285
Glu Arg Ala Leu Val His Gly Ser Asn Asp Phe Tyr Gly Met Asn His
    290                 295                 300
Tyr Thr Ser Asn Tyr Ile Arg His Arg Ser Ser Pro Ala Ser Ala Asp
305                 310                 315                 320
Asp Thr Val Gly Asn Val Asp Val Leu Phe Thr Asn Lys Gln Gly Asn
                325                 330                 335
Cys Ile Gly Pro Glu Thr Gln Ser Pro Trp Leu Arg Pro Cys Ala Ala
            340                 345                 350
Gly Phe Arg Asp Phe Leu Val Trp Ile Ser Lys Arg Tyr Gly Tyr Pro
        355                 360                 365
Pro Ile Tyr Val Thr Glu Asn Gly Thr Ser Ile Lys Gly Glu Ser Asp
    370                 375                 380
Leu Pro Lys Glu Lys Ile Leu Glu Asp Asp Phe Arg Val Lys Tyr Tyr
385                 390                 395                 400
Asn Glu Tyr Ile Arg Ala Met Val Thr Ala Val Glu Leu Asp Gly Val
                405                 410                 415
Asn Val Lys Gly Tyr Phe Ala Trp Ser Leu Met Asp Asn Phe Glu Trp
            420                 425                 430
Ala Asp Gly Tyr Val Thr Arg Phe Gly Val Thr Tyr Val Asp Tyr Glu
        435                 440                 445
Asn Gly Gln Lys Arg Phe Pro Lys Lys Ser Ala Lys Ser Leu Lys Pro
    450                 455                 460
Leu Phe Asp Glu Leu Ile Ala Ala Ala
465                 470
```

<210> 360
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> ChainC, Crystal Structure Of Beta-Glucosidase 2
From Fungus Trichoderma Reesei In Complex With
Tris 473 aa protein 3AHY_C GI:33324837

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

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


<210> 361
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, Crystal Structure Of Beta-Glucosidase 2
      From Fungus Trichoderma Reesei In Complex With
      Tris 473 aa protein 3AHY_B GI:303324836

<400> 361
Met His His His His His His Met Leu Pro Lys Asp Phe Gln Trp Gly
 1               5                  10                  15
Phe Ala Thr Ala Ala Tyr Gln Ile Glu Gly Ala Val Asp Gln Asp Gly
            20                  25                  30
Arg Gly Pro Ser Ile Trp Asp Thr Phe Cys Ala Gln Pro Gly Lys Ile
        35                  40                  45
Ala Asp Gly Ser Ser Gly Val Thr Ala Cys Asp Ser Tyr Asn Arg Thr
    50                  55                  60
Ala Glu Asp Ile Ala Leu Leu Lys Ser Leu Gly Ala Lys Ser Tyr Arg
65                  70                  75                  80
Phe Ser Ile Ser Trp Ser Arg Ile Ile Pro Glu Gly Gly Arg Gly Asp
                85                  90                  95
Ala Val Asn Gln Ala Gly Ile Asp His Tyr Val Lys Phe Val Asp Asp
            100                 105                 110
Leu Leu Asp Ala Gly Ile Thr Pro Phe Ile Thr Leu Phe His Trp Asp
        115                 120                 125
Leu Pro Glu Gly Leu His Gln Arg Tyr Gly Gly Leu Leu Asn Arg Thr
    130                 135                 140
Glu Phe Pro Leu Asp Phe Glu Asn Tyr Ala Arg Val Met Phe Arg Ala
145                 150                 155                 160
Leu Pro Lys Val Arg Asn Trp Ile Thr Phe Asn Glu Pro Leu Cys Ser
                165                 170                 175
Ala Ile Pro Gly Tyr Gly Ser Gly Thr Phe Ala Pro Gly Arg Gln Ser
            180                 185                 190
```

```
Thr Ser Glu Pro Trp Thr Val Gly His Asn Ile Leu Val Ala His Gly
        195                 200                 205
Arg Ala Val Lys Ala Tyr Arg Asp Asp Phe Lys Pro Ala Ser Gly Asp
    210                 215                 220
Gly Gln Ile Gly Ile Val Leu Asn Gly Asp Phe Thr Tyr Pro Trp Asp
225                 230                 235                 240
Ala Ala Asp Pro Ala Asp Lys Glu Ala Ala Glu Arg Arg Leu Glu Phe
                245                 250                 255
Phe Thr Ala Trp Phe Ala Asp Pro Ile Tyr Leu Gly Asp Tyr Pro Ala
            260                 265                 270
Ser Met Arg Lys Gln Leu Gly Asp Arg Leu Pro Thr Phe Thr Pro Glu
        275                 280                 285
Glu Arg Ala Leu Val His Gly Ser Asn Asp Phe Tyr Gly Met Asn His
    290                 295                 300
Tyr Thr Ser Asn Tyr Ile Arg His Arg Ser Ser Pro Ala Ser Ala Asp
305                 310                 315                 320
Asp Thr Val Gly Asn Val Asp Val Leu Phe Thr Asn Lys Gln Gly Asn
                325                 330                 335
Cys Ile Gly Pro Glu Thr Gln Ser Pro Trp Leu Arg Pro Cys Ala Ala
            340                 345                 350
Gly Phe Arg Asp Phe Leu Val Trp Ile Ser Lys Arg Tyr Gly Tyr Pro
        355                 360                 365
Pro Ile Tyr Val Thr Glu Asn Gly Thr Ser Ile Lys Gly Glu Ser Asp
    370                 375                 380
Leu Pro Lys Glu Lys Ile Leu Glu Asp Asp Phe Arg Val Lys Tyr Tyr
385                 390                 395                 400
Asn Glu Tyr Ile Arg Ala Met Val Thr Ala Val Glu Leu Asp Gly Val
                405                 410                 415
Asn Val Lys Gly Tyr Phe Ala Trp Ser Leu Met Asp Asn Phe Glu Trp
            420                 425                 430
Ala Asp Gly Tyr Val Thr Arg Phe Gly Val Thr Tyr Val Asp Tyr Glu
        435                 440                 445
Asn Gly Gln Lys Arg Phe Pro Lys Lys Ser Ala Lys Ser Leu Lys Pro
    450                 455                 460
Leu Phe Asp Glu Leu Ile Ala Ala Ala
465                 470


<210> 362
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Crystal Structure Of Beta-Glucosidase 2
      From Fungus Trichoderma Reesei In Complex With
      Tris 473 aa protein 3AHY_A GI:303324835

<400> 362
Met His His His His His His Met Leu Pro Lys Asp Phe Gln Trp Gly
 1               5                  10                  15
Phe Ala Thr Ala Ala Tyr Gln Ile Glu Gly Ala Val Asp Gln Asp Gly
            20                  25                  30
Arg Gly Pro Ser Ile Trp Asp Thr Phe Cys Ala Gln Pro Gly Lys Ile
```

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

465 470

<210> 363
<211> 949
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-glucosidaselike protein [Trichoderma reesei]
949 aa protein BAP59016.1 GI:690966592

<400> 363
Met Arg Leu Lys His Trp Lys Thr Ala Ala Phe Ala Ala Ala Ser Ile
1 5 10 15
Val Ser Gln Val Glu Ala Gly Phe Trp Asn Phe Gly Arg Asp Thr Ser
20 25 30
Ser Ser Thr Arg Pro Pro Thr Lys Asp Gln Phe Ile Glu Ser Leu Ile
35 40 45
Ser Lys Leu Thr Leu Glu Asp Leu Val Leu Gln Leu His Leu Met Phe
50 55 60
Ala Asp Asp Ile Val Gly Ala Ala Ser His Asn Glu Leu Tyr Asp Gln
65 70 75 80
Thr Met His Leu Ser Pro Lys Ser Pro Ile Gly Thr Ile His Asp Trp
85 90 95
Tyr Pro Met Asn Lys Ser Tyr Phe Asn Val Leu Gln Lys Leu Gln Leu
100 105 110
Asp Asn Ser His Val Lys Ile Pro Met Met Leu Val Glu Glu Cys Leu
115 120 125
His Gly Val Gly Ser Phe Lys Gln Ser Ile Phe Pro Gln Asn Ile Ala
130 135 140
Met Ala Ala Ser Phe Asp Thr Asp Ile Val Tyr Arg Val Gly Arg Ala
145 150 155 160
Ile Gly Thr Glu Ala Arg Ser Ile Gly Ile His Gly Cys Phe Ser Pro
165 170 175
Val Leu Asp Leu Ala Gln Asp Pro Arg Trp Gly Arg Val Gln Glu Asp
180 185 190
Phe Gly Glu Asp Lys Ile Leu Thr Ser His Ile Gly Ser Ala Tyr Ser
195 200 205
Ser Gly Leu Ser Lys Asn Lys Thr Trp Ser Asp Pro Asp Ala Val Phe
210 215 220
Pro Ile Met Lys His Phe Ala Ala His Gly Ala Ala Gln Ala Gly His
225 230 235 240
Asn Thr Ala Pro Phe Thr Gly Leu Gly Pro Arg Gln Ile Lys Gln Asp
245 250 255
Leu Leu Val Pro Phe Lys Ala Asn Tyr Asp Leu Gly Gly Ala Arg Gly
260 265 270
Val Met Met Ala Tyr Asn Glu Ile Asp Gly Val Pro Ser Cys Val Asn
275 280 285
Pro Met Leu Tyr Glu Val Leu Asp Asp Trp Gly Tyr Asp Gly Ile Val
290 295 300
Ile Gly Asp Asp Thr Ala Met Arg Asn Leu Leu Thr Gln His Arg Val
305 310 315 320
Thr Thr Ser Glu Ala Asp Thr Leu Gln Gln Trp Tyr Asn Ala Gly Gly

```
                325                 330                 335
Gln Ile Asp Phe Tyr Asp Phe Asp Leu Asp Ser Lys Ile Asn Ile Thr
            340                 345                 350
Lys Ala Leu Val Ala Asn Gly Thr Val Pro Leu Lys Thr Leu Gln Ser
        355                 360                 365
His Val Arg Lys Ile Leu Gly Val Lys Trp Asp Leu Gly Leu Phe Glu
    370                 375                 380
Asn Pro Tyr Ile Pro Glu His Ile Asp Pro Leu Ala Val Val Ala Ser
385                 390                 395                 400
His Gln Asp Val Ala Leu Glu Ala Ala His Lys Ser Ile Ile Leu Leu
                405                 410                 415
Lys Asn Asp Asn Arg Thr Leu Pro Leu Ser Ser Pro Lys Lys Ile Ala
            420                 425                 430
Leu Ile Gly Pro Phe Ala Asp Thr Ile Asn Leu Gly Asp Tyr Ser Gly
        435                 440                 445
Ala Leu Gly Gln Tyr Pro Ala Lys Tyr Thr Gln Thr Leu Arg Glu Gly
    450                 455                 460
Val Leu Arg His Ala Asn Lys Ser Gly His Thr Val Arg Thr Ser Trp
465                 470                 475                 480
Gly Thr Asn Ser Trp Glu Tyr Asn Asn Gln Tyr Val Ile Pro Gly Tyr
                485                 490                 495
Leu Leu Ser Thr Asn Gly Lys Pro Gly Gly Leu Lys Ala Thr Tyr Tyr
            500                 505                 510
Ala His Thr Asn Phe Thr Ser Pro Lys Ala Thr Arg Val Glu Val Pro
        515                 520                 525
Ala Gln Asp Trp Gly Leu Tyr Pro Pro Pro Gly Leu Ser Ser Asn Asn
    530                 535                 540
Phe Ser Ala Val Trp Glu Gly Glu Leu Glu Ser Pro Thr Asp Leu Asp
545                 550                 555                 560
Val Asn Gly Trp Ile Gly Leu Ala Ile Gly Pro Asn Ser Thr Ser Lys
                565                 570                 575
Leu Tyr Val Asp Gly Lys Leu Ile Ser Ser Lys Gly Tyr Ser Gly Ser
            580                 585                 590
Gly Asn Leu Leu Gly Thr Ile Glu Gly Tyr Ala Trp Thr Gln Ala Asn
        595                 600                 605
Ser Thr Leu Pro Pro Gln Gly Gly Val Glu Phe Thr Phe Lys Lys Asn
    610                 615                 620
Ala Lys His His Val Arg Ile Glu Phe Gln Ser Trp Asn Asn Tyr Lys
625                 630                 635                 640
Lys Thr Ala Asn Val Asn Ser Val Asn Ser Gln Leu Ile Phe Trp Trp
                645                 650                 655
Asn Leu Val Ser Pro Asn Gly Lys Ala Leu Asp Gln Ala Val Ser Ile
            660                 665                 670
Ala Lys Asp Ser Asp Val Val Ile Leu Ala Val Gly Ala Ala Trp Asn
        675                 680                 685
Ser Asp Gly Glu Ser Gly Asp Arg Gly Thr Leu Gly Leu Ala Pro Ser
    690                 695                 700
Gln Asp Glu Leu Ala Arg Glu Val Phe Ala Leu Gly Lys Pro Val Val
705                 710                 715                 720
Leu Val Leu Glu Gly Gly Arg Pro Ser Ala Ile Pro Asp His Tyr Gly
                725                 730                 735
Asn Ser Ser Ala Val Leu Ser Thr Phe Phe Gly Gly Gln Ala Gly Gly
            740                 745                 750
Gln Ala Ile Ala Asp Val Leu Phe Gly Asp Phe Asn Pro Gly Ala Arg
```

```
        755                 760                 765
Val Pro Ile Thr Val Pro Trp Ser Val Gly Gln Ile Pro Ala Tyr Tyr
    770                 775                 780
Asn Tyr Lys Pro Ser Ala Arg Ala Ala Gln Tyr Leu Asp Ile Pro Ser
785                 790                 795                 800
Glu Pro Ile Tyr Pro Phe Gly Tyr Gly Leu Ser Tyr Thr Thr Phe Ser
                805                 810                 815
Thr Ser Ser Pro Thr Ala Ser Val Ser Gly Ser Ser Lys Arg Ser Ser
            820                 825                 830
Val Asp Ala Gln Thr Ser Gln Ser Phe Gly Ser Gly Asp Trp Ile Thr
        835                 840                 845
Phe Ser Val Thr Val Lys Asn Thr Gly Ser Val Ala Gly Ser Tyr Val
    850                 855                 860
Ala Gln Val Tyr Leu Leu Gly Arg Val Ser Thr Ile Thr Gln Pro Val
865                 870                 875                 880
Lys Gln Leu Val Gly Phe Gln Arg Val Tyr Leu Glu Ala Gly Gln Lys
                885                 890                 895
Lys Thr Ala Asn Ile Gln Leu Glu Val Asp Arg Tyr Leu Lys Ile Ile
            900                 905                 910
Asn Arg Lys Asp Glu Trp Glu Leu Glu Lys Gly Ser Tyr Thr Phe Ala
        915                 920                 925
Leu Leu Glu His Gly Gly Ser Asn Ala Asp Thr Ser Lys Asn Val Thr
    930                 935                 940
Leu Gln Cys Val Gly
945
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<210> 364
<211> 744
<212> PRT
<213> Artificial Sequence

<220>
<223> extracellularbeta glucosidase 744 aa protein
1713235A GI:227874

<400> 364

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

```
    130                 135                 140
Ala Gly Pro Leu Gly Lys Thr Pro Gln Gly Gly Arg Asn Trp Glu Gly
145                 150                 155                 160
Phe Gly Val Asp Pro Tyr Leu Thr Gly Ile Ala Met Gly Gln Thr Ile
                165                 170                 175
Asn Gly Ile Gln Ser Val Gly Val Gln Ala Thr Ala Lys His Tyr Ile
            180                 185                 190
Leu Asn Glu Gln Glu Leu Asn Arg Glu Thr Ile Ser Ser Asn Pro Asp
        195                 200                 205
Asp Arg Thr Leu His Glu Leu Tyr Thr Trp Pro Phe Ala Asp Ala Val
    210                 215                 220
Gln Ala Asn Val Ala Ser Val Met Cys Ser Tyr Asn Lys Val Asn Thr
225                 230                 235                 240
Thr Trp Ala Cys Glu Asp Gln Tyr Thr Leu Gln Thr Val Leu Lys Asp
                245                 250                 255
Gln Leu Gly Phe Pro Gly Tyr Val Met Thr Asp Trp Asp Ala Gln His
            260                 265                 270
Thr Thr Val Gln Ser Ala Asn Ser Gly Leu Asp Met Ser Met Pro Gly
        275                 280                 285
Thr Asp Phe Asn Gly Asn Asn Arg Leu Trp Gly Pro Ala Leu Thr Asn
    290                 295                 300
Ala Val Asn Ser Asn Gln Val Pro Thr Ser Arg Val Asp Asp Met Val
305                 310                 315                 320
Thr Arg Ile Leu Ala Ala Trp Tyr Leu Thr Gly Gln Asp Gln Ala Gly
                325                 330                 335
Tyr Pro Ser Phe Asn Ile Ser Arg Asn Val Gln Gly Asn His Lys Thr
            340                 345                 350
Asn Val Arg Ala Ile Ala Arg Asp Gly Ile Val Leu Leu Lys Asn Asp
        355                 360                 365
Ala Asn Ile Leu Pro Leu Lys Lys Pro Ala Ser Ile Ala Val Val Gly
    370                 375                 380
Ser Ala Ala Ile Ile Gly Asn His Ala Arg Asn Ser Pro Ser Cys Asn
385                 390                 395                 400
Asp Lys Gly Cys Asp Asp Gly Ala Leu Gly Met Gly Trp Gly Ser Gly
                405                 410                 415
Ala Val Asn Tyr Pro Tyr Phe Val Ala Pro Tyr Asp Ala Ile Asn Thr
            420                 425                 430
Arg Ala Ser Ser Gln Gly Thr Gln Val Thr Leu Ser Asn Thr Asp Asn
        435                 440                 445
Thr Ser Ser Gly Ala Ser Ala Ala Arg Gly Lys Asp Val Ala Ile Val
    450                 455                 460
Phe Ile Thr Ala Asp Ser Gly Glu Gly Tyr Ile Thr Val Glu Gly Asn
465                 470                 475                 480
Ala Gly Asp Arg Asn Asn Leu Asp Pro Trp His Asn Gly Asn Ala Leu
                485                 490                 495
Val Gln Ala Val Ala Gly Ala Asn Ser Asn Val Ile Val Val Val His
            500                 505                 510
Ser Val Gly Ala Ile Ile Leu Glu Gln Ile Leu Ala Leu Pro Gln Val
        515                 520                 525
Lys Ala Val Val Trp Ala Gly Leu Pro Ser Gln Glu Ser Gly Asn Ala
    530                 535                 540
Leu Val Asp Val Leu Trp Gly Asp Val Ser Pro Ser Gly Lys Leu Val
545                 550                 555                 560
Tyr Thr Ile Ala Lys Ser Pro Asn Asp Tyr Asn Thr Arg Ile Val Ser
```

```
                565                 570                 575
Gly Gly Ser Asp Ser Phe Ser Glu Gly Leu Phe Ile Asp Tyr Lys His
            580                 585                 590
Phe Asp Asp Ala Asn Ile Thr Pro Arg Tyr Glu Phe Gly Tyr Gly Leu
        595                 600                 605
Ser Tyr Thr Lys Phe Asn Tyr Ser Arg Leu Ser Val Leu Ser Thr Ala
    610                 615                 620
Lys Ser Gly Pro Ala Thr Gly Ala Val Val Pro Gly Gly Pro Ser Asp
625                 630                 635                 640
Leu Phe Gln Asn Val Ala Thr Val Thr Val Asp Ile Ala Asn Ser Gly
                645                 650                 655
Gln Val Thr Gly Ala Glu Val Ala Gln Leu Tyr Ile Thr Tyr Pro Ser
            660                 665                 670
Ser Ala Pro Arg Thr Pro Pro Lys Gln Leu Arg Gly Phe Ala Lys Leu
        675                 680                 685
Asn Leu Thr Pro Gly Gln Ser Gly Thr Ala Thr Phe Asn Ile Arg Arg
    690                 695                 700
Arg Asp Leu Ser Tyr Trp Asp Thr Ala Ser Gln Lys Trp Val Val Pro
705                 710                 715                 720
Ser Gly Ser Phe Gly Ile Ser Val Gly Ala Ser Ser Arg Asp Ile Arg
                725                 730                 735
Leu Thr Ser Thr Leu Ser Val Ala
            740
```

<210> 365
<211> 713
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Crystal Structure Of A Glycoside
Hydrolase Family 3 Beta-glucosidase, Bgl1 From
Hypocrea Jecorina At 2.1a Resolution713 aa protein
3ZZ1_A GI:429544273

<400> 365

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

```
    130                 135                 140
Ile Asn Gly Ile Gln Ser Val Gly Val Gln Ala Thr Ala Lys His Tyr
145                 150                 155                 160
Ile Leu Asn Glu Gln Glu Leu Asn Arg Glu Thr Ile Ser Ser Asn Pro
                165                 170                 175
Asp Asp Arg Thr Leu His Glu Leu Tyr Thr Trp Pro Phe Ala Asp Ala
            180                 185                 190
Val Gln Ala Asn Val Ala Ser Val Met Cys Ser Tyr Asn Lys Val Asn
        195                 200                 205
Thr Thr Trp Ala Cys Glu Asp Gln Tyr Thr Leu Gln Thr Val Leu Lys
    210                 215                 220
Asp Gln Leu Gly Phe Pro Gly Tyr Val Met Thr Asp Trp Asn Ala Gln
225                 230                 235                 240
His Thr Thr Val Gln Ser Ala Asn Ser Gly Leu Asp Met Ser Met Pro
                245                 250                 255
Gly Thr Asp Phe Asn Gly Asn Asn Arg Leu Trp Gly Pro Ala Leu Thr
            260                 265                 270
Asn Ala Val Asn Ser Asn Gln Val Pro Thr Ser Arg Val Asp Asp Met
        275                 280                 285
Val Thr Arg Ile Leu Ala Ala Trp Tyr Leu Thr Gly Gln Asp Gln Ala
    290                 295                 300
Gly Tyr Pro Ser Phe Asn Ile Ser Arg Asn Val Gln Gly Asn His Lys
305                 310                 315                 320
Thr Asn Val Arg Ala Ile Ala Arg Asp Gly Ile Val Leu Leu Lys Asn
                325                 330                 335
Asp Ala Asn Ile Leu Pro Leu Lys Lys Pro Ala Ser Ile Ala Val Val
            340                 345                 350
Gly Ser Ala Ala Ile Ile Gly Asn His Ala Arg Asn Ser Pro Ser Cys
        355                 360                 365
Asn Asp Lys Gly Cys Asp Asp Gly Ala Leu Gly Met Gly Trp Gly Ser
    370                 375                 380
Gly Ala Val Asn Tyr Pro Tyr Phe Val Ala Pro Tyr Asp Ala Ile Asn
385                 390                 395                 400
Thr Arg Ala Ser Ser Gln Gly Thr Gln Val Thr Leu Ser Asn Thr Asp
                405                 410                 415
Asn Thr Ser Ser Gly Ala Ser Ala Ala Arg Gly Lys Asp Val Ala Ile
            420                 425                 430
Val Phe Ile Thr Ala Asp Ser Gly Glu Gly Tyr Ile Thr Val Glu Gly
        435                 440                 445
Asn Ala Gly Asp Arg Asn Asn Leu Asp Pro Trp His Asn Gly Asn Ala
    450                 455                 460
Leu Val Gln Ala Val Ala Gly Ala Asn Ser Asn Val Ile Val Val Val
465                 470                 475                 480
His Ser Val Gly Ala Ile Ile Leu Glu Gln Ile Leu Ala Leu Pro Gln
                485                 490                 495
Val Lys Ala Val Val Trp Ala Gly Leu Pro Ser Gln Glu Ser Gly Asn
            500                 505                 510
Ala Leu Val Asp Val Leu Trp Gly Asp Val Ser Pro Ser Gly Lys Leu
        515                 520                 525
Val Tyr Thr Ile Ala Lys Ser Pro Asn Asp Tyr Asn Thr Arg Ile Val
    530                 535                 540
Ser Gly Gly Ser Asp Ser Phe Ser Glu Gly Leu Phe Ile Asp Tyr Lys
545                 550                 555                 560
His Phe Asp Asp Ala Asn Ile Thr Pro Arg Tyr Glu Phe Gly Tyr Gly
```

```
                565                 570                 575
Leu Ser Tyr Thr Lys Phe Asn Tyr Ser Arg Leu Ser Val Leu Ser Thr
            580                 585                 590
Ala Lys Ser Gly Pro Ala Thr Gly Ala Val Val Pro Gly Gly Pro Ser
        595                 600                 605
Asp Leu Phe Gln Asn Val Ala Thr Val Thr Val Asp Ile Ala Asn Ser
    610                 615                 620
Gly Gln Val Thr Gly Ala Glu Val Ala Gln Leu Tyr Ile Thr Tyr Pro
625                 630                 635                 640
Ser Ser Ala Pro Arg Thr Pro Pro Lys Gln Leu Arg Gly Phe Ala Lys
                645                 650                 655
Leu Asn Leu Thr Pro Gly Gln Ser Gly Thr Ala Thr Phe Asn Ile Arg
            660                 665                 670
Arg Arg Asp Leu Ser Tyr Trp Asp Thr Ala Ser Gln Lys Trp Val Val
        675                 680                 685
Pro Ser Gly Ser Phe Gly Ile Ser Val Gly Ala Ser Ser Arg Asp Ile
    690                 695                 700
Arg Leu Thr Ser Thr Leu Ser Val Ala
705                 710


<210> 366
<211> 713
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Crystal Structure Of A Glycoside
      Hydrolase Family 3 Beta-glucosidase, Bgl1 From
      Hypocrea Jecorina At 2.1a Resolution 713 aa
      protein 3ZYZ_A GI:429544272

<400> 366
Val Val Pro Pro Ala Gly Thr Pro Trp Gly Thr Ala Tyr Asp Lys Ala
 1               5                  10                  15
Lys Ala Ala Leu Ala Lys Leu Asn Leu Gln Asp Lys Val Gly Ile Val
            20                  25                  30
Ser Gly Val Gly Trp Asn Gly Gly Pro Cys Val Gly Asn Thr Ser Pro
        35                  40                  45
Ala Ser Lys Ile Ser Tyr Pro Ser Leu Cys Leu Gln Asp Gly Pro Leu
    50                  55                  60
Gly Val Arg Tyr Ser Thr Gly Ser Thr Ala Phe Thr Pro Gly Val Gln
65                  70                  75                  80
Ala Ala Ser Thr Trp Asp Val Asn Leu Ile Arg Glu Arg Gly Gln Phe
                85                  90                  95
Ile Gly Glu Glu Val Lys Ala Ser Gly Ile His Val Ile Leu Gly Pro
            100                 105                 110
Val Ala Gly Pro Leu Gly Lys Thr Pro Gln Gly Gly Arg Asn Trp Glu
        115                 120                 125
Gly Phe Gly Val Asp Pro Tyr Leu Thr Gly Ile Ala Met Gly Gln Thr
    130                 135                 140
Ile Asn Gly Ile Gln Ser Val Gly Val Gln Ala Thr Ala Lys His Tyr
145                 150                 155                 160
Ile Leu Asn Glu Gln Glu Leu Asn Arg Glu Thr Ile Ser Ser Asn Pro
```

```
                165                 170                 175
Asp Asp Arg Thr Leu His Glu Leu Tyr Thr Trp Pro Phe Ala Asp Ala
            180                 185                 190
Val Gln Ala Asn Val Ala Ser Val Met Cys Ser Tyr Asn Lys Val Asn
        195                 200                 205
Thr Thr Trp Ala Cys Glu Asp Gln Tyr Thr Leu Gln Thr Val Leu Lys
    210                 215                 220
Asp Gln Leu Gly Phe Pro Gly Tyr Val Met Thr Asp Trp Asn Ala Gln
225                 230                 235                 240
His Thr Thr Val Gln Ser Ala Asn Ser Gly Leu Asp Met Ser Met Pro
                245                 250                 255
Gly Thr Asp Phe Asn Gly Asn Asn Arg Leu Trp Gly Pro Ala Leu Thr
            260                 265                 270
Asn Ala Val Asn Ser Asn Gln Val Pro Thr Ser Arg Val Asp Asp Met
        275                 280                 285
Val Thr Arg Ile Leu Ala Ala Trp Tyr Leu Thr Gly Gln Asp Gln Ala
    290                 295                 300
Gly Tyr Pro Ser Phe Asn Ile Ser Arg Asn Val Gln Gly Asn His Lys
305                 310                 315                 320
Thr Asn Val Arg Ala Ile Ala Arg Asp Gly Ile Val Leu Leu Lys Asn
                325                 330                 335
Asp Ala Asn Ile Leu Pro Leu Lys Lys Pro Ala Ser Ile Ala Val Val
            340                 345                 350
Gly Ser Ala Ala Ile Ile Gly Asn His Ala Arg Asn Ser Pro Ser Cys
        355                 360                 365
Asn Asp Lys Gly Cys Asp Asp Gly Ala Leu Gly Met Gly Trp Gly Ser
    370                 375                 380
Gly Ala Val Asn Tyr Pro Tyr Phe Val Ala Pro Tyr Asp Ala Ile Asn
385                 390                 395                 400
Thr Arg Ala Ser Ser Gln Gly Thr Gln Val Thr Leu Ser Asn Thr Asp
                405                 410                 415
Asn Thr Ser Ser Gly Ala Ser Ala Ala Arg Gly Lys Asp Val Ala Ile
            420                 425                 430
Val Phe Ile Thr Ala Asp Ser Gly Glu Gly Tyr Ile Thr Val Glu Gly
        435                 440                 445
Asn Ala Gly Asp Arg Asn Asn Leu Asp Pro Trp His Asn Gly Asn Ala
    450                 455                 460
Leu Val Gln Ala Val Ala Gly Ala Asn Ser Asn Val Ile Val Val Val
465                 470                 475                 480
His Ser Val Gly Ala Ile Ile Leu Glu Gln Ile Leu Ala Leu Pro Gln
                485                 490                 495
Val Lys Ala Val Val Trp Ala Gly Leu Pro Ser Gln Glu Ser Gly Asn
            500                 505                 510
Ala Leu Val Asp Val Leu Trp Gly Asp Val Ser Pro Ser Gly Lys Leu
        515                 520                 525
Val Tyr Thr Ile Ala Lys Ser Pro Asn Asp Tyr Asn Thr Arg Ile Val
    530                 535                 540
Ser Gly Gly Ser Asp Ser Phe Ser Glu Gly Leu Phe Ile Asp Tyr Lys
545                 550                 555                 560
His Phe Asp Asp Ala Asn Ile Thr Pro Arg Tyr Glu Phe Gly Tyr Gly
                565                 570                 575
Leu Ser Tyr Thr Lys Phe Asn Tyr Ser Arg Leu Ser Val Leu Ser Thr
            580                 585                 590
Ala Lys Ser Gly Pro Ala Thr Gly Ala Val Val Pro Gly Gly Pro Ser
```

```
        595                 600                 605
Asp Leu Phe Gln Asn Val Ala Thr Val Thr Val Asp Ile Ala Asn Ser
    610                 615                 620
Gly Gln Val Thr Gly Ala Glu Val Ala Gln Leu Tyr Ile Thr Tyr Pro
625                 630                 635                 640
Ser Ser Ala Pro Arg Thr Pro Pro Lys Gln Leu Arg Gly Phe Ala Lys
                645                 650                 655
Leu Asn Leu Thr Pro Gly Gln Ser Gly Thr Ala Thr Phe Asn Ile Arg
            660                 665                 670
Arg Arg Asp Leu Ser Tyr Trp Asp Thr Ala Ser Gln Lys Trp Val Val
        675                 680                 685
Pro Ser Gly Ser Phe Gly Ile Ser Val Gly Ala Ser Ser Arg Asp Ile
    690                 695                 700
Arg Leu Thr Ser Thr Leu Ser Val Ala
705                 710


<210> 367
<211> 714
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, Crystal Structure Of Beta-d-glucoside
      Glucohydrolase From Trichoderma Reesei 714 aa
      protein 4I8D_B GI:430801090

<400> 367
Ala Val Val Pro Pro Ala Gly Thr Pro Trp Gly Thr Ala Tyr Asp Lys
 1               5                  10                  15
Ala Lys Ala Ala Leu Ala Lys Leu Asn Leu Gln Asp Lys Val Gly Ile
            20                  25                  30
Val Ser Gly Val Gly Trp Asn Gly Gly Pro Cys Val Gly Asn Thr Ser
        35                  40                  45
Pro Ala Ser Lys Ile Ser Tyr Pro Ser Leu Cys Leu Gln Asp Gly Pro
    50                  55                  60
Leu Gly Val Arg Tyr Ser Thr Gly Ser Thr Ala Phe Thr Pro Gly Val
65                  70                  75                  80
Gln Ala Ala Ser Thr Trp Asp Val Asn Leu Ile Arg Glu Arg Gly Gln
                85                  90                  95
Phe Ile Gly Glu Glu Val Lys Ala Ser Gly Ile His Val Ile Leu Gly
            100                 105                 110
Pro Val Ala Gly Pro Leu Gly Lys Thr Pro Gln Gly Gly Arg Asn Trp
        115                 120                 125
Glu Gly Phe Gly Val Asp Pro Tyr Leu Thr Gly Ile Ala Met Gly Gln
    130                 135                 140
Thr Ile Asn Gly Ile Gln Ser Val Gly Val Gln Ala Thr Ala Lys His
145                 150                 155                 160
Tyr Ile Leu Asn Glu Gln Glu Leu Asn Arg Glu Thr Ile Ser Ser Asn
                165                 170                 175
Pro Asp Asp Arg Thr Leu His Glu Leu Tyr Thr Trp Pro Phe Ala Asp
            180                 185                 190
Ala Val Gln Ala Asn Val Ala Ser Val Met Cys Ser Tyr Asn Lys Val
        195                 200                 205
```

```
Asn Thr Thr Trp Ala Cys Glu Asp Gln Tyr Thr Leu Gln Thr Val Leu
    210                 215                 220
Lys Asp Gln Leu Gly Phe Pro Gly Tyr Val Met Thr Asp Trp Asn Ala
225                 230                 235                 240
Gln His Thr Thr Val Gln Ser Ala Asn Ser Gly Leu Asp Met Ser Met
                245                 250                 255
Pro Gly Thr Asp Phe Asn Gly Asn Asn Arg Leu Trp Gly Pro Ala Leu
            260                 265                 270
Thr Asn Ala Val Asn Ser Asn Gln Val Pro Thr Ser Arg Val Asp Asp
        275                 280                 285
Met Val Thr Arg Ile Leu Ala Ala Trp Tyr Leu Thr Gly Gln Asp Gln
    290                 295                 300
Ala Gly Tyr Pro Ser Phe Asn Ile Ser Arg Asn Val Gln Gly Asn His
305                 310                 315                 320
Lys Thr Asn Val Arg Ala Ile Ala Arg Asp Gly Ile Val Leu Leu Lys
                325                 330                 335
Asn Asp Ala Asn Ile Leu Pro Leu Lys Lys Pro Ala Ser Ile Ala Val
            340                 345                 350
Val Gly Ser Ala Ala Ile Ile Gly Asn His Ala Arg Asn Ser Pro Ser
        355                 360                 365
Cys Asn Asp Lys Gly Cys Asp Asp Gly Ala Leu Gly Met Gly Trp Gly
    370                 375                 380
Ser Gly Ala Val Asn Tyr Pro Tyr Phe Val Ala Pro Tyr Asp Ala Ile
385                 390                 395                 400
Asn Thr Arg Ala Ser Ser Gln Gly Thr Gln Val Thr Leu Ser Asn Thr
                405                 410                 415
Asp Asn Thr Ser Ser Gly Ala Ser Ala Ala Arg Gly Lys Asp Val Ala
            420                 425                 430
Ile Val Phe Ile Thr Ala Asp Ser Gly Glu Gly Tyr Ile Thr Val Glu
        435                 440                 445
Gly Asn Ala Gly Asp Arg Asn Asn Leu Asp Pro Trp His Asn Gly Asn
    450                 455                 460
Ala Leu Val Gln Ala Val Ala Gly Ala Asn Ser Asn Val Ile Val Val
465                 470                 475                 480
Val His Ser Val Gly Ala Ile Ile Leu Glu Gln Ile Leu Ala Leu Pro
                485                 490                 495
Gln Val Lys Ala Val Val Trp Ala Gly Leu Pro Ser Gln Glu Ser Gly
            500                 505                 510
Asn Ala Leu Val Asp Val Leu Trp Gly Asp Val Ser Pro Ser Gly Lys
        515                 520                 525
Leu Val Tyr Thr Ile Ala Lys Ser Pro Asn Asp Tyr Asn Thr Arg Ile
    530                 535                 540
Val Ser Gly Gly Ser Asp Ser Phe Ser Glu Gly Leu Phe Ile Asp Tyr
545                 550                 555                 560
Lys His Phe Asp Asp Ala Asn Ile Thr Pro Arg Tyr Glu Phe Gly Tyr
                565                 570                 575
Gly Leu Ser Tyr Thr Lys Phe Asn Tyr Ser Arg Leu Ser Val Leu Ser
            580                 585                 590
Thr Ala Lys Ser Gly Pro Ala Thr Gly Ala Val Val Pro Gly Gly Pro
        595                 600                 605
Ser Asp Leu Phe Gln Asn Val Ala Thr Val Thr Val Asp Ile Ala Asn
    610                 615                 620
Ser Gly Gln Val Thr Gly Ala Glu Val Ala Gln Leu Tyr Ile Thr Tyr
625                 630                 635                 640
```

Pro Ser Ser Ala Pro Arg Thr Pro Pro Lys Gln Leu Arg Gly Phe Ala
645 650 655
Lys Leu Asn Leu Thr Pro Gly Gln Ser Gly Thr Ala Thr Phe Asn Ile
660 665 670
Arg Arg Arg Asp Leu Ser Tyr Trp Asp Thr Ala Ser Gln Lys Trp Val
675 680 685
Val Pro Ser Gly Ser Phe Gly Ile Ser Val Gly Ala Ser Ser Arg Asp
690 695 700
Ile Arg Leu Thr Ser Thr Leu Ser Val Ala
705 710

<210> 368
<211> 714
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Crystal Structure Of Beta-d-glucoside
Glucohydrolase From Trichoderma Reesei 714 aa
protein 4I8D_A GI:430801089

<400> 368
Ala Val Val Pro Pro Ala Gly Thr Pro Trp Gly Thr Ala Tyr Asp Lys
1 5 10 15
Ala Lys Ala Ala Leu Ala Lys Leu Asn Leu Gln Asp Lys Val Gly Ile
20 25 30
Val Ser Gly Val Gly Trp Asn Gly Gly Pro Cys Val Gly Asn Thr Ser
35 40 45
Pro Ala Ser Lys Ile Ser Tyr Pro Ser Leu Cys Leu Gln Asp Gly Pro
50 55 60
Leu Gly Val Arg Tyr Ser Thr Gly Ser Thr Ala Phe Thr Pro Gly Val
65 70 75 80
Gln Ala Ala Ser Thr Trp Asp Val Asn Leu Ile Arg Glu Arg Gly Gln
85 90 95
Phe Ile Gly Glu Glu Val Lys Ala Ser Gly Ile His Val Ile Leu Gly
100 105 110
Pro Val Ala Gly Pro Leu Gly Lys Thr Pro Gln Gly Gly Arg Asn Trp
115 120 125
Glu Gly Phe Gly Val Asp Pro Tyr Leu Thr Gly Ile Ala Met Gly Gln
130 135 140
Thr Ile Asn Gly Ile Gln Ser Val Gly Val Gln Ala Thr Ala Lys His
145 150 155 160
Tyr Ile Leu Asn Glu Gln Glu Leu Asn Arg Glu Thr Ile Ser Ser Asn
165 170 175
Pro Asp Asp Arg Thr Leu His Glu Leu Tyr Thr Trp Pro Phe Ala Asp
180 185 190
Ala Val Gln Ala Asn Val Ala Ser Val Met Cys Ser Tyr Asn Lys Val
195 200 205
Asn Thr Thr Trp Ala Cys Glu Asp Gln Tyr Thr Leu Gln Thr Val Leu
210 215 220
Lys Asp Gln Leu Gly Phe Pro Gly Tyr Val Met Thr Asp Trp Asn Ala
225 230 235 240
Gln His Thr Thr Val Gln Ser Ala Asn Ser Gly Leu Asp Met Ser Met

```
                245                 250                 255
Pro Gly Thr Asp Phe Asn Gly Asn Asn Arg Leu Trp Gly Pro Ala Leu
            260                 265                 270
Thr Asn Ala Val Asn Ser Asn Gln Val Pro Thr Ser Arg Val Asp Asp
        275                 280                 285
Met Val Thr Arg Ile Leu Ala Ala Trp Tyr Leu Thr Gly Gln Asp Gln
    290                 295                 300
Ala Gly Tyr Pro Ser Phe Asn Ile Ser Arg Asn Val Gln Gly Asn His
305                 310                 315                 320
Lys Thr Asn Val Arg Ala Ile Ala Arg Asp Gly Ile Val Leu Leu Lys
                325                 330                 335
Asn Asp Ala Asn Ile Leu Pro Leu Lys Lys Pro Ala Ser Ile Ala Val
            340                 345                 350
Val Gly Ser Ala Ala Ile Ile Gly Asn His Ala Arg Asn Ser Pro Ser
        355                 360                 365
Cys Asn Asp Lys Gly Cys Asp Asp Gly Ala Leu Gly Met Gly Trp Gly
    370                 375                 380
Ser Gly Ala Val Asn Tyr Pro Tyr Phe Val Ala Pro Tyr Asp Ala Ile
385                 390                 395                 400
Asn Thr Arg Ala Ser Ser Gln Gly Thr Gln Val Thr Leu Ser Asn Thr
                405                 410                 415
Asp Asn Thr Ser Ser Gly Ala Ser Ala Ala Arg Gly Lys Asp Val Ala
            420                 425                 430
Ile Val Phe Ile Thr Ala Asp Ser Gly Glu Gly Tyr Ile Thr Val Glu
        435                 440                 445
Gly Asn Ala Gly Asp Arg Asn Asn Leu Asp Pro Trp His Asn Gly Asn
    450                 455                 460
Ala Leu Val Gln Ala Val Ala Gly Ala Asn Ser Asn Val Ile Val Val
465                 470                 475                 480
Val His Ser Val Gly Ala Ile Ile Leu Glu Gln Ile Leu Ala Leu Pro
                485                 490                 495
Gln Val Lys Ala Val Val Trp Ala Gly Leu Pro Ser Gln Glu Ser Gly
            500                 505                 510
Asn Ala Leu Val Asp Val Leu Trp Gly Asp Val Ser Pro Ser Gly Lys
        515                 520                 525
Leu Val Tyr Thr Ile Ala Lys Ser Pro Asn Asp Tyr Asn Thr Arg Ile
    530                 535                 540
Val Ser Gly Gly Ser Asp Ser Phe Ser Glu Gly Leu Phe Ile Asp Tyr
545                 550                 555                 560
Lys His Phe Asp Asp Ala Asn Ile Thr Pro Arg Tyr Glu Phe Gly Tyr
                565                 570                 575
Gly Leu Ser Tyr Thr Lys Phe Asn Tyr Ser Arg Leu Ser Val Leu Ser
            580                 585                 590
Thr Ala Lys Ser Gly Pro Ala Thr Gly Ala Val Val Pro Gly Gly Pro
        595                 600                 605
Ser Asp Leu Phe Gln Asn Val Ala Thr Val Thr Val Asp Ile Ala Asn
    610                 615                 620
Ser Gly Gln Val Thr Gly Ala Glu Val Ala Gln Leu Tyr Ile Thr Tyr
625                 630                 635                 640
Pro Ser Ser Ala Pro Arg Thr Pro Pro Lys Gln Leu Arg Gly Phe Ala
                645                 650                 655
Lys Leu Asn Leu Thr Pro Gly Gln Ser Gly Thr Ala Thr Phe Asn Ile
            660                 665                 670
Arg Arg Arg Asp Leu Ser Tyr Trp Asp Thr Ala Ser Gln Lys Trp Val
```

```
        675                 680                 685
Val Pro Ser Gly Ser Phe Gly Ile Ser Val Gly Ala Ser Ser Arg Asp
    690                 695                 700
Ile Arg Leu Thr Ser Thr Leu Ser Val Ala
705                 710
```

<210> 369
<211> 700
<212> PRT
<213> Artificial Sequence

<220>
<223> Cel3d [Trichoderma reesei] 700 aa protein
AAP57759.1 GI:31747172

<400> 369

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

```
    290                 295                 300
Met Phe Trp Gly Thr Leu Val Gly Glu Phe Ile Pro Thr Ala Thr Gly
305                 310                 315                 320
Ile Trp Glu Phe Gly Leu Ser Val Phe Gly Thr Ala Asp Leu Tyr Ile
                325                 330                 335
Asp Asn Glu Leu Val Ile Glu Asn Thr Thr His Gln Thr Arg Gly Thr
            340                 345                 350
Ala Phe Phe Gly Lys Gly Thr Thr Glu Lys Val Ala Thr Arg Arg Met
        355                 360                 365
Val Ala Gly Ser Thr Tyr Lys Leu Arg Leu Glu Phe Gly Ser Ala Asn
    370                 375                 380
Thr Thr Lys Met Glu Thr Thr Gly Val Val Asn Phe Gly Gly Gly Ala
385                 390                 395                 400
Val His Leu Gly Ala Cys Leu Lys Val Asp Pro Gln Glu Met Ile Ala
                405                 410                 415
Arg Ala Val Lys Ala Ala Ala Asp Ala Asp Tyr Thr Ile Ile Cys Thr
            420                 425                 430
Gly Leu Ser Gly Glu Trp Glu Ser Glu Gly Phe Asp Arg Pro His Met
        435                 440                 445
Asp Leu Pro Pro Gly Val Asp Thr Met Ile Ser Gln Val Leu Asp Ala
    450                 455                 460
Ala Pro Asn Ala Val Val Val Asn Gln Ser Gly Thr Pro Val Thr Met
465                 470                 475                 480
Ser Trp Ala His Lys Ala Lys Ala Ile Val Gln Ala Trp Tyr Gly Gly
                485                 490                 495
Asn Glu Thr Gly His Gly Ile Ser Asp Val Leu Phe Gly Asn Val Asn
            500                 505                 510
Pro Ser Gly Lys Leu Ser Leu Ser Trp Pro Val Asp Val Lys His Asn
        515                 520                 525
Pro Ala Tyr Leu Asn Tyr Ala Ser Val Gly Gly Arg Val Leu Tyr Gly
    530                 535                 540
Glu Asp Val Tyr Val Gly Tyr Lys Phe Tyr Asp Lys Thr Glu Arg Glu
545                 550                 555                 560
Val Leu Phe Pro Phe Gly His Gly Leu Ser Tyr Ala Thr Phe Lys Leu
                565                 570                 575
Pro Asp Ser Thr Val Arg Thr Val Pro Glu Thr Phe His Pro Asp Gln
            580                 585                 590
Pro Thr Val Ala Ile Val Lys Ile Lys Asn Thr Ser Ser Val Pro Gly
        595                 600                 605
Ala Gln Val Leu Gln Leu Tyr Ile Ser Ala Pro Asn Ser Pro Thr His
    610                 615                 620
Arg Pro Val Lys Glu Leu His Gly Phe Glu Lys Val Tyr Leu Glu Ala
625                 630                 635                 640
Gly Glu Glu Lys Glu Val Gln Ile Pro Ile Asp Gln Tyr Ala Thr Ser
                645                 650                 655
Phe Trp Asp Glu Ile Glu Ser Met Trp Lys Ser Glu Arg Gly Ile Tyr
            660                 665                 670
Asp Val Leu Val Gly Phe Ser Ser Gln Glu Ile Ser Gly Lys Gly Lys
        675                 680                 685
Leu Ile Val Pro Glu Thr Arg Phe Trp Met Gly Leu
    690                 695                 700
```

<210> 370

<211> 833
<212> PRT
<213> Artificial Sequence

<220>
<223> Cel3c[Trichoderma reesei] 833 aa protein
AAP57756.1 GI:31747168

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

```
        355                 360                 365
Leu Glu Thr Pro Pro Ser Tyr Thr Val Gly Ala Tyr Thr Thr Val Pro
    370                 375                 380
Pro Ile Leu Gly Glu Gln Cys Leu Thr Pro Asp Gly Ala Pro Gly Met
385                 390                 395                 400
Arg Trp Arg Val Phe Asn Glu Pro Pro Gly Thr Pro Asn Arg Gln His
                405                 410                 415
Ile Asp Glu Leu Phe Phe Thr Lys Thr Asp Met His Leu Val Asp Tyr
            420                 425                 430
Tyr His Pro Lys Ala Ala Asp Thr Trp Tyr Ala Asp Met Glu Gly Thr
        435                 440                 445
Tyr Thr Ala Asp Glu Asp Cys Thr Tyr Glu Leu Gly Leu Val Val Cys
    450                 455                 460
Gly Thr Ala Lys Ala Tyr Val Asp Asp Gln Leu Val Val Asp Asn Ala
465                 470                 475                 480
Thr Lys Gln Val Pro Gly Asp Ala Phe Phe Gly Ser Ala Thr Arg Glu
                485                 490                 495
Glu Thr Gly Arg Ile Asn Leu Val Lys Gly Asn Thr Tyr Lys Phe Lys
            500                 505                 510
Ile Glu Phe Gly Ser Ala Pro Thr Tyr Thr Leu Lys Gly Asp Thr Ile
        515                 520                 525
Val Pro Gly His Gly Ser Leu Arg Val Gly Gly Cys Lys Val Ile Asp
    530                 535                 540
Asp Gln Ala Glu Ile Glu Lys Ser Val Ala Leu Ala Lys Glu His Asp
545                 550                 555                 560
Gln Val Ile Ile Cys Ala Gly Leu Asn Ala Asp Trp Glu Thr Glu Gly
                565                 570                 575
Ala Asp Arg Ala Ser Met Lys Leu Pro Gly Val Leu Asp Gln Leu Ile
            580                 585                 590
Ala Asp Val Ala Ala Ala Asn Pro Asn Thr Val Val Val Met Gln Thr
        595                 600                 605
Gly Thr Pro Glu Glu Met Pro Trp Leu Asp Ala Thr Pro Ala Val Ile
    610                 615                 620
Gln Ala Trp Tyr Gly Gly Asn Glu Thr Gly Asn Ser Ile Ala Asp Val
625                 630                 635                 640
Val Phe Gly Asp Tyr Asn Pro Ser Gly Lys Leu Ser Leu Ser Phe Pro
                645                 650                 655
Lys Arg Leu Gln Asp Asn Pro Ala Phe Leu Asn Phe Arg Thr Glu Ala
            660                 665                 670
Gly Arg Thr Leu Tyr Gly Glu Asp Val Tyr Val Gly Tyr Arg Tyr Tyr
        675                 680                 685
Glu Phe Ala Asp Lys Asp Val Asn Phe Pro Phe Gly His Gly Leu Ser
    690                 695                 700
Tyr Thr Thr Phe Ala Phe Ser Asn Leu Ser Val Ser His Lys Asp Gly
705                 710                 715                 720
Lys Leu Ser Val Ser Leu Ser Val Lys Asn Thr Gly Ser Val Pro Gly
                725                 730                 735
Ala Gln Val Ala Gln Leu Tyr Val Lys Pro Leu Gln Ala Ala Lys Ile
            740                 745                 750
Asn Arg Pro Val Lys Glu Leu Lys Gly Phe Ala Lys Val Glu Leu Gln
        755                 760                 765
Pro Gly Glu Thr Lys Ala Val Thr Ile Glu Glu Gln Glu Lys Tyr Val
    770                 775                 780
Ala Ala Tyr Phe Asp Glu Glu Arg Asp Gln Trp Cys Val Glu Lys Gly
```

785 790 795 800
Asp Tyr Glu Val Ile Val Ser Asp Ser Ser Ala Ala Lys Asp Gly Val
805 810 815
Ala Leu Arg Gly Lys Phe Thr Val Gly Glu Thr Tyr Trp Trp Ser Gly
820 825 830
Val

<210> 371
<211> 874
<212> PRT
<213> Artificial Sequence

<220>
<223> Cel3b [Trichoderma reesei] 874 aa protein
AAP57755.1 GI:31747166

<400> 371
Met Lys Thr Leu Ser Val Phe Ala Ala Ala Leu Leu Ala Ala Val Ala
1 5 10 15
Glu Ala Asn Pro Tyr Pro Pro Pro His Ser Asn Gln Ala Tyr Ser Pro
20 25 30
Pro Phe Tyr Pro Ser Pro Trp Met Asp Pro Ser Ala Pro Gly Trp Glu
35 40 45
Gln Ala Tyr Ala Gln Ala Lys Glu Phe Val Ser Gly Leu Thr Leu Leu
50 55 60
Glu Lys Val Asn Leu Thr Thr Gly Val Gly Trp Met Gly Glu Lys Cys
65 70 75 80
Val Gly Asn Val Gly Thr Val Pro Arg Leu Gly Met Arg Ser Leu Cys
85 90 95
Met Gln Asp Gly Pro Leu Gly Leu Arg Phe Asn Thr Tyr Asn Ser Ala
100 105 110
Phe Ser Val Gly Leu Thr Ala Ala Ala Ser Trp Ser Arg His Leu Trp
115 120 125
Val Asp Arg Gly Thr Ala Leu Gly Ser Glu Ala Lys Gly Lys Gly Val
130 135 140
Asp Val Leu Leu Gly Pro Val Ala Gly Pro Leu Gly Arg Asn Pro Asn
145 150 155 160
Gly Gly Arg Asn Val Glu Gly Phe Gly Ser Asp Pro Tyr Leu Ala Gly
165 170 175
Leu Ala Leu Ala Asp Thr Val Thr Gly Ile Gln Asn Ala Gly Thr Ile
180 185 190
Ala Cys Ala Lys His Phe Leu Leu Asn Glu Gln Glu His Phe Arg Gln
195 200 205
Val Gly Glu Ala Asn Gly Tyr Gly Tyr Pro Ile Thr Glu Ala Leu Ser
210 215 220
Ser Asn Val Asp Asp Lys Thr Ile His Glu Val Tyr Gly Trp Pro Phe
225 230 235 240
Gln Asp Ala Val Lys Ala Gly Val Gly Ser Phe Met Cys Ser Tyr Asn
245 250 255
Gln Val Asn Asn Ser Tyr Ala Cys Gln Asn Ser Lys Leu Ile Asn Gly
260 265 270
Leu Leu Lys Glu Glu Tyr Gly Phe Gln Gly Phe Val Met Ser Asp Trp

```
        275                 280                 285
Gln Ala Gln His Thr Gly Val Ala Ser Ala Val Ala Gly Leu Asp Met
    290                 295                 300
Thr Met Pro Gly Asp Thr Ala Phe Asn Thr Gly Ala Ser Tyr Phe Gly
305                 310                 315                 320
Ser Asn Leu Thr Leu Ala Val Leu Asn Gly Thr Val Pro Glu Trp Arg
                325                 330                 335
Ile Asp Asp Met Val Met Arg Ile Met Ala Pro Phe Phe Lys Val Gly
            340                 345                 350
Lys Thr Val Asp Ser Leu Ile Asp Thr Asn Phe Asp Ser Trp Thr Asn
        355                 360                 365
Gly Glu Tyr Gly Tyr Val Gln Ala Ala Val Asn Glu Asn Trp Glu Lys
    370                 375                 380
Val Asn Tyr Gly Val Asp Val Arg Ala Asn His Ala Asn His Ile Arg
385                 390                 395                 400
Glu Val Gly Ala Lys Gly Thr Val Ile Phe Lys Asn Asn Gly Ile Leu
                405                 410                 415
Pro Leu Lys Lys Pro Lys Phe Leu Thr Val Ile Gly Glu Asp Ala Gly
            420                 425                 430
Gly Asn Pro Ala Gly Pro Asn Gly Cys Gly Asp Arg Gly Cys Asp Asp
        435                 440                 445
Gly Thr Leu Ala Met Glu Trp Gly Ser Gly Thr Thr Asn Phe Pro Tyr
    450                 455                 460
Leu Val Thr Pro Asp Ala Ala Leu Gln Ser Gln Ala Leu Gln Asp Gly
465                 470                 475                 480
Thr Arg Tyr Glu Ser Ile Leu Ser Asn Tyr Ala Ile Ser Gln Thr Gln
                485                 490                 495
Ala Leu Val Ser Gln Pro Asp Ala Ile Ala Ile Val Phe Ala Asn Ser
            500                 505                 510
Asp Ser Gly Glu Gly Tyr Ile Asn Val Asp Gly Asn Glu Gly Asp Arg
        515                 520                 525
Lys Asn Leu Thr Leu Trp Lys Asn Gly Asp Asp Leu Ile Lys Thr Val
    530                 535                 540
Ala Ala Val Asn Pro Lys Thr Ile Val Val Ile His Ser Thr Gly Pro
545                 550                 555                 560
Val Ile Leu Lys Asp Tyr Ala Asn His Pro Asn Ile Ser Ala Ile Leu
                565                 570                 575
Trp Ala Gly Ala Pro Gly Gln Glu Ser Gly Asn Ser Leu Val Asp Ile
            580                 585                 590
Leu Tyr Gly Lys Gln Ser Pro Gly Arg Thr Pro Phe Thr Trp Gly Pro
        595                 600                 605
Ser Leu Glu Ser Tyr Gly Val Ser Val Met Thr Thr Pro Asn Asn Gly
    610                 615                 620
Asn Gly Ala Pro Gln Asp Asn Phe Asn Glu Gly Ala Phe Ile Asp Tyr
625                 630                 635                 640
Arg Tyr Phe Asp Lys Val Ala Pro Gly Lys Pro Arg Ser Ser Asp Lys
                645                 650                 655
Ala Pro Thr Tyr Glu Phe Gly Phe Gly Leu Ser Trp Ser Thr Phe Lys
            660                 665                 670
Phe Ser Asn Leu His Ile Gln Lys Asn Asn Val Gly Pro Met Ser Pro
        675                 680                 685
Pro Asn Gly Lys Thr Ile Ala Ala Pro Ser Leu Gly Ser Phe Ser Lys
    690                 695                 700
Asn Leu Lys Asp Tyr Gly Phe Pro Lys Asn Val Arg Arg Ile Lys Glu
```

705 710 715 720
Phe Ile Tyr Pro Tyr Leu Ser Thr Thr Thr Ser Gly Lys Glu Ala Ser
725 730 735
Gly Asp Ala His Tyr Gly Gln Thr Ala Lys Glu Phe Leu Pro Ala Gly
740 745 750
Ala Leu Asp Gly Ser Pro Gln Pro Arg Ser Ala Ala Ser Gly Glu Pro
755 760 765
Gly Gly Asn Arg Gln Leu Tyr Asp Ile Leu Tyr Thr Val Thr Ala Thr
770 775 780
Ile Thr Asn Thr Gly Ser Val Met Asp Asp Ala Val Pro Gln Leu Tyr
785 790 795 800
Leu Ser His Gly Gly Pro Asn Glu Pro Pro Lys Val Leu Arg Gly Phe
805 810 815
Asp Arg Ile Glu Arg Ile Ala Pro Gly Gln Ser Val Thr Phe Lys Ala
820 825 830
Asp Leu Thr Arg Arg Asp Leu Ser Asn Trp Asp Thr Lys Lys Gln Gln
835 840 845
Trp Val Ile Thr Asp Tyr Pro Lys Thr Val Tyr Val Gly Ser Ser Ser
850 855 860
Arg Asp Leu Pro Leu Ser Ala Arg Leu Pro
865 870

<210> 372
<211> 744
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-D-glucoside glucohydrolase [Trichoderma
reesei] 744 aa protein AAA18473.1 GI:493580

<400> 372
Met Arg Tyr Arg Thr Ala Ala Ala Leu Ala Leu Ala Thr Gly Pro Phe
1 5 10 15
Ala Arg Ala Asp Ser His Ser Thr Ser Gly Ala Ser Ala Glu Ala Val
20 25 30
Val Pro Pro Ala Gly Thr Pro Trp Gly Thr Ala Tyr Asp Lys Ala Lys
35 40 45
Ala Ala Leu Ala Lys Leu Asn Leu Gln Asp Lys Val Gly Ile Val Ser
50 55 60
Gly Val Gly Trp Asn Gly Gly Pro Cys Val Gly Asn Thr Ser Pro Ala
65 70 75 80
Ser Lys Ile Ser Tyr Pro Ser Leu Cys Leu Gln Asp Gly Pro Leu Gly
85 90 95
Val Arg Tyr Ser Thr Gly Ser Thr Ala Phe Thr Pro Gly Val Gln Ala
100 105 110
Ala Ser Thr Trp Asp Val Asn Leu Ile Arg Glu Arg Gly Gln Phe Ile
115 120 125
Gly Glu Glu Val Lys Ala Ser Gly Ile His Val Ile Leu Gly Pro Val
130 135 140
Ala Gly Pro Leu Gly Lys Thr Pro Gln Gly Gly Arg Asn Trp Glu Gly
145 150 155 160
Phe Gly Val Asp Pro Tyr Leu Thr Gly Ile Ala Met Gly Gln Thr Ile

```
                165                 170                 175
Asn Gly Ile Gln Ser Val Gly Val Gln Ala Thr Ala Lys His Tyr Ile
            180                 185                 190
Leu Asn Glu Gln Glu Leu Asn Arg Glu Thr Ile Ser Ser Asn Pro Asp
        195                 200                 205
Asp Arg Thr Leu His Glu Leu Tyr Thr Trp Pro Phe Ala Asp Ala Val
    210                 215                 220
Gln Ala Asn Val Ala Ser Val Met Cys Ser Tyr Asn Lys Val Asn Thr
225                 230                 235                 240
Thr Trp Ala Cys Glu Asp Gln Tyr Thr Leu Gln Thr Val Leu Lys Asp
                245                 250                 255
Gln Leu Gly Phe Pro Gly Tyr Val Met Thr Asp Trp Asn Ala Gln His
            260                 265                 270
Thr Thr Val Gln Ser Ala Asn Ser Gly Leu Asp Met Ser Met Pro Gly
        275                 280                 285
Thr Asp Phe Asn Gly Asn Asn Arg Leu Trp Gly Pro Ala Leu Thr Asn
    290                 295                 300
Ala Val Asn Ser Asn Gln Val Pro Thr Ser Arg Val Asp Asp Met Val
305                 310                 315                 320
Thr Arg Ile Leu Ala Ala Trp Tyr Leu Thr Gly Gln Asp Gln Ala Gly
                325                 330                 335
Tyr Pro Ser Phe Asn Ile Ser Arg Asn Val Gln Gly Asn His Lys Thr
            340                 345                 350
Asn Val Arg Ala Ile Ala Arg Asp Gly Ile Val Leu Leu Lys Asn Asp
        355                 360                 365
Ala Asn Ile Leu Pro Leu Lys Lys Pro Ala Ser Ile Ala Val Val Gly
    370                 375                 380
Ser Ala Ala Ile Ile Gly Asn His Ala Arg Asn Ser Pro Ser Cys Asn
385                 390                 395                 400
Asp Lys Gly Cys Asp Asp Gly Ala Leu Gly Met Gly Trp Gly Ser Gly
                405                 410                 415
Ala Val Asn Tyr Pro Tyr Phe Val Ala Pro Tyr Asp Ala Ile Asn Thr
            420                 425                 430
Arg Ala Ser Ser Gln Gly Thr Gln Val Thr Leu Ser Asn Thr Asp Asn
        435                 440                 445
Thr Ser Ser Gly Ala Ser Ala Ala Arg Gly Lys Asp Val Ala Ile Val
    450                 455                 460
Phe Ile Thr Ala Asp Ser Gly Glu Gly Tyr Ile Thr Val Glu Gly Asn
465                 470                 475                 480
Ala Gly Asp Arg Asn Asn Leu Asp Pro Trp His Asn Gly Asn Ala Leu
                485                 490                 495
Val Gln Ala Val Ala Gly Ala Asn Ser Asn Val Ile Val Val Val His
            500                 505                 510
Ser Val Gly Ala Ile Ile Leu Glu Gln Ile Leu Ala Leu Pro Gln Val
        515                 520                 525
Lys Ala Val Val Trp Ala Gly Leu Pro Ser Gln Glu Ser Gly Asn Ala
    530                 535                 540
Leu Val Asp Val Leu Trp Gly Asp Val Ser Pro Ser Gly Lys Leu Val
545                 550                 555                 560
Tyr Thr Ile Ala Lys Ser Pro Asn Asp Tyr Asn Thr Arg Ile Val Ser
                565                 570                 575
Gly Gly Ser Asp Ser Phe Ser Glu Gly Leu Phe Ile Asp Tyr Lys His
            580                 585                 590
Phe Asp Asp Ala Asn Ile Thr Pro Arg Tyr Glu Phe Gly Tyr Gly Leu
```

```
        595                 600                 605
Ser Tyr Thr Lys Phe Asn Tyr Ser Arg Leu Ser Val Leu Ser Thr Ala
    610                 615                 620
Lys Ser Gly Pro Ala Thr Gly Ala Val Val Pro Gly Gly Pro Ser Asp
625                 630                 635                 640
Leu Phe Gln Asn Val Ala Thr Val Thr Val Asp Ile Ala Asn Ser Gly
                645                 650                 655
Gln Val Thr Gly Ala Glu Val Ala Gln Leu Tyr Ile Thr Tyr Pro Ser
            660                 665                 670
Ser Ala Pro Arg Thr Pro Pro Lys Gln Leu Arg Gly Phe Ala Lys Leu
        675                 680                 685
Asn Leu Thr Pro Gly Gln Ser Gly Thr Ala Thr Phe Asn Ile Arg Arg
    690                 695                 700
Arg Asp Leu Ser Tyr Trp Asp Thr Ala Ser Gln Lys Trp Val Val Pro
705                 710                 715                 720
Ser Gly Ser Phe Gly Ile Ser Val Gly Ala Ser Ser Arg Asp Ile Arg
                725                 730                 735
Leu Thr Ser Thr Leu Ser Val Ala
            740
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<210> 373
<211> 862
<212> PRT
<213> Artificial Sequence

<220>
<223> putative beta-glucosidase 1 precursor [Trichoderma reesei RUT C-30] 862 aa protein
ETS02983.1 GI:572279864

<400> 373

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

```
Glu Gln Gly Val Ile Ala Thr Ile Lys His Phe Ile Gly Asn Glu Gln
            180                 185                 190
Glu Met Tyr Arg Met Tyr Asn Pro Phe Gln Tyr Ala Tyr Ser Ser Asn
        195                 200                 205
Ile Asp Asp Arg Thr Leu His Glu Val Tyr Ala Trp Pro Phe Ala Glu
    210                 215                 220
Gly Ile Arg Ala Gly Val Gly Ala Val Met Met Ala Tyr Asn Ala Val
225                 230                 235                 240
Asn Gly Thr Ala Cys Ser Gln His Pro Tyr Leu Met Ser Ala Leu Leu
                245                 250                 255
Lys Asp Glu Met Gly Phe Gln Gly Phe Ile Met Thr Asp Trp Leu Ala
            260                 265                 270
His Met Ser Gly Val Ala Ser Ala Ile Ala Gly Leu Asp Met Asp Met
        275                 280                 285
Pro Gly Asp Val Gln Ile Pro Phe Phe Gly Gly Ser Tyr Trp Met Tyr
    290                 295                 300
Glu Leu Thr Arg Ser Ala Leu Asn Gly Ser Val Pro Met Asp Arg Ile
305                 310                 315                 320
Asn Asp Ala Ala Thr Arg Ile Ala Ala Ala Trp Tyr Lys Met Gly Gln
                325                 330                 335
Asp Lys Gly Phe Pro Ala Thr Asn Phe Asp Thr Asn Ser Arg Ala Ala
            340                 345                 350
Phe Asn Pro Leu Tyr Pro Ala Ala Leu Pro Leu Ser Pro Phe Gly Ile
        355                 360                 365
Thr Asn Glu Phe Val Pro Val Gln Asp Asp His Asp Val Ile Ala Arg
    370                 375                 380
Gln Ile Ser Gln Glu Ala Ile Thr Leu Leu Lys Asn Asp Gly Asp Ile
385                 390                 395                 400
Leu Pro Leu Ser Pro Ser Gln His Leu Lys Val Phe Gly Thr Asp Ala
                405                 410                 415
Gln Lys Asn Pro Asp Gly Ile Asn Ser Cys Thr Asp Arg Asn Cys Asn
            420                 425                 430
Lys Gly Thr Leu Gly Gln Gly Trp Gly Ser Gly Thr Val Asp Tyr Pro
        435                 440                 445
Tyr Leu Asp Asp Pro Ile Ser Ala Ile Thr Ala Glu Ala Asp Asn Val
    450                 455                 460
Thr Phe Tyr Asn Thr Asp Lys Phe Pro Ser Val Gly Glu Val Ser Asp
465                 470                 475                 480
Ser Asp Val Ala Ile Val Phe Val Asn Ser Asp Ala Gly Glu Asn Thr
                485                 490                 495
Tyr Thr Val Glu Gly Asn His Gly Asp Arg Asp Lys Ser Gly Leu Tyr
            500                 505                 510
Ala Trp His Asp Gly Asp Lys Leu Val Gln Asp Ala Ala Ser Lys Phe
        515                 520                 525
Ser Asn Val Ile Val Val Ile His Thr Val Gly Pro Leu Ile Leu Glu
    530                 535                 540
Lys Trp Ile Asp Leu Pro Ser Val Lys Ala Val Leu Val Ala His Leu
545                 550                 555                 560
Pro Gly Gln Glu Ala Gly Lys Ser Leu Thr Asn Val Leu Phe Gly His
                565                 570                 575
Ala Ser Pro Cys Gly His Leu Pro Tyr Ser Ile Thr Lys Glu Glu Asp
            580                 585                 590
Asp Leu Pro Lys Ser Val Thr Thr Leu Ile Asp Ser Glu Phe Leu Asn
        595                 600                 605
```

```
Gln Pro Gln Asp Thr Tyr Thr Glu Gly Leu Tyr Ile Asp Tyr Arg Trp
    610                 615                 620
Leu Asn Lys Asn Lys Thr Lys Pro Arg Tyr Ala Phe Gly His Gly Leu
625                 630                 635                 640
Ser Tyr Thr Asn Phe Thr Phe Lys Ala Ala Ser Ile Lys Gln Val Ala
                645                 650                 655
Arg Leu Ser Ala Tyr Pro Pro Ala Arg Pro Ala Lys Gly Ser Thr Pro
            660                 665                 670
Asp Phe Ala Gln Ser Ile Pro Ser Ala Ser Glu Ala Val Ala Pro Ser
        675                 680                 685
Gly Phe Gly Lys Ile Pro Arg Tyr Ile Tyr Ser Trp Leu Ser Gln Gly
    690                 695                 700
Asp Ala Asn Arg Ala Ile Ser Asp Gly Lys Thr Gly Lys Tyr Pro Tyr
705                 710                 715                 720
Pro Asp Gly Tyr Ser Thr Thr Gln Lys Pro Gly Ala Arg Ala Gly Gly
                725                 730                 735
Gly Glu Gly Gly Asn Pro Ala Leu Trp Asp Val Ala Tyr Ser Leu Thr
            740                 745                 750
Val Thr Val Gln Asn Thr Gly Asp Glu Tyr Ala Gly Lys Ala Ser Val
        755                 760                 765
Gln Ala Tyr Leu Gln Phe Pro Asp Asp Ile Asp Tyr Asp Thr Pro Ile
    770                 775                 780
Ile Gln Leu Arg Asp Phe Glu Lys Thr Lys Glu Leu Lys Pro Gly Glu
785                 790                 795                 800
Thr Thr Thr Val Thr Leu Thr Leu Thr Arg Lys Asp Val Ser Val Trp
                805                 810                 815
Asp Val Val Ala Gln Asp Trp Lys Val Pro Ala Val Asp Gly Gly Tyr
            820                 825                 830
Lys Val Trp Ile Gly Asp Ala Ser Asp Ser Leu Ser Ile Val Cys His
        835                 840                 845
Thr Asp Thr Leu Glu Cys Glu Thr Gly Val Val Gly Pro Val
    850                 855                 860


<210> 374
<211> 781
<212> PRT
<213> Artificial Sequence

<220>
<223> Putative beta-glucosidase [Trichoderma reesei RUT
      C-30] 781 aa protein ETS01786.1 GI:572278616

<400> 374
Met Val Ala Val Lys Gln Ile Ala Leu Leu Ala Gly Leu Ala His Trp
 1               5                  10                  15
Ala Asp Ala Ala Glu Lys Val Ile Thr Asn Asp Thr His Phe Tyr Gly
            20                  25                  30
Gln Ser Pro Pro Val Tyr Pro Ser Pro Glu Met Thr Gly Gly Asn Glu
        35                  40                  45
Trp Glu Ala Ala Tyr Gln Lys Ala Lys Ala Phe Val Gly Gln Leu Thr
    50                  55                  60
Leu Glu Glu Lys Val Asn Leu Thr Ala Gly Val Pro Pro Asn Thr Thr
65                  70                  75                  80
```

```
Cys Ser Gly Val Ile Pro Ala Ile Glu Arg Leu Lys Phe Pro Gly Met
                85                  90                  95
Cys Leu Ser Asp Ala Gly Asn Gly Leu Arg Asn Thr Asp Phe Val Ser
            100                 105                 110
Gly Phe Pro Ser Gly Ile His Val Gly Ala Ser Trp Ser Lys Asp Leu
        115                 120                 125
Ala Phe Arg Arg Ala Val Ala Met Gly Ala Glu Phe Arg Lys Lys Gly
    130                 135                 140
Val Asn Val Leu Leu Gly Pro Val Val Gly Pro Ala Gly Arg Thr Val
145                 150                 155                 160
Arg Gly Gly Arg Asn Trp Glu Gly Phe Ser Val Asp Pro Trp Leu Ala
                165                 170                 175
Gly Val Leu Val Ser Glu Thr Val Ser Gly Ile Gln Glu Gln Gly Val
            180                 185                 190
Ile Thr Ser Thr Lys His Tyr Ile Leu Asn Glu Gln Glu Thr His Arg
        195                 200                 205
Met Pro Glu Ala Asn Val Ser Ala Val Ser Ser Asn Ile Asp Asp Lys
    210                 215                 220
Thr Met His Glu Tyr Tyr Leu Trp Pro Phe Gln Asp Ala Val Arg Ala
225                 230                 235                 240
Gly Ser Gly Asn Ile Met Cys Ser Tyr Gln Arg Ile Asn Asn Ser Tyr
                245                 250                 255
Gly Cys Ser Asn Ser Lys Thr Leu Asn Gly Leu Leu Lys Thr Glu Leu
            260                 265                 270
Gly Phe Gln Gly Phe Val Val Ser Asp Trp Ser Ala Gln His Ala Gly
        275                 280                 285
Val Ala Ser Ala Glu Ala Gly Met Asp Met Ala Met Pro Gly Pro Ala
    290                 295                 300
Glu Phe Trp Gly Glu His Leu Val Glu Ala Val Lys Asn Gly Ser Leu
305                 310                 315                 320
Pro Glu Ser Arg Ile Thr Asp Met Ala Thr Arg Ile Ile Ala Thr Trp
                325                 330                 335
Tyr Gln Phe Asp Gln Asp Asn Gly Ile Pro Lys Pro Gly Ile Gly Met
            340                 345                 350
Pro Ser Asn Val Leu Asp Ser His Glu Ile Val Asp Ala Arg Asp Pro
        355                 360                 365
Ala Ala Val Pro Val Leu Leu Asn Gly Ala Ile Glu Gly His Val Leu
    370                 375                 380
Val Lys Asn Thr Lys Asn Thr Leu Pro Leu Lys Lys Pro Arg Lys Leu
385                 390                 395                 400
Ser Leu Phe Gly Tyr Ser Ala Thr Thr Pro Asp Phe Phe Ser Pro Ser
                405                 410                 415
Arg Asp Glu Gln Leu Ser Asp Ser Trp Ile Phe Gly Lys Glu Ala Tyr
            420                 425                 430
Asn Ser Asn Tyr Leu Ser Pro Asp Gly Phe Ala Thr Phe Gly Arg Asn
        435                 440                 445
Gly Thr Thr Phe Gly Gly Cys Gly Ser Gly Ala Ile Thr Pro Ala Leu
    450                 455                 460
Ala Ile Ser Pro Phe Glu Ala Leu Lys Trp Arg Ala Ala Gln Asp Gly
465                 470                 475                 480
Thr Ala Thr Phe Asn Asn Phe Leu Ser Asp Lys Pro Asp Val Asp Pro
                485                 490                 495
Thr Ser Asp Ala Cys Ile Val Phe Gly Asn Ala Tyr Ala Cys Glu Gly
            500                 505                 510
```

```
Asn Asp Arg Pro Ala Ile Gln Asp Asp Tyr Thr Asp Asp Leu Ile Lys
        515                 520                 525
Ala Val Ala Ser Gln Cys Asn Lys Thr Ile Val Val Leu His Asn Ala
    530                 535                 540
Gly Ile Arg Leu Val Asp Gly Phe Val Asp His Pro Asn Ile Thr Ala
545                 550                 555                 560
Val Ile Phe Ala His Leu Pro Gly Gln Glu Ser Gly Pro Ala Leu Thr
                565                 570                 575
Ser Leu Leu Tyr Gly Glu Thr Ser Pro Ser Gly Arg Leu Pro Tyr Thr
            580                 585                 590
Val Ala Lys Asn Asp Thr Asp Tyr Gly Val Val Leu Asp Pro Ala Gln
        595                 600                 605
Ala Thr Gly Glu Phe Ala Tyr Phe Pro Gln Ala Asp Phe Lys Glu Gly
    610                 615                 620
Val Tyr Leu Asp Tyr Arg Tyr Phe Asp Lys Glu Gly Ile Glu Pro Arg
625                 630                 635                 640
Tyr Glu Phe Gly Phe Gly Leu Ser Tyr Thr Thr Phe Ala Tyr Leu Asn
                645                 650                 655
Leu Ser Val Asp His Val Ser Gly Ala Asn Thr Tyr Pro Trp Pro Gly
            660                 665                 670
Gly Pro Ile Val Ser Gly Gly Gln Thr Asp Leu Trp Asp Ala Ile Ala
        675                 680                 685
Thr Val Ser Val Asp Ile Arg Asn Thr Gly Ser Val Ala Ser Tyr Glu
    690                 695                 700
Val Ala Gln Leu Tyr Ile Gly Ile Pro Gly Ala Pro Ala Lys Gln Leu
705                 710                 715                 720
Arg Gly Phe Glu Lys Pro Phe Leu Arg Pro Asn Glu Ser Gln Ser Val
                725                 730                 735
Thr Phe His Leu Thr Arg Arg Asp Leu Ser Val Trp Ser Val Glu Arg
            740                 745                 750
Gln Lys Trp Gln Leu Gln Gln Gly Thr Tyr Lys Ile Tyr Val Gly Ser
        755                 760                 765
Ser Ser Arg Arg Leu His Val Asn Gly Thr Leu Asp Ile
    770                 775                 780


<210> 375
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> predicted protein, partial [Trichoderma reesei
      QM6a] 457 aa protein EGR51923.1 GI:340521689

<400> 375
His Leu Arg Ser His Thr Val Glu Ser Pro Asn Ser Ile Val Lys Arg
 1               5                  10                  15
Gly Thr Cys Ala Phe Pro Thr Asp Asp Pro Asn Leu Val Ala Val Thr
            20                  25                  30
Pro Asp Ala Glu Asn Ala Gly Trp Ala Met Ser Pro Asp Gln Pro Cys
        35                  40                  45
Lys Pro Gly His Tyr Cys Pro Ile Ala Cys Lys Pro Gly Met Val Met
    50                  55                  60
```

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

<210> 376
<211> 781

<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 3 [Trichoderma reesei
QM6a] 781 aa protein EGR50829.1 GI:340520593

<400> 376
Met Val Ala Val Lys Gln Ile Ala Leu Leu Ala Gly Leu Ala His Trp
1 5 10 15
Ala Asp Ala Ala Glu Lys Val Ile Thr Asn Asp Thr His Phe Tyr Gly
20 25 30
Gln Ser Pro Pro Val Tyr Pro Ser Pro Glu Met Thr Gly Gly Asn Glu
35 40 45
Trp Glu Ala Ala Tyr Gln Lys Ala Lys Ala Phe Val Gly Gln Leu Thr
50 55 60
Leu Glu Glu Lys Val Asn Leu Thr Ala Gly Val Pro Pro Asn Thr Thr
65 70 75 80
Cys Ser Gly Val Ile Pro Ala Ile Glu Arg Leu Lys Phe Pro Gly Met
85 90 95
Cys Leu Ser Asp Ala Gly Asn Gly Leu Arg Asn Thr Asp Phe Val Ser
100 105 110
Gly Phe Pro Ser Gly Ile His Val Gly Ala Ser Trp Ser Lys Asp Leu
115 120 125
Ala Phe Arg Arg Ala Val Ala Met Gly Ala Glu Phe Arg Lys Lys Gly
130 135 140
Val Asn Val Leu Leu Gly Pro Val Val Gly Pro Ala Gly Arg Thr Val
145 150 155 160
Arg Gly Gly Arg Asn Trp Glu Gly Phe Ser Val Asp Pro Trp Leu Ala
165 170 175
Gly Val Leu Val Ser Glu Thr Val Ser Gly Ile Gln Glu Gln Gly Val
180 185 190
Ile Thr Ser Thr Lys His Tyr Ile Leu Asn Glu Gln Glu Thr His Arg
195 200 205
Met Pro Glu Ala Asn Val Ser Ala Val Ser Ser Asn Ile Asp Asp Lys
210 215 220
Thr Met His Glu Tyr Tyr Leu Trp Pro Phe Gln Asp Ala Val Arg Ala
225 230 235 240
Gly Ser Gly Asn Ile Met Cys Ser Tyr Gln Arg Ile Asn Asn Ser Tyr
245 250 255
Gly Cys Ser Asn Ser Lys Thr Leu Asn Gly Leu Leu Lys Thr Glu Leu
260 265 270
Gly Phe Gln Gly Phe Val Val Ser Asp Trp Ser Ala Gln His Ala Gly
275 280 285
Val Ala Ser Ala Glu Ala Gly Met Asp Met Ala Met Pro Gly Pro Ala
290 295 300
Glu Phe Trp Gly Glu His Leu Val Glu Ala Val Lys Asn Gly Ser Leu
305 310 315 320
Pro Glu Ser Arg Ile Thr Asp Met Ala Thr Arg Ile Ile Ala Thr Trp
325 330 335
Tyr Gln Phe Asp Gln Asp Asn Gly Ile Pro Lys Pro Gly Ile Gly Met
340 345 350
Pro Ser Asn Val Leu Asp Ser His Glu Ile Val Asp Ala Arg Asp Pro
355 360 365

```
Ala Ala Val Pro Val Leu Leu Asn Gly Ala Ile Glu Gly His Val Leu
    370                 375                 380
Val Lys Asn Thr Lys Asn Thr Leu Pro Leu Lys Lys Pro Arg Lys Leu
385                 390                 395                 400
Ser Leu Phe Gly Tyr Ser Ala Thr Thr Pro Asp Phe Phe Ser Pro Ser
                405                 410                 415
Arg Asp Glu Gln Leu Ser Asp Ser Trp Ile Phe Gly Lys Glu Ala Tyr
            420                 425                 430
Asn Ser Asn Tyr Leu Ser Pro Asp Gly Phe Ala Thr Phe Gly Arg Asn
        435                 440                 445
Gly Thr Thr Phe Gly Gly Cys Gly Ser Gly Ala Ile Thr Pro Ala Leu
    450                 455                 460
Ala Ile Ser Pro Phe Glu Ala Leu Lys Trp Arg Ala Ala Gln Asp Gly
465                 470                 475                 480
Thr Ala Thr Phe Asn Asn Phe Leu Ser Asp Lys Pro Asp Val Asp Pro
                485                 490                 495
Thr Ser Asp Ala Cys Ile Val Phe Gly Asn Ala Tyr Ala Cys Glu Gly
            500                 505                 510
Asn Asp Arg Pro Ala Ile Gln Asp Asp Tyr Thr Asp Asp Leu Ile Lys
        515                 520                 525
Ala Val Ala Ser Gln Cys Asn Lys Thr Ile Val Val Leu His Asn Ala
    530                 535                 540
Gly Ile Arg Leu Val Asp Gly Phe Val Asp His Pro Asn Ile Thr Ala
545                 550                 555                 560
Val Ile Phe Ala His Leu Pro Gly Gln Glu Ser Gly Pro Ala Leu Thr
                565                 570                 575
Ser Leu Leu Tyr Gly Glu Thr Ser Pro Ser Gly Arg Leu Pro Tyr Thr
            580                 585                 590
Val Ala Lys Asn Asp Thr Asp Tyr Gly Val Val Leu Asp Pro Ala Gln
        595                 600                 605
Ala Thr Gly Glu Phe Ala Tyr Phe Pro Gln Ala Asp Phe Lys Glu Gly
    610                 615                 620
Val Tyr Leu Asp Tyr Arg Tyr Phe Asp Lys Glu Gly Ile Glu Pro Arg
625                 630                 635                 640
Tyr Glu Phe Gly Phe Gly Leu Ser Tyr Thr Thr Phe Ala Tyr Leu Asn
                645                 650                 655
Leu Ser Val Asp His Val Ser Gly Ala Asn Thr Tyr Pro Trp Pro Gly
            660                 665                 670
Gly Pro Ile Val Ser Gly Gly Gln Thr Asp Leu Trp Asp Ala Ile Ala
        675                 680                 685
Thr Val Ser Val Asp Ile Arg Asn Thr Gly Ser Val Ala Ser Tyr Glu
    690                 695                 700
Val Ala Gln Leu Tyr Ile Gly Ile Pro Gly Ala Pro Ala Lys Gln Leu
705                 710                 715                 720
Arg Gly Phe Glu Lys Pro Phe Leu Arg Pro Asn Glu Ser Gln Ser Val
                725                 730                 735
Thr Phe His Leu Thr Arg Arg Asp Leu Ser Val Trp Ser Val Glu Arg
            740                 745                 750
Gln Lys Trp Gln Leu Gln Gln Gly Thr Tyr Lys Ile Tyr Val Gly Ser
        755                 760                 765
Ser Ser Arg Arg Leu His Val Asn Gly Thr Leu Asp Ile
    770                 775                 780
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<210> 377
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> cell wall protein [Trichoderma reesei QM6a] 436 aa
protein EGR50785.1 GI:340520549

<400> 377
Met Leu Ala Cys Ile Thr Arg Ala Thr Leu Pro Thr Val Val Ala Ala
 1               5                  10                  15
Thr Pro Ser His His His His His Ala His Arg His Ala Lys Lys His
            20                  25                  30
Ala Ala Ala Arg Val Glu Lys Arg Ala Pro Asp Val Val Thr Glu Val
        35                  40                  45
Val Val Gly Ala Thr Ala Thr Val Phe Glu Leu Asp Gly Lys Ile Val
    50                  55                  60
Asp Ala Ala Thr Ala Lys Ala Gly Leu Ala Glu Gly Glu Tyr Ile Ile
65                  70                  75                  80
Val Gly Glu Thr Thr Pro Thr Phe Val Pro Pro Pro Pro Pro Pro Pro
                85                  90                  95
Ala Thr Ser Ser Ala Ala Pro Leu Arg Ala Gln Phe Val Glu Glu Pro
            100                 105                 110
Ile Ser Ser Pro Ala Ala Pro Thr Thr Thr Ser Ala Pro Pro Pro Pro
        115                 120                 125
Pro Thr Thr Thr Ala Gln Ala Thr Thr Ser Ser Ala Pro Pro Pro Pro
    130                 135                 140
Lys Thr Ser Lys Pro Ala Gln Ser Ser Pro Ser Ser Gly Ala Thr Gly
145                 150                 155                 160
Leu Asp Ala Asp Phe Pro Ser Gly Lys Ile Ser Cys Lys Thr Phe Pro
                165                 170                 175
Ser Glu Tyr Gly Ala Val Ala Leu Asp Trp Leu Gly Thr Gly Gly Trp
            180                 185                 190
Ser Gly Leu Gln Phe Val Pro Asn Tyr Ser Pro Asp Ala Gln Ser Ile
        195                 200                 205
Ser Asp Ile Ile Thr Gly Ile Ala Gly Gln Thr Cys Ser Lys Gly Ala
    210                 215                 220
Met Cys Ser Tyr Ala Cys Pro Pro Gly Tyr Gln Lys Thr Gln Trp Pro
225                 230                 235                 240
Lys Ala Gln Gly Ala Thr Leu Gln Ser Ile Gly Gly Leu Tyr Cys Asn
                245                 250                 255
Glu Asp Gly Phe Leu Glu Leu Thr Arg Pro Asp His Pro Lys Leu Cys
            260                 265                 270
Glu Ala Gly Ala Gly Gly Val Thr Ile Lys Asn Asp Leu Asp Asp Ser
        275                 280                 285
Val Cys Thr Cys Arg Thr Asp Tyr Pro Gly Ile Glu Ser Met Val Ile
    290                 295                 300
Pro Ala Cys Thr Ser Ala Gly Glu Thr Ile Glu Leu Thr Asn Pro Asp
305                 310                 315                 320
Glu Thr Asp Tyr Tyr Val Trp Asp Gly Lys Thr Thr Ser Ala Gln Tyr
                325                 330                 335
Tyr Val Asn Lys Lys Gly Tyr Ala Val Glu Asp Ala Cys Val Trp Asn
            340                 345                 350

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


<210> 378
<211> 700
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 3 [Trichoderma reesei
      QM6a] 700 aa protein EGR49878.1 GI:340519640

<400> 378
Met Ile Leu Gly Cys Glu Ser Thr Gly Val Ile Ser Ala Val Lys His
 1               5                  10                  15
Phe Val Ala Asn Asp Gln Glu His Glu Arg Arg Ala Val Asp Cys Leu
            20                  25                  30
Ile Thr Gln Arg Ala Leu Arg Glu Val Tyr Leu Arg Pro Phe Gln Ile
        35                  40                  45
Val Ala Arg Asp Ala Arg Pro Gly Ala Leu Met Thr Ser Tyr Asn Lys
    50                  55                  60
Val Asn Gly Lys His Val Ala Asp Ser Ala Glu Phe Leu Gln Gly Ile
65                  70                  75                  80
Leu Arg Thr Glu Trp Asn Trp Asp Pro Leu Ile Val Ser Asp Trp Tyr
                85                  90                  95
Gly Thr Tyr Thr Thr Ile Asp Ala Ile Lys Ala Gly Leu Asp Leu Glu
            100                 105                 110
Met Pro Gly Val Ser Arg Tyr Arg Gly Lys Tyr Ile Glu Ser Ala Leu
        115                 120                 125
Gln Ala Arg Leu Leu Lys Gln Ser Thr Ile Asp Glu Arg Ala Arg Arg
    130                 135                 140
Val Leu Arg Phe Ala Gln Lys Ala Ser His Leu Lys Val Ser Glu Val
145                 150                 155                 160
Glu Gln Gly Arg Asp Phe Pro Glu Asp Arg Val Leu Asn Arg Gln Ile
                165                 170                 175
Cys Gly Ser Ser Ile Val Leu Leu Lys Asn Glu Asn Ser Ile Leu Pro
            180                 185                 190
Leu Pro Lys Ser Val Lys Lys Val Ala Leu Val Gly Ser His Val Arg
        195                 200                 205
Leu Pro Ala Ile Ser Gly Gly Gly Ser Ala Ser Leu Val Pro Tyr Tyr
    210                 215                 220
Ala Ile Ser Leu Tyr Asp Ala Val Ser Glu Val Leu Ala Gly Ala Thr
225                 230                 235                 240
```

```
Ile Thr His Glu Val Gly Ala Tyr Ala His Gln Met Leu Pro Val Ile
                245                 250                 255
Asp Ala Met Ile Ser Asn Ala Val Ile His Phe Tyr Asn Asp Pro Ile
            260                 265                 270
Asp Val Lys Asp Arg Lys Leu Leu Gly Ser Glu Asn Val Ser Ser Thr
        275                 280                 285
Ser Phe Gln Leu Met Asp Tyr Asn Asn Ile Pro Thr Leu Asn Lys Ala
    290                 295                 300
Met Phe Trp Gly Thr Leu Val Gly Glu Phe Ile Pro Thr Ala Thr Gly
305                 310                 315                 320
Ile Trp Glu Phe Gly Leu Ser Val Phe Gly Thr Ala Asp Leu Tyr Ile
                325                 330                 335
Asp Asn Glu Leu Val Ile Glu Asn Thr Thr His Gln Thr Arg Gly Thr
            340                 345                 350
Ala Phe Phe Gly Lys Gly Thr Thr Glu Lys Val Ala Thr Arg Arg Met
        355                 360                 365
Val Ala Gly Ser Thr Tyr Lys Leu Arg Leu Glu Phe Gly Ser Ala Asn
    370                 375                 380
Thr Thr Lys Met Glu Thr Thr Gly Val Val Asn Phe Gly Gly Gly Ala
385                 390                 395                 400
Val His Leu Gly Ala Cys Leu Lys Val Asp Pro Gln Glu Met Ile Ala
                405                 410                 415
Arg Ala Val Lys Ala Ala Ala Asp Ala Asp Tyr Thr Ile Ile Cys Thr
            420                 425                 430
Gly Leu Ser Gly Glu Trp Glu Ser Glu Gly Phe Asp Arg Pro His Met
        435                 440                 445
Asp Leu Pro Pro Gly Val Asp Thr Met Ile Ser Gln Val Leu Asp Ala
    450                 455                 460
Ala Pro Asn Ala Val Val Val Asn Gln Ser Gly Thr Pro Val Thr Met
465                 470                 475                 480
Ser Trp Ala His Lys Ala Lys Ala Ile Val Gln Ala Trp Tyr Gly Gly
                485                 490                 495
Asn Glu Thr Gly His Gly Ile Ser Asp Val Leu Phe Gly Asn Val Asn
            500                 505                 510
Pro Ser Gly Lys Leu Ser Leu Ser Trp Pro Val Asp Val Lys His Asn
        515                 520                 525
Pro Ala Tyr Leu Asn Tyr Ala Ser Val Gly Gly Arg Val Leu Tyr Gly
    530                 535                 540
Glu Asp Val Tyr Val Gly Tyr Lys Phe Tyr Asp Lys Thr Glu Arg Glu
545                 550                 555                 560
Val Leu Phe Pro Phe Gly His Gly Leu Ser Tyr Ala Thr Phe Lys Leu
                565                 570                 575
Pro Asp Ser Thr Val Arg Thr Val Pro Glu Thr Phe His Pro Asp Gln
            580                 585                 590
Pro Thr Val Ala Ile Val Lys Ile Lys Asn Thr Ser Ser Val Pro Gly
        595                 600                 605
Ala Gln Val Leu Gln Leu Tyr Ile Ser Ala Pro Asn Ser Pro Thr His
    610                 615                 620
Arg Pro Val Lys Glu Leu His Gly Phe Glu Lys Val Tyr Leu Glu Ala
625                 630                 635                 640
Gly Glu Glu Lys Glu Val Gln Ile Pro Ile Asp Gln Tyr Ala Thr Ser
                645                 650                 655
Phe Trp Asp Glu Ile Glu Ser Met Trp Lys Ser Glu Arg Gly Ile Tyr
            660                 665                 670
```

Asp Val Leu Val Gly Phe Ser Ser Gln Glu Ile Ser Gly Lys Gly Lys
        675                 680                 685
Leu Ile Val Pro Glu Thr Arg Phe Trp Met Gly Leu
    690                 695                 700


<210> 379
<211> 744
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 3 [Trichoderma reesei
      QM6a] 744 aa protein EGR49703.1 GI:340519465

<400> 379
Met Arg Tyr Arg Thr Ala Ala Ala Leu Ala Leu Ala Thr Gly Pro Phe
 1               5                  10                  15
Ala Arg Ala Asp Ser His Ser Thr Ser Gly Ala Ser Ala Glu Ala Val
            20                  25                  30
Val Pro Pro Ala Gly Thr Pro Trp Gly Thr Ala Tyr Asp Lys Ala Lys
        35                  40                  45
Ala Ala Leu Ala Lys Leu Asn Leu Gln Asp Lys Val Gly Ile Val Ser
    50                  55                  60
Gly Val Gly Trp Asn Gly Gly Pro Cys Val Gly Asn Thr Ser Pro Ala
65                  70                  75                  80
Ser Lys Ile Ser Tyr Pro Ser Leu Cys Leu Gln Asp Gly Pro Leu Gly
                85                  90                  95
Val Arg Tyr Ser Thr Gly Ser Thr Ala Phe Thr Pro Gly Val Gln Ala
            100                 105                 110
Ala Ser Thr Trp Asp Val Asn Leu Ile Arg Glu Arg Gly Gln Phe Ile
        115                 120                 125
Gly Glu Glu Val Lys Ala Ser Gly Ile His Val Ile Leu Gly Pro Val
    130                 135                 140
Ala Gly Pro Leu Gly Lys Thr Pro Gln Gly Gly Arg Asn Trp Glu Gly
145                 150                 155                 160
Phe Gly Val Asp Pro Tyr Leu Thr Gly Ile Ala Met Gly Gln Thr Ile
                165                 170                 175
Asn Gly Ile Gln Ser Val Gly Val Gln Ala Thr Ala Lys His Tyr Ile
            180                 185                 190
Leu Asn Glu Gln Glu Leu Asn Arg Glu Thr Ile Ser Ser Asn Pro Asp
        195                 200                 205
Asp Arg Thr Leu His Glu Leu Tyr Thr Trp Pro Phe Ala Asp Ala Val
    210                 215                 220
Gln Ala Asn Val Ala Ser Val Met Cys Ser Tyr Asn Lys Val Asn Thr
225                 230                 235                 240
Thr Trp Ala Cys Glu Asp Gln Tyr Thr Leu Gln Thr Val Leu Lys Asp
                245                 250                 255
Gln Leu Gly Phe Pro Gly Tyr Val Met Thr Asp Trp Asn Ala Gln His
            260                 265                 270
Thr Thr Val Gln Ser Ala Asn Ser Gly Leu Asp Met Ser Met Pro Gly
        275                 280                 285
Thr Asp Phe Asn Gly Asn Asn Arg Leu Trp Gly Pro Ala Leu Thr Asn
    290                 295                 300

```
Ala Val Asn Ser Asn Gln Val Pro Thr Ser Arg Val Asp Asp Met Val
305                 310                 315                 320
Thr Arg Ile Leu Ala Ala Trp Tyr Leu Thr Gly Gln Asp Gln Ala Gly
                325                 330                 335
Tyr Pro Ser Phe Asn Ile Ser Arg Asn Val Gln Gly Asn His Lys Thr
            340                 345                 350
Asn Val Arg Ala Ile Ala Arg Asp Gly Ile Val Leu Leu Lys Asn Asp
        355                 360                 365
Ala Asn Ile Leu Pro Leu Lys Lys Pro Ala Ser Ile Ala Val Val Gly
    370                 375                 380
Ser Ala Ala Ile Ile Gly Asn His Ala Arg Asn Ser Pro Ser Cys Asn
385                 390                 395                 400
Asp Lys Gly Cys Asp Asp Gly Ala Leu Gly Met Gly Trp Gly Ser Gly
                405                 410                 415
Ala Val Asn Tyr Pro Tyr Phe Val Ala Pro Tyr Asp Ala Ile Asn Thr
            420                 425                 430
Arg Ala Ser Ser Gln Gly Thr Gln Val Thr Leu Ser Asn Thr Asp Asn
        435                 440                 445
Thr Ser Ser Gly Ala Ser Ala Ala Arg Gly Lys Asp Val Ala Ile Val
    450                 455                 460
Phe Ile Thr Ala Asp Ser Gly Glu Gly Tyr Ile Thr Val Glu Gly Asn
465                 470                 475                 480
Ala Gly Asp Arg Asn Asn Leu Asp Pro Trp His Asn Gly Asn Ala Leu
                485                 490                 495
Val Gln Ala Val Ala Gly Ala Asn Ser Asn Val Ile Val Val Val His
            500                 505                 510
Ser Val Gly Ala Ile Ile Leu Glu Gln Ile Leu Ala Leu Pro Gln Val
        515                 520                 525
Lys Ala Val Val Trp Ala Gly Leu Pro Ser Gln Glu Ser Gly Asn Ala
    530                 535                 540
Leu Val Asp Val Leu Trp Gly Asp Val Ser Pro Ser Gly Lys Leu Val
545                 550                 555                 560
Tyr Thr Ile Ala Lys Ser Pro Asn Asp Tyr Asn Thr Arg Ile Val Ser
                565                 570                 575
Gly Gly Ser Asp Ser Phe Ser Glu Gly Leu Phe Ile Asp Tyr Lys His
            580                 585                 590
Phe Asp Asp Ala Asn Ile Thr Pro Arg Tyr Glu Phe Gly Tyr Gly Leu
        595                 600                 605
Ser Tyr Thr Lys Phe Asn Tyr Ser Arg Leu Ser Val Leu Ser Thr Ala
    610                 615                 620
Lys Ser Gly Pro Ala Thr Gly Ala Val Val Pro Gly Gly Pro Ser Asp
625                 630                 635                 640
Leu Phe Gln Asn Val Ala Thr Val Thr Val Asp Ile Ala Asn Ser Gly
                645                 650                 655
Gln Val Thr Gly Ala Glu Val Ala Gln Leu Tyr Ile Thr Tyr Pro Ser
            660                 665                 670
Ser Ala Pro Arg Thr Pro Pro Lys Gln Leu Arg Gly Phe Ala Lys Leu
        675                 680                 685
Asn Leu Thr Pro Gly Gln Ser Gly Thr Ala Thr Phe Asn Ile Arg Arg
    690                 695                 700
Arg Asp Leu Ser Tyr Trp Asp Thr Ala Ser Gln Lys Trp Val Val Pro
705                 710                 715                 720
Ser Gly Ser Phe Gly Ile Ser Val Gly Ala Ser Ser Arg Asp Ile Arg
                725                 730                 735
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Leu Thr Ser Thr Leu Ser Val Ala
740

<210> 380
<211> 814
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 3 [Trichoderma reesei QM6a] 814 aa protein EGR49559.1 GI:340519320

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

```
Thr Asn Glu Phe Val Pro Val Gln Asp Asp His Asp Val Ile Ala Arg
                325                 330                 335
Gln Ile Ser Gln Glu Ala Ile Thr Leu Leu Lys Asn Asp Gly Asp Ile
            340                 345                 350
Leu Pro Leu Ser Pro Ser Gln His Leu Lys Val Phe Gly Thr Asp Ala
        355                 360                 365
Gln Lys Asn Pro Asp Gly Ile Asn Ser Cys Thr Asp Arg Asn Cys Asn
    370                 375                 380
Lys Gly Thr Leu Gly Gln Gly Trp Gly Ser Gly Thr Val Asp Tyr Pro
385                 390                 395                 400
Tyr Leu Asp Asp Pro Ile Ser Ala Ile Thr Ala Glu Ala Asp Asn Val
                405                 410                 415
Thr Phe Tyr Asn Thr Asp Lys Phe Pro Ser Val Gly Glu Val Ser Asp
            420                 425                 430
Ser Asp Val Ala Ile Val Phe Val Asn Ser Asp Ala Gly Glu Asn Thr
        435                 440                 445
Tyr Thr Val Glu Gly Asn His Gly Asp Arg Asp Lys Ser Gly Leu Tyr
    450                 455                 460
Ala Trp His Asp Gly Asp Lys Leu Val Gln Asp Ala Ala Ser Lys Phe
465                 470                 475                 480
Ser Asn Val Ile Val Val Ile His Thr Val Gly Pro Leu Ile Leu Glu
                485                 490                 495
Lys Trp Ile Asp Leu Pro Ser Val Lys Ala Val Leu Val Ala His Leu
            500                 505                 510
Pro Gly Gln Glu Ala Gly Lys Ser Leu Thr Asn Val Leu Phe Gly His
        515                 520                 525
Ala Ser Pro Cys Gly His Leu Pro Tyr Ser Ile Thr Lys Glu Glu Asp
    530                 535                 540
Asp Leu Pro Lys Ser Val Thr Thr Leu Ile Asp Ser Glu Phe Leu Asn
545                 550                 555                 560
Gln Pro Gln Asp Thr Tyr Thr Glu Gly Leu Tyr Ile Asp Tyr Arg Trp
                565                 570                 575
Leu Asn Lys Asn Lys Thr Lys Pro Arg Tyr Ala Phe Gly His Gly Leu
            580                 585                 590
Ser Tyr Thr Asn Phe Thr Phe Lys Ala Ala Ser Ile Lys Gln Val Ala
        595                 600                 605
Arg Leu Ser Ala Tyr Pro Pro Ala Arg Pro Ala Lys Gly Ser Thr Pro
    610                 615                 620
Asp Phe Ala Gln Ser Ile Pro Ser Ala Ser Glu Ala Val Ala Pro Ser
625                 630                 635                 640
Gly Phe Gly Lys Ile Pro Arg Tyr Ile Tyr Ser Trp Leu Ser Gln Gly
                645                 650                 655
Asp Ala Asn Arg Ala Ile Ser Asp Gly Lys Thr Gly Lys Tyr Pro Tyr
            660                 665                 670
Pro Asp Gly Tyr Ser Thr Thr Gln Lys Pro Gly Ala Arg Ala Gly Gly
        675                 680                 685
Gly Glu Gly Gly Asn Pro Ala Leu Trp Asp Val Ala Tyr Ser Leu Thr
    690                 695                 700
Val Thr Val Gln Asn Thr Gly Asp Glu Tyr Ala Gly Lys Ala Ser Val
705                 710                 715                 720
Gln Ala Tyr Leu Gln Phe Pro Asp Asp Ile Asp Tyr Asp Thr Pro Ile
                725                 730                 735
Ile Gln Leu Arg Asp Phe Glu Lys Thr Lys Glu Leu Lys Pro Gly Glu
            740                 745                 750
```

```
Thr Thr Thr Val Thr Leu Thr Leu Thr Arg Lys Asp Val Ser Val Trp
        755                 760                 765
Asp Val Val Ala Gln Asp Trp Lys Val Pro Ala Val Asp Gly Gly Tyr
    770                 775                 780
Lys Val Trp Ile Gly Asp Ala Ser Asp Ser Leu Ser Ile Val Cys His
785                 790                 795                 800
Thr Asp Thr Leu Glu Cys Glu Thr Gly Val Val Gly Pro Val
                805                 810
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<210> 381
<211> 874
<212> PRT
<213> Artificial Sequence

<220>
<223> glycosidehydrolase family 3 [Trichoderma reesei QM6a] 874 aa protein EGR48517.1 GI:340518276

<400> 381

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

```
Leu Leu Lys Glu Glu Tyr Gly Phe Gln Gly Phe Val Met Ser Asp Trp
        275                 280                 285
Gln Ala Gln His Thr Gly Val Ala Ser Ala Val Ala Gly Leu Asp Met
    290                 295                 300
Thr Met Pro Gly Asp Thr Ala Phe Asn Thr Gly Ala Ser Tyr Phe Gly
305                 310                 315                 320
Ser Asn Leu Thr Leu Ala Val Leu Asn Gly Thr Val Pro Glu Trp Arg
                325                 330                 335
Ile Asp Asp Met Val Met Arg Ile Met Ala Pro Phe Phe Lys Val Gly
            340                 345                 350
Lys Thr Val Asp Ser Leu Ile Asp Thr Asn Phe Asp Ser Trp Thr Asn
        355                 360                 365
Gly Glu Tyr Gly Tyr Val Gln Ala Ala Val Asn Glu Asn Trp Glu Lys
    370                 375                 380
Val Asn Tyr Gly Val Asp Val Arg Ala Asn His Ala Asn His Ile Arg
385                 390                 395                 400
Glu Val Gly Ala Lys Gly Thr Val Ile Phe Lys Asn Asn Gly Ile Leu
                405                 410                 415
Pro Leu Lys Lys Pro Lys Phe Leu Thr Val Ile Gly Glu Asp Ala Gly
            420                 425                 430
Gly Asn Pro Ala Gly Pro Asn Gly Cys Gly Asp Arg Gly Cys Asp Asp
        435                 440                 445
Gly Thr Leu Ala Met Glu Trp Gly Ser Gly Thr Thr Asn Phe Pro Tyr
    450                 455                 460
Leu Val Thr Pro Asp Ala Ala Leu Gln Ser Gln Ala Leu Gln Asp Gly
465                 470                 475                 480
Thr Arg Tyr Glu Ser Ile Leu Ser Asn Tyr Ala Ile Ser Gln Thr Gln
                485                 490                 495
Ala Leu Val Ser Gln Pro Asp Ala Ile Ala Ile Val Phe Ala Asn Ser
            500                 505                 510
Asp Ser Gly Glu Gly Tyr Ile Asn Val Asp Gly Asn Glu Gly Asp Arg
        515                 520                 525
Lys Asn Leu Thr Leu Trp Lys Asn Gly Asp Asp Leu Ile Lys Thr Val
    530                 535                 540
Ala Ala Val Asn Pro Lys Thr Ile Val Val Ile His Ser Thr Gly Pro
545                 550                 555                 560
Val Ile Leu Lys Asp Tyr Ala Asn His Pro Asn Ile Ser Ala Ile Leu
                565                 570                 575
Trp Ala Gly Ala Pro Gly Gln Glu Ser Gly Asn Ser Leu Val Asp Ile
            580                 585                 590
Leu Tyr Gly Lys Gln Ser Pro Gly Arg Thr Pro Phe Thr Trp Gly Pro
        595                 600                 605
Ser Leu Glu Ser Tyr Gly Val Ser Val Met Thr Thr Pro Asn Asn Gly
    610                 615                 620
Asn Gly Ala Pro Gln Asp Asn Phe Asn Glu Gly Ala Phe Ile Asp Tyr
625                 630                 635                 640
Arg Tyr Phe Asp Lys Val Ala Pro Gly Lys Pro Arg Ser Ser Asp Lys
                645                 650                 655
Ala Pro Thr Tyr Glu Phe Gly Phe Gly Leu Ser Trp Ser Thr Phe Lys
            660                 665                 670
Phe Ser Asn Leu His Ile Gln Lys Asn Asn Val Gly Pro Met Ser Pro
        675                 680                 685
Pro Asn Gly Lys Thr Ile Ala Ala Pro Ser Leu Gly Ser Phe Ser Lys
    690                 695                 700
```

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Asn Leu Lys Asp Tyr Gly Phe Pro Lys Asn Val Arg Arg Ile Lys Glu
705                 710                 715                 720
Phe Ile Tyr Pro Tyr Leu Ser Thr Thr Thr Ser Gly Lys Glu Ala Ser
                725                 730                 735
Gly Asp Ala His Tyr Gly Gln Thr Ala Lys Glu Phe Leu Pro Ala Gly
            740                 745                 750
Ala Leu Asp Gly Ser Pro Gln Pro Arg Ser Ala Ala Ser Gly Glu Pro
        755                 760                 765
Gly Gly Asn Arg Gln Leu Tyr Asp Ile Leu Tyr Thr Val Thr Ala Thr
    770                 775                 780
Ile Thr Asn Thr Gly Ser Val Met Asp Asp Ala Val Pro Gln Leu Tyr
785                 790                 795                 800
Leu Ser His Gly Gly Pro Asn Glu Pro Pro Lys Val Leu Arg Gly Phe
                805                 810                 815
Asp Arg Ile Glu Arg Ile Ala Pro Gly Gln Ser Val Thr Phe Lys Ala
            820                 825                 830
Asp Leu Thr Arg Arg Asp Leu Ser Asn Trp Asp Thr Lys Lys Gln Gln
        835                 840                 845
Trp Val Ile Thr Asp Tyr Pro Lys Thr Val Tyr Val Gly Ser Ser Ser
    850                 855                 860
Arg Asp Leu Pro Leu Ser Ala Arg Leu Pro
865                 870


<210> 382
<211> 932
<212> PRT
<213> Artificial Sequence

<220>
<223> glycosidehydrolase family 3 [Trichoderma reesei
      QM6a] 932 aa protein EGR47352.1 GI:340517106

<400> 382
Met Ala Asn Ser Ile Gly Gly Ser Ser Ala Asp Lys Phe Asp Leu Asp
 1               5                  10                  15
Pro Leu Trp Gln Asn Leu Asp Trp Ala Ile Gly Gln Met Met Leu Met
            20                  25                  30
Gly Trp Asp Gly Thr Gln Val Thr Pro Gln Ile Arg Ser Leu Ile Glu
        35                  40                  45
Asp His His Leu Gly Ser Ile Ile Leu Thr Ala Lys Asn Leu Lys Ser
    50                  55                  60
Ala His His Thr Ala Leu Leu Val Gln Glu Leu Gln Met Ile Ala Lys
65                  70                  75                  80
Asn Ser Gly His Pro Gln Pro Leu Leu Ile Ala Val Asp Gln Glu Asn
                85                  90                  95
Gly Gly Val Asn Ser Leu Phe Asp Glu Asp Phe Val Cys Gln Phe Pro
            100                 105                 110
Ser Ala Met Ala Ile Ala Ala Thr Gly Ser Leu Glu Leu Ser Tyr Glu
        115                 120                 125
Val Asn Lys Ala Thr Ala Thr Glu Ile Ser Ala Cys Gly Val Asn Leu
    130                 135                 140
Met Leu Gly Pro Val Leu Asp Val Leu Asn Asn Ala Arg Tyr Gln Val
145                 150                 155                 160
```

```
Ile Gly Val Arg Ala Ser Gly Asp Asp Pro Gln Glu Val Ser Gln Tyr
                165                 170                 175
Gly Leu Ala Ala Leu Ser Gly Ile Arg Asp Ala Gly Val Ala Ser Cys
            180                 185                 190
Gly Lys His Phe Pro Ser Tyr Gly Asn Leu Asp Phe Leu Gly Ser Asn
        195                 200                 205
Leu Asp Val Pro Ile Ile Thr Gln Thr Leu Glu Glu Leu Ser Leu Ser
    210                 215                 220
Ala Leu Val Pro Phe Arg Asn Ala Ile Ala Ser Gly Lys Leu Asp Ala
225                 230                 235                 240
Met Phe Ile Gly Gly Cys Gly Ile Ser Asn Pro Ser Met Asn Val Ser
                245                 250                 255
His Ala Cys Leu Ser Asp Gln Val Val Asp Asp Leu Leu Arg Asn Glu
            260                 265                 270
Leu Gly Phe Lys Gly Val Ala Ile Ser Glu Cys Leu Glu Met Glu Ala
        275                 280                 285
Leu Ser Gln Asp Leu Gly Val Gln Asn Gly Val Val Met Ala Val Glu
    290                 295                 300
Ala Gly Cys Asp Ile Val Leu Leu Cys Arg Ala Tyr Asp Val Gln Leu
305                 310                 315                 320
Glu Ala Ile Lys Gly Leu Lys Leu Gly Tyr Glu Asn Gly Ile Ile Thr
                325                 330                 335
Lys Glu Arg Ile Phe Thr Ser Leu Lys Arg Ile Phe His Leu Lys Ser
            340                 345                 350
Thr Cys Thr Ser Trp Ala Lys Ala Leu Asn Pro Pro Gly Ile Asn Leu
        355                 360                 365
Leu Ser Gln Ile Arg Pro Ser His Leu Ala Leu Ser Arg Arg Ala Tyr
    370                 375                 380
Asp Asp Ser Ile Thr Ile Val Arg Asp Lys Glu Lys Leu Leu Pro Leu
385                 390                 395                 400
Ser Leu Ser Met His Pro Gly Glu Glu Leu Leu Leu Leu Thr Pro Leu
                405                 410                 415
Val Lys Pro Leu Pro Ala Ser Ser Leu Thr Lys Ser Leu Leu Glu Ser
            420                 425                 430
Lys Asn Asp Pro Ser Leu Val Ser Thr Glu His Asp Arg Trp Asn His
        435                 440                 445
Gln Ile Arg Glu Arg Ser Ala Ile Met Ser Gly Glu Gly Val Phe Arg
    450                 455                 460
Glu Phe Gly Lys Thr Leu Ala Arg Tyr Arg Asn Glu Lys Leu Leu His
465                 470                 475                 480
Thr Ser Tyr Thr Ala Asn Gly Val Arg Pro Val His Glu Asn Leu Ile
                485                 490                 495
Asn Arg Ala Ser Cys Ile Ile Ile Phe Thr Ala Asp Ala Asn Arg Asn
            500                 505                 510
Leu Tyr Gln Ala Gly Phe Thr Lys His Val Asp Met Met Cys Ser Met
        515                 520                 525
Leu Arg Ser Arg Gly Gln Lys Lys Gln Leu Ile Val Val Ala Val Ser
    530                 535                 540
Ser Pro Tyr Asp Phe Ala Met Asp Lys Ser Ile Gly Thr Tyr Ile Cys
545                 550                 555                 560
Thr Tyr Asp Phe Thr Glu Asn Ala Met Ala Ala Leu Val Arg Ala Leu
                565                 570                 575
Val Gly Asp Ser Asn Pro Val Gly Thr Met Pro Gly Thr Leu Arg Lys
            580                 585                 590
```

```
Ser Lys Lys Val Leu Lys Ser Arg Gln His Trp Leu Val Glu Glu Phe
        595                 600                 605
Asp Ser Ser Arg Asp Arg Lys Gly Leu Asn Asp Leu Ile Arg Ala Val
    610                 615                 620
His Arg Ala Ser Asp Gln Asp Phe Arg Tyr Leu Gln Thr Ala Thr Ala
625                 630                 635                 640
Asp Thr Phe Leu Leu Ala Asn Gln Asn Ile Lys Glu Thr His Phe Val
                645                 650                 655
Val Arg Asn Ser Ser Thr Gln Ala Leu Tyr Gly Phe Ala Ala Thr Tyr
            660                 665                 670
Phe Val Gln Asn Val Gly Ile Leu Gly Ala Leu Ile Val Asp Pro Thr
        675                 680                 685
Lys Arg Asn Met Ser Ile Gly Arg Ser Leu His Arg Arg Ala Ile Lys
    690                 695                 700
Ser Leu Thr Gln Gln Arg Gly Ile Lys Lys Val Gln Leu Gly Ser Cys
705                 710                 715                 720
Phe Pro Ala Leu Phe Leu Gly Ile Pro Leu Asp Ile Glu Val Thr Thr
                725                 730                 735
Thr Lys Glu Trp Phe Ser Asn Ser Gly Trp Asp Thr Gln Phe Pro Arg
            740                 745                 750
Arg Leu Thr Asn Met Val Ile Gln Asp Leu Ser Ala Trp Tyr Ala Pro
        755                 760                 765
Glu Gly Leu Ser Gln Ser Ile Gln Arg Ala Asn Ile Ser Phe Asp Leu
    770                 775                 780
Ile Tyr Gly Val Glu Ser Gly Asp Thr Val Met His His Val Arg Thr
785                 790                 795                 800
His Ala Asn Pro Glu Val Leu Glu Leu Tyr Arg Thr Ala Leu Glu Glu
                805                 810                 815
Ser Lys Ala Cys Gly Ile Val Arg Ala Lys Asp Ala Ala Gly Asn Leu
            820                 825                 830
Leu Gly Thr Ile Ile Ile Cys Arg Pro Asn Ser Pro Leu Ala Arg Tyr
        835                 840                 845
Val Pro Pro Leu Val Ser Leu Gly Gln Asp Ile Gly Gly Leu Leu Ala
    850                 855                 860
Pro Ile Val Pro Pro Ala Pro Leu Ser Thr Leu Val Leu Gln Gly Leu
865                 870                 875                 880
Ala Leu Met Gly Val Arg Gln Asn Lys Gly His Lys Ala Thr Lys Ser
                885                 890                 895
Val Leu Ser Trp Val Val Asp Asp Ala Tyr Glu Pro Leu Val Ala Met
            900                 905                 910
Gly Phe Asp Val Leu Gln Ala Phe Glu Glu Ile Thr Asn Ser Pro Glu
        915                 920                 925
Thr Phe Gln Thr
    930
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<210> 383
<211> 890
<212> PRT
<213> Artificial Sequence

<220>
<223> carbohydrate esterase family 4 [Trichoderma reesei QM6a] 890 aa protein EGR46266.1 GI:340516015

<400> 383

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

```
Ile Ala Ala Glu Gly Thr Val Leu Leu Lys Asn Glu Gly Val Leu Pro
            420                 425                 430
Leu Ser Val Asp Gly Leu Leu Gly Gly Gly Gly Gly Ser Asn Ser Thr
        435                 440                 445
Lys Arg Glu Gly Gln Val Arg Ile Gly Ile Phe Gly Glu Asp Ala Gly
    450                 455                 460
Pro Gly Lys Gly Pro Asn Tyr Cys Glu Asp Arg Ser Cys Asn Gln Gly
465                 470                 475                 480
Thr Leu Ala Ser Gly Trp Gly Ser Gly Ala Val Glu Phe Pro Tyr Leu
                485                 490                 495
Val Ser Pro Ile Glu Ala Leu Arg Lys Lys Phe Asn Lys Asp Lys Val
            500                 505                 510
Lys Leu Thr Glu His Leu Lys Asn Asp Glu Leu Asp Thr Gly Val Ile
        515                 520                 525
Lys Ser Gln Asp Ile Cys Met Val Phe Ile Asn Ser Asp Ser Gly Glu
    530                 535                 540
Gly Tyr Arg Ala Trp Glu Gly Val Arg Gly Asp Arg Asn Asp Leu Lys
545                 550                 555                 560
Pro Gln Lys Gly Gly Val Gly Leu Val Thr His Val Gly Leu Asn Cys
                565                 570                 575
Gly Asn Gly Ser Gly Thr Thr Ile Val Val Leu His Ser Val Gly Pro
            580                 585                 590
Val Val Val Asp Pro Trp Ile Asp Met Pro Gly Ile Lys Ala Leu Ile
        595                 600                 605
Ser Ala Asn Leu Pro Gly Gln Glu Ser Gly Asn Ala Leu Ala Ser Ile
    610                 615                 620
Leu Phe Gly Glu Glu Asn Pro Ser Gly Lys Leu Pro Tyr Thr Val Gly
625                 630                 635                 640
Lys Ser Leu Ser Asp Tyr Gly Pro Gly Gly Gln Val Met Tyr Leu Pro
                645                 650                 655
Asn Gly Ala Val Pro Gln Gln Asp Phe Ser Glu Gly Leu Tyr Ile Asp
            660                 665                 670
Tyr Arg His Phe Asp Lys Phe Asn Ile Glu Pro Arg Tyr Glu Phe Gly
        675                 680                 685
Phe Gly Leu Ser Tyr Thr Asn Phe Asp Tyr Lys Asn Leu Lys Ile Thr
    690                 695                 700
Glu Thr Lys Pro Arg Ser Pro Leu Pro Asp Glu Arg Pro Ala Ala Glu
705                 710                 715                 720
Val Glu Pro Pro Ser Phe Asp Thr Thr Ile Pro Gln Ala Glu Glu Ala
                725                 730                 735
Leu Phe Pro Ser Gly Ile Arg Arg Leu Lys Lys Tyr Val Tyr Pro Tyr
            740                 745                 750
Ile Glu Ser Val Lys Asp Ile Lys Glu Gly Gln Tyr Ser Tyr Pro Asp
        755                 760                 765
Gly Tyr Asp Lys Glu Gln Pro Leu Ser Gly Ala Gly Gly Gly Glu Gly
    770                 775                 780
Gly Asn Pro Ser Leu Trp Asp Ser His Val Ile Val Ser Val Glu Val
785                 790                 795                 800
Thr Asn Thr Gly Lys Leu Gly Gly Lys Ala Val Pro Gln Leu Tyr Leu
                805                 810                 815
Ser Tyr Pro Ala Ser Glu Thr Val Asp Phe Pro Val Arg Val Leu Arg
            820                 825                 830
Gly Phe Asp Lys Val Tyr Ile Gly Lys Gly Glu Thr Lys Thr Val Glu
        835                 840                 845
```

Phe Ser Leu Thr Arg Arg Asp Leu Ser Tyr Trp Asp Val Glu Arg Gln
    850                 855                 860
Asn Trp Val Ile Pro Glu Gly Glu Tyr Thr Phe Ala Val Gly Glu Ser
865                 870                 875                 880
Ser Arg Asp Leu Arg Val Ser Gly Thr Trp
                885                 890


<210> 384
<211> 489
<212> PRT
<213> Artificial Sequence

<220>
<223> glycosidehydrolase family 3, partial [Trichoderma
      reesei QM6a] 489 aa protein EGR44807.1
      GI:340514546

<400> 384
Gln Leu Phe Ala Val Gly Phe His Gly Arg Glu Ile Asn Gln Glu Ile
 1               5                  10                  15
Thr Thr Leu Ile Arg Asp Tyr Gly Val Gly Ala Ile Val Leu Phe Lys
            20                  25                  30
Arg Asn Glu Asn Gly Leu Val Thr Arg Ile Ser Pro Pro Ile Ala Ser
        35                  40                  45
Gln Gln Pro Gly Pro Met Thr Leu Gly Ala Ala Gly Ser Leu Glu Tyr
    50                  55                  60
Ala Tyr Glu Val Ala Lys Ala Thr Ala Glu Met Leu Arg Tyr Phe Gly
65                  70                  75                  80
Ile Asn Met Asn Tyr Ala Pro Val Gly Asp Val Asn Ser Glu Pro Leu
                85                  90                  95
Asn Pro Val Ile Gly Val Arg Ser Pro Ser Asp Gln Ala Glu Thr Val
            100                 105                 110
Ser Lys Phe Ala Ala Ala Cys Thr Lys Gly Leu Arg Glu His Lys Val
        115                 120                 125
Val Pro Cys Ile Lys His Phe Pro Gly His Gly Asp Thr Ala Val Asp
    130                 135                 140
Ser His Tyr Gly Leu Pro Val Ile Asn Lys Ser Arg Ala Asp Met Glu
145                 150                 155                 160
Lys Leu Glu Leu Ile Pro Phe Arg Asp Ala Val Ala Asp Asn Ile Glu
                165                 170                 175
Met Val Met Thr Ala His Ile Ser Leu Pro Gln Leu Ala Lys Asp Gly
            180                 185                 190
Leu Pro Ala Thr Leu Ser Pro Asp Thr Ile Gly Ile Leu Arg Asn Glu
        195                 200                 205
Trp Lys Tyr Glu Gly Val Ile Met Thr Asp Cys Leu Glu Met Asp Gly
    210                 215                 220
Ile Arg Ala Thr Tyr Gly Thr Val Glu Gly Ser Leu Met Ala Phe Gln
225                 230                 235                 240
Ala Gly Val Asp Asn Val Met Ile Cys His Thr Phe Asp Val Gln Ala
                245                 250                 255
Ala Ala Val Asp Tyr Ile Cys Gly Ala Ile Glu Ser Gly Lys Leu Ser
            260                 265                 270
Gln Glu Arg Val Asp Gln Ser Leu Glu Arg Leu Arg Lys Leu Lys Glu

```
        275                 280                 285
Arg Tyr Thr Asn Trp Asp Ile Ala Leu His Ala Glu Pro Pro Glu Ala
    290                 295                 300
Leu Glu Ala Ile Asn Glu Arg Gly Glu Lys Leu Ala Arg Gln Val Tyr
305                 310                 315                 320
Ala Asp Ala Thr Thr Leu Val Arg Ala Gln Glu Gly Leu Leu Pro Leu
                325                 330                 335
Lys Ala Thr Ala Lys Ile Ala Phe Val Ser Pro Gly Pro Asp Val Pro
            340                 345                 350
Ile Gly Gly Ala Val Asp Ser Gly Thr Leu Pro Thr Arg Val Pro Trp
        355                 360                 365
Ile Ala Asp Thr Phe Gly Glu Gln Ile Arg Lys Arg Ala Pro Glu Met
    370                 375                 380
Ser Asp Val Arg Phe Thr Ser Ser Asn Leu Thr Glu Glu Gln Trp Glu
385                 390                 395                 400
Gln Ile Asp Glu Ala Asp Val Val Ile Leu Ala Thr Arg Asn Ala Arg
                405                 410                 415
Glu Ser Lys Tyr Gln Lys Glu Leu Gly Leu Glu Val Ala Lys Arg Arg
            420                 425                 430
Gly Ser Arg Pro Leu Ile Ser Ile Ala Thr Cys Ala Pro Tyr Asp Phe
        435                 440                 445
Leu Asp Asp Glu Glu Ile Arg Thr Tyr Ile Ala Val Tyr Glu Pro Thr
    450                 455                 460
Val Glu Ala Phe Ser Ala Ala Val Asp Ile Leu Phe Gly Asp Ala Gln
465                 470                 475                 480
Pro Arg Gly Lys Leu Pro Val Ala His
                485
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<210> 385
<211> 834
<212> PRT
<213> Artificial Sequence

<220>
<223> glycosidehydrolase family 3 [Trichoderma reesei QM6a] 834 aa protein EGR44527.1 GI:340514262

<400> 385

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

```
        115                 120                 125
Ala Ala Ala Leu Ile Arg Gly Ile Gln Ser Thr Gly Val Gln Ala Thr
    130                 135                 140
Ile Lys His Phe Leu Cys Asn Asp Gln Glu Asp Arg Arg Met Met Val
145                 150                 155                 160
Gln Ser Ile Val Thr Glu Arg Ala Leu Arg Glu Ile Tyr Ala Leu Pro
                165                 170                 175
Phe Gln Ile Ala Val Arg Asp Ser Gln Pro Gly Ala Phe Met Thr Ala
            180                 185                 190
Tyr Asn Gly Ile Asn Gly Val Ser Cys Ser Glu Asn Pro Lys Tyr Leu
        195                 200                 205
Asp Gly Met Leu Arg Lys Glu Trp Gly Trp Asp Gly Leu Ile Met Ser
    210                 215                 220
Asp Trp Tyr Gly Thr Tyr Ser Thr Thr Glu Ala Val Val Ala Gly Leu
225                 230                 235                 240
Asp Leu Glu Met Pro Gly Pro Pro Arg Phe Arg Gly Glu Thr Leu Lys
                245                 250                 255
Phe Asn Val Ser Asn Gly Lys Pro Phe Ile His Val Ile Asp Gln Arg
            260                 265                 270
Ala Arg Glu Val Leu Gln Phe Val Lys Lys Cys Ala Ala Ser Gly Val
        275                 280                 285
Thr Glu Asn Gly Pro Glu Thr Thr Val Asn Asn Thr Pro Glu Thr Ala
    290                 295                 300
Ala Leu Leu Arg Lys Val Gly Asn Glu Gly Ile Val Leu Leu Lys Asn
305                 310                 315                 320
Glu Asn Asn Val Leu Pro Leu Ser Lys Lys Lys Lys Thr Leu Ile Val
                325                 330                 335
Gly Pro Asn Ala Lys Gln Ala Thr Tyr His Gly Gly Gly Ser Ala Ala
            340                 345                 350
Leu Arg Ala Tyr Tyr Ala Val Thr Pro Phe Asp Gly Leu Ser Lys Gln
        355                 360                 365
Leu Glu Thr Pro Pro Ser Tyr Thr Val Gly Ala Tyr Thr His Arg Phe
    370                 375                 380
Leu Pro Ile Leu Gly Glu Gln Cys Leu Thr Pro Asp Gly Ala Pro Gly
385                 390                 395                 400
Met Arg Trp Arg Val Phe Asn Glu Pro Pro Gly Thr Pro Asn Arg Gln
                405                 410                 415
His Ile Asp Glu Leu Phe Phe Thr Lys Thr Asp Met His Leu Val Asp
            420                 425                 430
Tyr Tyr His Pro Lys Ala Ala Asp Thr Trp Tyr Ala Asp Met Glu Gly
        435                 440                 445
Thr Tyr Thr Ala Asp Glu Asp Cys Thr Tyr Glu Leu Gly Leu Val Val
    450                 455                 460
Cys Gly Thr Ala Lys Ala Tyr Val Asp Asp Gln Leu Val Val Asp Asn
465                 470                 475                 480
Ala Thr Lys Gln Val Pro Gly Asp Ala Phe Phe Gly Ser Ala Thr Arg
                485                 490                 495
Glu Glu Thr Gly Arg Ile Asn Leu Val Lys Gly Asn Thr Tyr Lys Phe
            500                 505                 510
Lys Ile Glu Phe Gly Ser Ala Pro Thr Tyr Thr Leu Lys Gly Asp Thr
        515                 520                 525
Ile Val Pro Gly His Gly Ser Leu Arg Val Gly Gly Cys Lys Val Ile
    530                 535                 540
Asp Asp Gln Ala Glu Ile Glu Lys Ser Val Ala Leu Ala Lys Glu His
```

545 550 555 560
Asp Gln Val Ile Ile Cys Ala Gly Leu Asn Ala Asp Trp Glu Thr Glu
565 570 575
Gly Ala Asp Arg Ala Ser Met Lys Leu Pro Gly Val Leu Asp Gln Leu
580 585 590
Ile Ala Asp Val Ala Ala Ala Asn Pro Asn Thr Val Val Val Met Gln
595 600 605
Thr Gly Thr Pro Glu Glu Met Pro Trp Leu Asp Ala Thr Pro Ala Val
610 615 620
Ile Gln Ala Trp Tyr Gly Gly Asn Glu Thr Gly Asn Ser Ile Ala Asp
625 630 635 640
Val Val Phe Gly Asp Tyr Asn Pro Ser Gly Lys Leu Ser Leu Ser Phe
645 650 655
Pro Lys Arg Leu Gln Asp Asn Pro Ala Phe Leu Asn Phe Arg Thr Glu
660 665 670
Ala Gly Arg Thr Leu Tyr Gly Glu Asp Val Tyr Val Gly Tyr Arg Tyr
675 680 685
Tyr Glu Phe Ala Asp Lys Asp Val Asn Phe Pro Phe Gly His Gly Leu
690 695 700
Ser Tyr Thr Thr Phe Ala Phe Ser Asn Leu Ser Val Ser His Lys Asp
705 710 715 720
Gly Lys Leu Ser Val Ser Leu Ser Val Lys Asn Thr Gly Ser Val Pro
725 730 735
Gly Ala Gln Val Ala Gln Leu Tyr Val Lys Pro Leu Gln Ala Ala Lys
740 745 750
Ile Asn Arg Pro Val Lys Glu Leu Lys Gly Phe Ala Lys Val Glu Leu
755 760 765
Gln Pro Gly Glu Thr Lys Ala Val Thr Ile Glu Glu Gln Glu Lys Tyr
770 775 780
Val Ala Ala Tyr Phe Asp Glu Glu Arg Asp Gln Trp Cys Val Glu Lys
785 790 795 800
Gly Asp Tyr Glu Val Ile Val Ser Asp Ser Ser Ala Ala Lys Asp Gly
805 810 815
Val Ala Leu Arg Gly Lys Phe Thr Val Gly Glu Thr Tyr Trp Trp Ser
820 825 830
Gly Val

<210> 386
<211> 834
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 3 [Trichoderma reesei QM6a] 834 aa protein XP_006969529.1 GI:589115013

<400> 386
Met Ala Asp Ile Asp Val Glu Ala Ile Leu Lys Lys Leu Thr Leu Ala
1 5 10 15
Glu Lys Val Asp Leu Leu Ala Gly Ile Asp Phe Trp His Thr Lys Ala
20 25 30
Leu Pro Lys His Gly Val Pro Ser Leu Arg Phe Thr Asp Gly Pro Asn

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

```
465                 470                 475                 480
Ala Thr Lys Gln Val Pro Gly Asp Ala Phe Phe Gly Ser Ala Thr Arg
                485                 490                 495
Glu Glu Thr Gly Arg Ile Asn Leu Val Lys Gly Asn Thr Tyr Lys Phe
            500                 505                 510
Lys Ile Glu Phe Gly Ser Ala Pro Thr Tyr Thr Leu Lys Gly Asp Thr
        515                 520                 525
Ile Val Pro Gly His Gly Ser Leu Arg Val Gly Gly Cys Lys Val Ile
    530                 535                 540
Asp Asp Gln Ala Glu Ile Glu Lys Ser Val Ala Leu Ala Lys Glu His
545                 550                 555                 560
Asp Gln Val Ile Ile Cys Ala Gly Leu Asn Ala Asp Trp Glu Thr Glu
                565                 570                 575
Gly Ala Asp Arg Ala Ser Met Lys Leu Pro Gly Val Leu Asp Gln Leu
            580                 585                 590
Ile Ala Asp Val Ala Ala Ala Asn Pro Asn Thr Val Val Val Met Gln
        595                 600                 605
Thr Gly Thr Pro Glu Glu Met Pro Trp Leu Asp Ala Thr Pro Ala Val
    610                 615                 620
Ile Gln Ala Trp Tyr Gly Gly Asn Glu Thr Gly Asn Ser Ile Ala Asp
625                 630                 635                 640
Val Val Phe Gly Asp Tyr Asn Pro Ser Gly Lys Leu Ser Leu Ser Phe
                645                 650                 655
Pro Lys Arg Leu Gln Asp Asn Pro Ala Phe Leu Asn Phe Arg Thr Glu
            660                 665                 670
Ala Gly Arg Thr Leu Tyr Gly Glu Asp Val Tyr Val Gly Tyr Arg Tyr
        675                 680                 685
Tyr Glu Phe Ala Asp Lys Asp Val Asn Phe Pro Phe Gly His Gly Leu
    690                 695                 700
Ser Tyr Thr Thr Phe Ala Phe Ser Asn Leu Ser Val Ser His Lys Asp
705                 710                 715                 720
Gly Lys Leu Ser Val Ser Leu Ser Val Lys Asn Thr Gly Ser Val Pro
                725                 730                 735
Gly Ala Gln Val Ala Gln Leu Tyr Val Lys Pro Leu Gln Ala Ala Lys
            740                 745                 750
Ile Asn Arg Pro Val Lys Glu Leu Lys Gly Phe Ala Lys Val Glu Leu
        755                 760                 765
Gln Pro Gly Glu Thr Lys Ala Val Thr Ile Glu Glu Gln Glu Lys Tyr
    770                 775                 780
Val Ala Ala Tyr Phe Asp Glu Glu Arg Asp Gln Trp Cys Val Glu Lys
785                 790                 795                 800
Gly Asp Tyr Glu Val Ile Val Ser Asp Ser Ser Ala Ala Lys Asp Gly
                805                 810                 815
Val Ala Leu Arg Gly Lys Phe Thr Val Gly Glu Thr Tyr Trp Trp Ser
            820                 825                 830
Gly Val
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<210> 387
<211> 489
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 3, partial [Trichoderma reesei QM6a] 489 aa protein XP_006969215.1 GI:589114385

<400> 387

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

```
Ser Asp Val Arg Phe Thr Ser Ser Asn Leu Thr Glu Glu Gln Trp Glu
385                 390                 395                 400
Gln Ile Asp Glu Ala Asp Val Val Ile Leu Ala Thr Arg Asn Ala Arg
                405                 410                 415
Glu Ser Lys Tyr Gln Lys Glu Leu Gly Leu Glu Val Ala Lys Arg Arg
            420                 425                 430
Gly Ser Arg Pro Leu Ile Ser Ile Ala Thr Cys Ala Pro Tyr Asp Phe
        435                 440                 445
Leu Asp Asp Glu Glu Ile Arg Thr Tyr Ile Ala Val Tyr Glu Pro Thr
    450                 455                 460
Val Glu Ala Phe Ser Ala Ala Val Asp Ile Leu Phe Gly Asp Ala Gln
465                 470                 475                 480
Pro Arg Gly Lys Leu Pro Val Ala His
                485
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<210> 388
<211> 860
<212> PRT
<213> Artificial Sequence

<220>
<223> carbohydrate esterase family 4 [Trichoderma reesei QM6a] 890 aa protein XP_006967911.1 GI:589111777

<400> 388

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

```
Glu Trp Val Leu Pro Asn Ala Leu Ser Ser Asn Ile Asp Asp Arg Thr
225                 230                 235                 240
Met His Glu Ile Tyr Ala Trp Pro Phe Gly Asp Ala Val Lys Ala Gly
                245                 250                 255
Val Ala Ser Val Met Cys Ser Tyr Asn Met Val Asn Asn Ser Tyr Ala
            260                 265                 270
Cys Gly Asn Ser Lys Leu Leu Asn Gly Ile Leu Lys Asp Glu Leu Gly
        275                 280                 285
Phe Gln Gly Phe Val Met Ser Asp Trp Leu Ala Gln Arg Ser Gly Val
    290                 295                 300
Gly Ser Ala Leu Ala Gly Leu Asp Met Ser Met Pro Gly Asp Gly Leu
305                 310                 315                 320
Arg Trp Gln Asp Gly Asn Ser Leu Trp Gly Pro Asn Leu Ser Arg Ala
                325                 330                 335
Val Leu Asn Gly Ser Leu Pro Leu Glu Arg Leu Asn Asp Met Val Val
            340                 345                 350
Arg Ile Val Ala Ala Trp Tyr Gln Leu Gly Gln Asp Asp Glu Lys Leu
        355                 360                 365
Phe Asp Arg Lys Gly Pro Asn Phe Ser Ser Trp Thr Asn Asp Arg Met
    370                 375                 380
Gly Val Thr Ala Pro Ala Ser Ser Ser Pro Gln Glu Lys Val Val Val
385                 390                 395                 400
Asn Gln Phe Val Asn Val Gln Ala Asn His Ser Ile Leu Ala Arg Gln
                405                 410                 415
Ile Ala Ala Glu Gly Thr Val Leu Leu Lys Asn Glu Gly Val Leu Pro
            420                 425                 430
Leu Ser Val Asp Gly Leu Leu Gly Gly Gly Gly Gly Ser Asn Ser Thr
        435                 440                 445
Lys Arg Glu Gly Gln Val Arg Ile Gly Ile Phe Gly Glu Asp Ala Gly
    450                 455                 460
Pro Gly Lys Gly Pro Asn Tyr Cys Glu Asp Arg Ser Cys Asn Gln Gly
465                 470                 475                 480
Thr Leu Ala Ser Gly Trp Gly Ser Gly Ala Val Glu Phe Pro Tyr Leu
                485                 490                 495
Val Ser Pro Ile Glu Ala Leu Arg Lys Lys Phe Asn Lys Asp Lys Val
            500                 505                 510
Lys Leu Thr Glu His Leu Lys Asn Asp Glu Leu Asp Thr Gly Val Ile
        515                 520                 525
Lys Ser Gln Asp Ile Cys Met Val Phe Ile Asn Ser Asp Ser Gly Glu
    530                 535                 540
Gly Tyr Arg Ala Trp Glu Gly Val Arg Gly Asp Arg Asn Asp Leu Lys
545                 550                 555                 560
Pro Gln Lys Gly Gly Val Gly Leu Val Thr His Val Gly Leu Asn Cys
                565                 570                 575
Gly Asn Gly Ser Gly Thr Thr Ile Val Val Leu His Ser Val Gly Pro
            580                 585                 590
Val Val Val Asp Pro Trp Ile Asp Met Pro Gly Ile Lys Ala Leu Ile
        595                 600                 605
Ser Ala Asn Leu Pro Gly Gln Glu Ser Gly Asn Ala Leu Ala Ser Ile
    610                 615                 620
Leu Phe Gly Glu Glu Asn Pro Ser Gly Lys Leu Pro Tyr Thr Val Gly
625                 630                 635                 640
Lys Ser Leu Ser Asp Tyr Gly Pro Gly Gly Gln Val Met Tyr Leu Pro
                645                 650                 655
```

```
Asn Gly Ala Val Pro Gln Gln Asp Phe Ser Glu Gly Leu Tyr Ile Asp
            660                 665                 670
Tyr Arg His Phe Asp Lys Phe Asn Ile Glu Pro Arg Tyr Glu Phe Gly
        675                 680                 685
Phe Gly Leu Ser Tyr Thr Asn Phe Asp Tyr Lys Asn Leu Lys Ile Thr
    690                 695                 700
Glu Thr Lys Pro Arg Ser Pro Leu Pro Asp Glu Arg Pro Ala Ala Glu
705                 710                 715                 720
Val Glu Pro Pro Ser Phe Asp Thr Thr Ile Pro Gln Ala Glu Glu Ala
                725                 730                 735
Leu Phe Pro Ser Gly Ile Arg Arg Leu Lys Lys Tyr Val Tyr Pro Tyr
            740                 745                 750
Ile Glu Ser Val Lys Asp Ile Lys Glu Gly Gln Tyr Ser Tyr Pro Asp
        755                 760                 765
Gly Tyr Asp Lys Glu Gln Pro Leu Ser Gly Ala Gly Gly Gly Glu Gly
    770                 775                 780
Gly Asn Pro Ser Leu Trp Asp Ser His Val Ile Val Ser Val Glu Val
785                 790                 795                 800
Thr Asn Thr Gly Lys Leu Gly Gly Lys Ala Lys Gly Glu Thr Lys Thr
                805                 810                 815
Val Glu Phe Ser Leu Thr Arg Arg Asp Leu Ser Tyr Trp Asp Val Glu
            820                 825                 830
Arg Gln Asn Trp Val Ile Pro Glu Gly Glu Tyr Thr Phe Ala Val Gly
        835                 840                 845
Glu Ser Ser Arg Asp Leu Arg Val Ser Gly Thr Trp
    850                 855                 860


<210> 389
<211> 932
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 3 [Trichoderma reesei
      QM6a] 932 aa protein XP_006966911.1 GI:589109777

<400> 389
Met Ala Asn Ser Ile Gly Gly Ser Ser Ala Asp Lys Phe Asp Leu Asp
 1               5                  10                  15
Pro Leu Trp Gln Asn Leu Asp Trp Ala Ile Gly Gln Met Met Leu Met
            20                  25                  30
Gly Trp Asp Gly Thr Gln Val Thr Pro Gln Ile Arg Ser Leu Ile Glu
        35                  40                  45
Asp His His Leu Gly Ser Ile Ile Leu Thr Ala Lys Asn Leu Lys Ser
    50                  55                  60
Ala His His Thr Ala Leu Leu Val Gln Glu Leu Gln Met Ile Ala Lys
65                  70                  75                  80
Asn Ser Gly His Pro Gln Pro Leu Leu Ile Ala Val Asp Gln Glu Asn
                85                  90                  95
Gly Gly Val Asn Ser Leu Phe Asp Glu Asp Phe Val Cys Gln Phe Pro
            100                 105                 110
Ser Ala Met Ala Ile Ala Ala Thr Gly Ser Leu Glu Leu Ser Tyr Glu
        115                 120                 125
```

```
Val Asn Lys Ala Thr Ala Thr Glu Ile Ser Ala Cys Gly Val Asn Leu
    130                 135                 140
Met Leu Gly Pro Val Leu Asp Val Leu Asn Asn Ala Arg Tyr Gln Val
145                 150                 155                 160
Ile Gly Val Arg Ala Ser Gly Asp Asp Pro Gln Glu Val Ser Gln Tyr
                165                 170                 175
Gly Leu Ala Ala Leu Ser Gly Ile Arg Asp Ala Gly Val Ala Ser Cys
            180                 185                 190
Gly Lys His Phe Pro Ser Tyr Gly Asn Leu Asp Phe Leu Gly Ser Asn
        195                 200                 205
Leu Asp Val Pro Ile Ile Thr Gln Thr Leu Glu Glu Leu Ser Leu Ser
    210                 215                 220
Ala Leu Val Pro Phe Arg Asn Ala Ile Ala Ser Gly Lys Leu Asp Ala
225                 230                 235                 240
Met Phe Ile Gly Gly Cys Gly Ile Ser Asn Pro Ser Met Asn Val Ser
                245                 250                 255
His Ala Cys Leu Ser Asp Gln Val Val Asp Asp Leu Leu Arg Asn Glu
            260                 265                 270
Leu Gly Phe Lys Gly Val Ala Ile Ser Glu Cys Leu Glu Met Glu Ala
        275                 280                 285
Leu Ser Gln Asp Leu Gly Val Gln Asn Gly Val Val Met Ala Val Glu
    290                 295                 300
Ala Gly Cys Asp Ile Val Leu Leu Cys Arg Ala Tyr Asp Val Gln Leu
305                 310                 315                 320
Glu Ala Ile Lys Gly Leu Lys Leu Gly Tyr Glu Asn Gly Ile Ile Thr
                325                 330                 335
Lys Glu Arg Ile Phe Thr Ser Leu Lys Arg Ile Phe His Leu Lys Ser
            340                 345                 350
Thr Cys Thr Ser Trp Ala Lys Ala Leu Asn Pro Pro Gly Ile Asn Leu
        355                 360                 365
Leu Ser Gln Ile Arg Pro Ser His Leu Ala Leu Ser Arg Arg Ala Tyr
    370                 375                 380
Asp Asp Ser Ile Thr Ile Val Arg Asp Lys Glu Lys Leu Leu Pro Leu
385                 390                 395                 400
Ser Leu Ser Met His Pro Gly Glu Glu Leu Leu Leu Leu Thr Pro Leu
                405                 410                 415
Val Lys Pro Leu Pro Ala Ser Ser Leu Thr Lys Ser Leu Leu Glu Ser
            420                 425                 430
Lys Asn Asp Pro Ser Leu Val Ser Thr Glu His Asp Arg Trp Asn His
        435                 440                 445
Gln Ile Arg Glu Arg Ser Ala Ile Met Ser Gly Glu Gly Val Phe Arg
    450                 455                 460
Glu Phe Gly Lys Thr Leu Ala Arg Tyr Arg Asn Glu Lys Leu Leu His
465                 470                 475                 480
Thr Ser Tyr Thr Ala Asn Gly Val Arg Pro Val His Glu Asn Leu Ile
                485                 490                 495
Asn Arg Ala Ser Cys Ile Ile Ile Phe Thr Ala Asp Ala Asn Arg Asn
            500                 505                 510
Leu Tyr Gln Ala Gly Phe Thr Lys His Val Asp Met Met Cys Ser Met
        515                 520                 525
Leu Arg Ser Arg Gly Gln Lys Lys Gln Leu Ile Val Val Ala Val Ser
    530                 535                 540
Ser Pro Tyr Asp Phe Ala Met Asp Lys Ser Ile Gly Thr Tyr Ile Cys
545                 550                 555                 560
```

```
Thr Tyr Asp Phe Thr Glu Asn Ala Met Ala Ala Leu Val Arg Ala Leu
                565                 570                 575
Val Gly Asp Ser Asn Pro Val Gly Thr Met Pro Gly Thr Leu Arg Lys
            580                 585                 590
Ser Lys Lys Val Leu Lys Ser Arg Gln His Trp Leu Val Glu Glu Phe
        595                 600                 605
Asp Ser Ser Arg Asp Arg Lys Gly Leu Asn Asp Leu Ile Arg Ala Val
    610                 615                 620
His Arg Ala Ser Asp Gln Asp Phe Arg Tyr Leu Gln Thr Ala Thr Ala
625                 630                 635                 640
Asp Thr Phe Leu Leu Ala Asn Gln Asn Ile Lys Glu Thr His Phe Val
                645                 650                 655
Val Arg Asn Ser Ser Thr Gln Ala Leu Tyr Gly Phe Ala Ala Thr Tyr
            660                 665                 670
Phe Val Gln Asn Val Gly Ile Leu Gly Ala Leu Ile Val Asp Pro Thr
        675                 680                 685
Lys Arg Asn Met Ser Ile Gly Arg Ser Leu His Arg Arg Ala Ile Lys
    690                 695                 700
Ser Leu Thr Gln Gln Arg Gly Ile Lys Lys Val Gln Leu Gly Ser Cys
705                 710                 715                 720
Phe Pro Ala Leu Phe Leu Gly Ile Pro Leu Asp Ile Glu Val Thr Thr
                725                 730                 735
Thr Lys Glu Trp Phe Ser Asn Ser Gly Trp Asp Thr Gln Phe Pro Arg
            740                 745                 750
Arg Leu Thr Asn Met Val Ile Gln Asp Leu Ser Ala Trp Tyr Ala Pro
        755                 760                 765
Glu Gly Leu Ser Gln Ser Ile Gln Arg Ala Asn Ile Ser Phe Asp Leu
    770                 775                 780
Ile Tyr Gly Val Glu Ser Gly Asp Thr Val Met His His Val Arg Thr
785                 790                 795                 800
His Ala Asn Pro Glu Val Leu Glu Leu Tyr Arg Thr Ala Leu Glu Glu
                805                 810                 815
Ser Lys Ala Cys Gly Ile Val Arg Ala Lys Asp Ala Ala Gly Asn Leu
            820                 825                 830
Leu Gly Thr Ile Ile Ile Cys Arg Pro Asn Ser Pro Leu Ala Arg Tyr
        835                 840                 845
Val Pro Pro Leu Val Ser Leu Gly Gln Asp Ile Gly Gly Leu Leu Ala
    850                 855                 860
Pro Ile Val Pro Pro Ala Pro Leu Ser Thr Leu Val Leu Gln Gly Leu
865                 870                 875                 880
Ala Leu Met Gly Val Arg Gln Asn Lys Gly His Lys Ala Thr Lys Ser
                885                 890                 895
Val Leu Ser Trp Val Val Asp Asp Ala Tyr Glu Pro Leu Val Ala Met
            900                 905                 910
Gly Phe Asp Val Leu Gln Ala Phe Glu Glu Ile Thr Asn Ser Pro Glu
        915                 920                 925
Thr Phe Gln Thr
    930
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<210> 390
<211> 874
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 3 [Trichoderma reesei QM6a] 874 aa protein XP_006965281.1 GI:589106517

<400> 390

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

```
Val Asn Tyr Gly Val Asp Val Arg Ala Asn His Ala Asn His Ile Arg
385                 390                 395                 400
Glu Val Gly Ala Lys Gly Thr Val Ile Phe Lys Asn Asn Gly Ile Leu
                405                 410                 415
Pro Leu Lys Lys Pro Lys Phe Leu Thr Val Ile Gly Glu Asp Ala Gly
            420                 425                 430
Gly Asn Pro Ala Gly Pro Asn Gly Cys Gly Asp Arg Gly Cys Asp Asp
        435                 440                 445
Gly Thr Leu Ala Met Glu Trp Gly Ser Gly Thr Thr Asn Phe Pro Tyr
    450                 455                 460
Leu Val Thr Pro Asp Ala Ala Leu Gln Ser Gln Ala Leu Gln Asp Gly
465                 470                 475                 480
Thr Arg Tyr Glu Ser Ile Leu Ser Asn Tyr Ala Ile Ser Gln Thr Gln
                485                 490                 495
Ala Leu Val Ser Gln Pro Asp Ala Ile Ala Ile Val Phe Ala Asn Ser
            500                 505                 510
Asp Ser Gly Glu Gly Tyr Ile Asn Val Asp Gly Asn Glu Gly Asp Arg
        515                 520                 525
Lys Asn Leu Thr Leu Trp Lys Asn Gly Asp Asp Leu Ile Lys Thr Val
    530                 535                 540
Ala Ala Val Asn Pro Lys Thr Ile Val Val Ile His Ser Thr Gly Pro
545                 550                 555                 560
Val Ile Leu Lys Asp Tyr Ala Asn His Pro Asn Ile Ser Ala Ile Leu
                565                 570                 575
Trp Ala Gly Ala Pro Gly Gln Glu Ser Gly Asn Ser Leu Val Asp Ile
            580                 585                 590
Leu Tyr Gly Lys Gln Ser Pro Gly Arg Thr Pro Phe Thr Trp Gly Pro
        595                 600                 605
Ser Leu Glu Ser Tyr Gly Val Ser Val Met Thr Thr Pro Asn Asn Gly
    610                 615                 620
Asn Gly Ala Pro Gln Asp Asn Phe Asn Glu Gly Ala Phe Ile Asp Tyr
625                 630                 635                 640
Arg Tyr Phe Asp Lys Val Ala Pro Gly Lys Pro Arg Ser Ser Asp Lys
                645                 650                 655
Ala Pro Thr Tyr Glu Phe Gly Phe Gly Leu Ser Trp Ser Thr Phe Lys
            660                 665                 670
Phe Ser Asn Leu His Ile Gln Lys Asn Asn Val Gly Pro Met Ser Pro
        675                 680                 685
Pro Asn Gly Lys Thr Ile Ala Ala Pro Ser Leu Gly Ser Phe Ser Lys
    690                 695                 700
Asn Leu Lys Asp Tyr Gly Phe Pro Lys Asn Val Arg Arg Ile Lys Glu
705                 710                 715                 720
Phe Ile Tyr Pro Tyr Leu Ser Thr Thr Thr Ser Gly Lys Glu Ala Ser
                725                 730                 735
Gly Asp Ala His Tyr Gly Gln Thr Ala Lys Glu Phe Leu Pro Ala Gly
            740                 745                 750
Ala Leu Asp Gly Ser Pro Gln Pro Arg Ser Ala Ala Ser Gly Glu Pro
        755                 760                 765
Gly Gly Asn Arg Gln Leu Tyr Asp Ile Leu Tyr Thr Val Thr Ala Thr
    770                 775                 780
Ile Thr Asn Thr Gly Ser Val Met Asp Asp Ala Val Pro Gln Leu Tyr
785                 790                 795                 800
Leu Ser His Gly Gly Pro Asn Glu Pro Pro Lys Val Leu Arg Gly Phe
                805                 810                 815
```

Asp Arg Ile Glu Arg Ile Ala Pro Gly Gln Ser Val Thr Phe Lys Ala
820 825 830
Asp Leu Thr Arg Arg Asp Leu Ser Asn Trp Asp Thr Lys Lys Gln Gln
835 840 845
Trp Val Ile Thr Asp Tyr Pro Lys Thr Val Tyr Val Gly Ser Ser Ser
850 855 860
Arg Asp Leu Pro Leu Ser Ala Arg Leu Pro
865 870

<210> 391
<211> 814
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 3 [Trichoderma reesei QM6a] 814 aa protein XP_006964430.1 GI:589104815

<400> 391
Met Thr Leu Ala Glu Lys Thr Asn Ile Thr Ala Gly Thr Gly Ile Tyr
1 5 10 15
Met Gly Glu Arg Cys Ala Gly Asn Thr Gly Ser Ala Phe Arg Val Ser
20 25 30
Phe Pro Gln Leu Cys Leu Asn Asp Ser Pro Ala Gly Val Arg His Ala
35 40 45
Asp Asn Val Thr Ala Phe Pro Asp Gly Ile Thr Val Gly Ala Thr Phe
50 55 60
Asp Lys Ala Leu Met Tyr Lys Arg Gly Val Ala Ile Gly Lys Glu Asn
65 70 75 80
Arg Gly Lys Gly Val Asn Val Trp Leu Gly Pro Thr Val Gly Pro Ile
85 90 95
Gly Arg Lys Pro Lys Gly Gly Arg Asn Trp Glu Gly Phe Gly Ala Asp
100 105 110
Pro Val Leu Gln Ala Val Gly Ala Arg Glu Thr Ile Lys Gly Val Gln
115 120 125
Glu Gln Gly Val Ile Ala Thr Ile Lys His Phe Ile Gly Asn Glu Gln
130 135 140
Glu Met Tyr Arg Met Tyr Asn Pro Phe Gln Tyr Ala Tyr Ser Ser Asn
145 150 155 160
Ile Asp Asp Arg Thr Leu His Glu Val Tyr Ala Trp Pro Phe Ala Glu
165 170 175
Gly Ile Arg Ala Gly Val Gly Ala Val Met Met Ala Tyr Asn Ala Val
180 185 190
Asn Gly Thr Ala Cys Ser Gln His Pro Tyr Leu Met Ser Ala Leu Leu
195 200 205
Lys Asp Glu Met Gly Phe Gln Gly Phe Ile Met Thr Asp Trp Leu Ala
210 215 220
His Met Ser Gly Val Ala Ser Ala Ile Ala Gly Leu Asp Met Asp Met
225 230 235 240
Pro Gly Asp Val Gln Ile Pro Phe Phe Gly Gly Ser Tyr Trp Met Tyr
245 250 255
Glu Leu Thr Arg Ser Ala Leu Asn Gly Ser Val Pro Met Asp Arg Ile
260 265 270

```
Asn Asp Ala Ala Thr Arg Ile Ala Ala Ala Trp Tyr Lys Met Gly Gln
        275                 280                 285
Asp Lys Gly Phe Pro Ala Thr Asn Phe Asp Thr Asn Ser Arg Ala Ala
    290                 295                 300
Phe Asn Pro Leu Tyr Pro Ala Ala Leu Pro Leu Ser Pro Phe Gly Ile
305                 310                 315                 320
Thr Asn Glu Phe Val Pro Val Gln Asp Asp His Asp Val Ile Ala Arg
                325                 330                 335
Gln Ile Ser Gln Glu Ala Ile Thr Leu Leu Lys Asn Asp Gly Asp Ile
            340                 345                 350
Leu Pro Leu Ser Pro Ser Gln His Leu Lys Val Phe Gly Thr Asp Ala
        355                 360                 365
Gln Lys Asn Pro Asp Gly Ile Asn Ser Cys Thr Asp Arg Asn Cys Asn
    370                 375                 380
Lys Gly Thr Leu Gly Gln Gly Trp Gly Ser Gly Thr Val Asp Tyr Pro
385                 390                 395                 400
Tyr Leu Asp Asp Pro Ile Ser Ala Ile Thr Ala Glu Ala Asp Asn Val
                405                 410                 415
Thr Phe Tyr Asn Thr Asp Lys Phe Pro Ser Val Gly Glu Val Ser Asp
            420                 425                 430
Ser Asp Val Ala Ile Val Phe Val Asn Ser Asp Ala Gly Glu Asn Thr
        435                 440                 445
Tyr Thr Val Glu Gly Asn His Gly Asp Arg Asp Lys Ser Gly Leu Tyr
    450                 455                 460
Ala Trp His Asp Gly Asp Lys Leu Val Gln Asp Ala Ala Ser Lys Phe
465                 470                 475                 480
Ser Asn Val Ile Val Val Ile His Thr Val Gly Pro Leu Ile Leu Glu
                485                 490                 495
Lys Trp Ile Asp Leu Pro Ser Val Lys Ala Val Leu Val Ala His Leu
            500                 505                 510
Pro Gly Gln Glu Ala Gly Lys Ser Leu Thr Asn Val Leu Phe Gly His
        515                 520                 525
Ala Ser Pro Cys Gly His Leu Pro Tyr Ser Ile Thr Lys Glu Glu Asp
    530                 535                 540
Asp Leu Pro Lys Ser Val Thr Thr Leu Ile Asp Ser Glu Phe Leu Asn
545                 550                 555                 560
Gln Pro Gln Asp Thr Tyr Thr Glu Gly Leu Tyr Ile Asp Tyr Arg Trp
                565                 570                 575
Leu Asn Lys Asn Lys Thr Lys Pro Arg Tyr Ala Phe Gly His Gly Leu
            580                 585                 590
Ser Tyr Thr Asn Phe Thr Phe Lys Ala Ala Ser Ile Lys Gln Val Ala
        595                 600                 605
Arg Leu Ser Ala Tyr Pro Pro Ala Arg Pro Ala Lys Gly Ser Thr Pro
    610                 615                 620
Asp Phe Ala Gln Ser Ile Pro Ser Ala Ser Glu Ala Val Ala Pro Ser
625                 630                 635                 640
Gly Phe Gly Lys Ile Pro Arg Tyr Ile Tyr Ser Trp Leu Ser Gln Gly
                645                 650                 655
Asp Ala Asn Arg Ala Ile Ser Asp Gly Lys Thr Gly Lys Tyr Pro Tyr
            660                 665                 670
Pro Asp Gly Tyr Ser Thr Thr Gln Lys Pro Gly Ala Arg Ala Gly Gly
        675                 680                 685
Gly Glu Gly Gly Asn Pro Ala Leu Trp Asp Val Ala Tyr Ser Leu Thr
    690                 695                 700
```

```
Val Thr Val Gln Asn Thr Gly Asp Glu Tyr Ala Gly Lys Ala Ser Val
705                 710                 715                 720
Gln Ala Tyr Leu Gln Phe Pro Asp Asp Ile Asp Tyr Asp Thr Pro Ile
                725                 730                 735
Ile Gln Leu Arg Asp Phe Glu Lys Thr Lys Glu Leu Lys Pro Gly Glu
            740                 745                 750
Thr Thr Thr Val Thr Leu Thr Leu Thr Arg Lys Asp Val Ser Val Trp
        755                 760                 765
Asp Val Val Ala Gln Asp Trp Lys Val Pro Ala Val Asp Gly Gly Tyr
    770                 775                 780
Lys Val Trp Ile Gly Asp Ala Ser Asp Ser Leu Ser Ile Val Cys His
785                 790                 795                 800
Thr Asp Thr Leu Glu Cys Glu Thr Gly Val Val Gly Pro Val
                805                 810
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<210> 392
<211> 744
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 3 [Trichoderma reesei QM6a] 744 aa protein XP_006964076.1 GI:589104107

<400> 392

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

```
Gln Ala Asn Val Ala Ser Val Met Cys Ser Tyr Asn Lys Val Asn Thr
225                 230                 235                 240
Thr Trp Ala Cys Glu Asp Gln Tyr Thr Leu Gln Thr Val Leu Lys Asp
                245                 250                 255
Gln Leu Gly Phe Pro Gly Tyr Val Met Thr Asp Trp Asn Ala Gln His
            260                 265                 270
Thr Thr Val Gln Ser Ala Asn Ser Gly Leu Asp Met Ser Met Pro Gly
        275                 280                 285
Thr Asp Phe Asn Gly Asn Asn Arg Leu Trp Gly Pro Ala Leu Thr Asn
    290                 295                 300
Ala Val Asn Ser Asn Gln Val Pro Thr Ser Arg Val Asp Asp Met Val
305                 310                 315                 320
Thr Arg Ile Leu Ala Ala Trp Tyr Leu Thr Gly Gln Asp Gln Ala Gly
                325                 330                 335
Tyr Pro Ser Phe Asn Ile Ser Arg Asn Val Gln Gly Asn His Lys Thr
            340                 345                 350
Asn Val Arg Ala Ile Ala Arg Asp Gly Ile Val Leu Leu Lys Asn Asp
        355                 360                 365
Ala Asn Ile Leu Pro Leu Lys Lys Pro Ala Ser Ile Ala Val Val Gly
    370                 375                 380
Ser Ala Ala Ile Ile Gly Asn His Ala Arg Asn Ser Pro Ser Cys Asn
385                 390                 395                 400
Asp Lys Gly Cys Asp Asp Gly Ala Leu Gly Met Gly Trp Gly Ser Gly
                405                 410                 415
Ala Val Asn Tyr Pro Tyr Phe Val Ala Pro Tyr Asp Ala Ile Asn Thr
            420                 425                 430
Arg Ala Ser Ser Gln Gly Thr Gln Val Thr Leu Ser Asn Thr Asp Asn
        435                 440                 445
Thr Ser Ser Gly Ala Ser Ala Ala Arg Gly Lys Asp Val Ala Ile Val
    450                 455                 460
Phe Ile Thr Ala Asp Ser Gly Glu Gly Tyr Ile Thr Val Glu Gly Asn
465                 470                 475                 480
Ala Gly Asp Arg Asn Asn Leu Asp Pro Trp His Asn Gly Asn Ala Leu
                485                 490                 495
Val Gln Ala Val Ala Gly Ala Asn Ser Asn Val Ile Val Val Val His
            500                 505                 510
Ser Val Gly Ala Ile Ile Leu Glu Gln Ile Leu Ala Leu Pro Gln Val
        515                 520                 525
Lys Ala Val Val Trp Ala Gly Leu Pro Ser Gln Glu Ser Gly Asn Ala
    530                 535                 540
Leu Val Asp Val Leu Trp Gly Asp Val Ser Pro Ser Gly Lys Leu Val
545                 550                 555                 560
Tyr Thr Ile Ala Lys Ser Pro Asn Asp Tyr Asn Thr Arg Ile Val Ser
                565                 570                 575
Gly Gly Ser Asp Ser Phe Ser Glu Gly Leu Phe Ile Asp Tyr Lys His
            580                 585                 590
Phe Asp Asp Ala Asn Ile Thr Pro Arg Tyr Glu Phe Gly Tyr Gly Leu
        595                 600                 605
Ser Tyr Thr Lys Phe Asn Tyr Ser Arg Leu Ser Val Leu Ser Thr Ala
    610                 615                 620
Lys Ser Gly Pro Ala Thr Gly Ala Val Val Pro Gly Gly Pro Ser Asp
625                 630                 635                 640
Leu Phe Gln Asn Val Ala Thr Val Thr Val Asp Ile Ala Asn Ser Gly
                645                 650                 655
```

```
Gln Val Thr Gly Ala Glu Val Ala Gln Leu Tyr Ile Thr Tyr Pro Ser
            660                 665                 670
Ser Ala Pro Arg Thr Pro Pro Lys Gln Leu Arg Gly Phe Ala Lys Leu
        675                 680                 685
Asn Leu Thr Pro Gly Gln Ser Gly Thr Ala Thr Phe Asn Ile Arg Arg
    690                 695                 700
Arg Asp Leu Ser Tyr Trp Asp Thr Ala Ser Gln Lys Trp Val Val Pro
705                 710                 715                 720
Ser Gly Ser Phe Gly Ile Ser Val Gly Ala Ser Ser Arg Asp Ile Arg
                725                 730                 735
Leu Thr Ser Thr Leu Ser Val Ala
            740
```

<210> 393
<211> 700
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 3 [Trichoderma reesei QM6a] 700 aa protein XP_006964050.1 GI:589104055

<400> 393

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

```
Ile Thr His Glu Val Gly Ala Tyr Ala His Gln Met Leu Pro Val Ile
                245                 250                 255
Asp Ala Met Ile Ser Asn Ala Val Ile His Phe Tyr Asn Asp Pro Ile
            260                 265                 270
Asp Val Lys Asp Arg Lys Leu Leu Gly Ser Glu Asn Val Ser Ser Thr
        275                 280                 285
Ser Phe Gln Leu Met Asp Tyr Asn Asn Ile Pro Thr Leu Asn Lys Ala
    290                 295                 300
Met Phe Trp Gly Thr Leu Val Gly Glu Phe Ile Pro Thr Ala Thr Gly
305                 310                 315                 320
Ile Trp Glu Phe Gly Leu Ser Val Phe Gly Thr Ala Asp Leu Tyr Ile
                325                 330                 335
Asp Asn Glu Leu Val Ile Glu Asn Thr Thr His Gln Thr Arg Gly Thr
            340                 345                 350
Ala Phe Phe Gly Lys Gly Thr Thr Glu Lys Val Ala Thr Arg Arg Met
        355                 360                 365
Val Ala Gly Ser Thr Tyr Lys Leu Arg Leu Glu Phe Gly Ser Ala Asn
    370                 375                 380
Thr Thr Lys Met Glu Thr Thr Gly Val Val Asn Phe Gly Gly Gly Ala
385                 390                 395                 400
Val His Leu Gly Ala Cys Leu Lys Val Asp Pro Gln Glu Met Ile Ala
                405                 410                 415
Arg Ala Val Lys Ala Ala Ala Asp Ala Asp Tyr Thr Ile Ile Cys Thr
            420                 425                 430
Gly Leu Ser Gly Glu Trp Glu Ser Glu Gly Phe Asp Arg Pro His Met
        435                 440                 445
Asp Leu Pro Pro Gly Val Asp Thr Met Ile Ser Gln Val Leu Asp Ala
    450                 455                 460
Ala Pro Asn Ala Val Val Val Asn Gln Ser Gly Thr Pro Val Thr Met
465                 470                 475                 480
Ser Trp Ala His Lys Ala Lys Ala Ile Val Gln Ala Trp Tyr Gly Gly
                485                 490                 495
Asn Glu Thr Gly His Gly Ile Ser Asp Val Leu Phe Gly Asn Val Asn
            500                 505                 510
Pro Ser Gly Lys Leu Ser Leu Ser Trp Pro Val Asp Val Lys His Asn
        515                 520                 525
Pro Ala Tyr Leu Asn Tyr Ala Ser Val Gly Gly Arg Val Leu Tyr Gly
    530                 535                 540
Glu Asp Val Tyr Val Gly Tyr Lys Phe Tyr Asp Lys Thr Glu Arg Glu
545                 550                 555                 560
Val Leu Phe Pro Phe Gly His Gly Leu Ser Tyr Ala Thr Phe Lys Leu
                565                 570                 575
Pro Asp Ser Thr Val Arg Thr Val Pro Glu Thr Phe His Pro Asp Gln
            580                 585                 590
Pro Thr Val Ala Ile Val Lys Ile Lys Asn Thr Ser Ser Val Pro Gly
        595                 600                 605
Ala Gln Val Leu Gln Leu Tyr Ile Ser Ala Pro Asn Ser Pro Thr His
    610                 615                 620
Arg Pro Val Lys Glu Leu His Gly Phe Glu Lys Val Tyr Leu Glu Ala
625                 630                 635                 640
Gly Glu Glu Lys Glu Val Gln Ile Pro Ile Asp Gln Tyr Ala Thr Ser
                645                 650                 655
Phe Trp Asp Glu Ile Glu Ser Met Trp Lys Ser Glu Arg Gly Ile Tyr
            660                 665                 670
```

Asp Val Leu Val Gly Phe Ser Ser Gln Glu Ile Ser Gly Lys Gly Lys
        675                 680                 685
Leu Ile Val Pro Glu Thr Arg Phe Trp Met Gly Leu
    690                 695                 700


<210> 394
<211> 781
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 3 [Trichoderma reesei
      QM6a] 781 aa protein XP_006963375.1 GI:589102705

<400> 394
Met Val Ala Val Lys Gln Ile Ala Leu Leu Ala Gly Leu Ala His Trp
 1               5                  10                  15
Ala Asp Ala Ala Glu Lys Val Ile Thr Asn Asp Thr His Phe Tyr Gly
            20                  25                  30
Gln Ser Pro Pro Val Tyr Pro Ser Pro Glu Met Thr Gly Gly Asn Glu
        35                  40                  45
Trp Glu Ala Ala Tyr Gln Lys Ala Lys Ala Phe Val Gly Gln Leu Thr
    50                  55                  60
Leu Glu Glu Lys Val Asn Leu Thr Ala Gly Val Pro Pro Asn Thr Thr
65                  70                  75                  80
Cys Ser Gly Val Ile Pro Ala Ile Glu Arg Leu Lys Phe Pro Gly Met
                85                  90                  95
Cys Leu Ser Asp Ala Gly Asn Gly Leu Arg Asn Thr Asp Phe Val Ser
            100                 105                 110
Gly Phe Pro Ser Gly Ile His Val Gly Ala Ser Trp Ser Lys Asp Leu
        115                 120                 125
Ala Phe Arg Arg Ala Val Ala Met Gly Ala Glu Phe Arg Lys Lys Gly
    130                 135                 140
Val Asn Val Leu Leu Gly Pro Val Val Gly Pro Ala Gly Arg Thr Val
145                 150                 155                 160
Arg Gly Gly Arg Asn Trp Glu Gly Phe Ser Val Asp Pro Trp Leu Ala
                165                 170                 175
Gly Val Leu Val Ser Glu Thr Val Ser Gly Ile Gln Glu Gln Gly Val
            180                 185                 190
Ile Thr Ser Thr Lys His Tyr Ile Leu Asn Glu Gln Glu Thr His Arg
        195                 200                 205
Met Pro Glu Ala Asn Val Ser Ala Val Ser Ser Asn Ile Asp Asp Lys
    210                 215                 220
Thr Met His Glu Tyr Tyr Leu Trp Pro Phe Gln Asp Ala Val Arg Ala
225                 230                 235                 240
Gly Ser Gly Asn Ile Met Cys Ser Tyr Gln Arg Ile Asn Asn Ser Tyr
                245                 250                 255
Gly Cys Ser Asn Ser Lys Thr Leu Asn Gly Leu Leu Lys Thr Glu Leu
            260                 265                 270
Gly Phe Gln Gly Phe Val Val Ser Asp Trp Ser Ala Gln His Ala Gly
        275                 280                 285
Val Ala Ser Ala Glu Ala Gly Met Asp Met Ala Met Pro Gly Pro Ala
    290                 295                 300

```
Glu Phe Trp Gly Glu His Leu Val Glu Ala Val Lys Asn Gly Ser Leu
305                 310                 315                 320
Pro Glu Ser Arg Ile Thr Asp Met Ala Thr Arg Ile Ile Ala Thr Trp
                325                 330                 335
Tyr Gln Phe Asp Gln Asp Asn Gly Ile Pro Lys Pro Gly Ile Gly Met
            340                 345                 350
Pro Ser Asn Val Leu Asp Ser His Glu Ile Val Asp Ala Arg Asp Pro
        355                 360                 365
Ala Ala Val Pro Val Leu Leu Asn Gly Ala Ile Glu Gly His Val Leu
    370                 375                 380
Val Lys Asn Thr Lys Asn Thr Leu Pro Leu Lys Lys Pro Arg Lys Leu
385                 390                 395                 400
Ser Leu Phe Gly Tyr Ser Ala Thr Thr Pro Asp Phe Phe Ser Pro Ser
                405                 410                 415
Arg Asp Glu Gln Leu Ser Asp Ser Trp Ile Phe Gly Lys Glu Ala Tyr
            420                 425                 430
Asn Ser Asn Tyr Leu Ser Pro Asp Gly Phe Ala Thr Phe Gly Arg Asn
        435                 440                 445
Gly Thr Thr Phe Gly Gly Cys Gly Ser Gly Ala Ile Thr Pro Ala Leu
    450                 455                 460
Ala Ile Ser Pro Phe Glu Ala Leu Lys Trp Arg Ala Ala Gln Asp Gly
465                 470                 475                 480
Thr Ala Thr Phe Asn Asn Phe Leu Ser Asp Lys Pro Asp Val Asp Pro
                485                 490                 495
Thr Ser Asp Ala Cys Ile Val Phe Gly Asn Ala Tyr Ala Cys Glu Gly
            500                 505                 510
Asn Asp Arg Pro Ala Ile Gln Asp Asp Tyr Thr Asp Asp Leu Ile Lys
        515                 520                 525
Ala Val Ala Ser Gln Cys Asn Lys Thr Ile Val Val Leu His Asn Ala
    530                 535                 540
Gly Ile Arg Leu Val Asp Gly Phe Val Asp His Pro Asn Ile Thr Ala
545                 550                 555                 560
Val Ile Phe Ala His Leu Pro Gly Gln Glu Ser Gly Pro Ala Leu Thr
                565                 570                 575
Ser Leu Leu Tyr Gly Glu Thr Ser Pro Ser Gly Arg Leu Pro Tyr Thr
            580                 585                 590
Val Ala Lys Asn Asp Thr Asp Tyr Gly Val Val Leu Asp Pro Ala Gln
        595                 600                 605
Ala Thr Gly Glu Phe Ala Tyr Phe Pro Gln Ala Asp Phe Lys Glu Gly
    610                 615                 620
Val Tyr Leu Asp Tyr Arg Tyr Phe Asp Lys Glu Gly Ile Glu Pro Arg
625                 630                 635                 640
Tyr Glu Phe Gly Phe Gly Leu Ser Tyr Thr Thr Phe Ala Tyr Leu Asn
                645                 650                 655
Leu Ser Val Asp His Val Ser Gly Ala Asn Thr Tyr Pro Trp Pro Gly
            660                 665                 670
Gly Pro Ile Val Ser Gly Gly Gln Thr Asp Leu Trp Asp Ala Ile Ala
        675                 680                 685
Thr Val Ser Val Asp Ile Arg Asn Thr Gly Ser Val Ala Ser Tyr Glu
    690                 695                 700
Val Ala Gln Leu Tyr Ile Gly Ile Pro Gly Ala Pro Ala Lys Gln Leu
705                 710                 715                 720
Arg Gly Phe Glu Lys Pro Phe Leu Arg Pro Asn Glu Ser Gln Ser Val
                725                 730                 735
```

```
Thr Phe His Leu Thr Arg Arg Asp Leu Ser Val Trp Ser Val Glu Arg
            740                 745                 750
Gln Lys Trp Gln Leu Gln Gln Gly Thr Tyr Lys Ile Tyr Val Gly Ser
        755                 760                 765
Ser Ser Arg Arg Leu His Val Asn Gly Thr Leu Asp Ile
    770                 775                 780


<210> 395
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> cell wall protein [Trichoderma reesei QM6a] 436 aa
      protein XP_006963339.1 GI:589102633

<400> 395
Met Leu Ala Cys Ile Thr Arg Ala Thr Leu Pro Thr Val Val Ala Ala
 1               5                  10                  15
Thr Pro Ser His His His His His Ala His Arg His Ala Lys Lys His
            20                  25                  30
Ala Ala Ala Arg Val Glu Lys Arg Ala Pro Asp Val Val Thr Glu Val
        35                  40                  45
Val Val Gly Ala Thr Ala Thr Val Phe Glu Leu Asp Gly Lys Ile Val
    50                  55                  60
Asp Ala Ala Thr Ala Lys Ala Gly Leu Ala Glu Gly Glu Tyr Ile Ile
65                  70                  75                  80
Val Gly Glu Thr Thr Pro Thr Phe Val Pro Pro Pro Pro Pro Pro Pro
                85                  90                  95
Ala Thr Ser Ser Ala Ala Pro Leu Arg Ala Gln Phe Val Glu Glu Pro
            100                 105                 110
Ile Ser Ser Pro Ala Ala Pro Thr Thr Thr Ser Ala Pro Pro Pro Pro
        115                 120                 125
Pro Thr Thr Thr Ala Gln Ala Thr Thr Ser Ser Ala Pro Pro Pro Pro
    130                 135                 140
Lys Thr Ser Lys Pro Ala Gln Ser Ser Pro Ser Ser Gly Ala Thr Gly
145                 150                 155                 160
Leu Asp Ala Asp Phe Pro Ser Gly Lys Ile Ser Cys Lys Thr Phe Pro
                165                 170                 175
Ser Glu Tyr Gly Ala Val Ala Leu Asp Trp Leu Gly Thr Gly Gly Trp
            180                 185                 190
Ser Gly Leu Gln Phe Val Pro Asn Tyr Ser Pro Asp Ala Gln Ser Ile
        195                 200                 205
Ser Asp Ile Ile Thr Gly Ile Ala Gly Gln Thr Cys Ser Lys Gly Ala
    210                 215                 220
Met Cys Ser Tyr Ala Cys Pro Pro Gly Tyr Gln Lys Thr Gln Trp Pro
225                 230                 235                 240
Lys Ala Gln Gly Ala Thr Leu Gln Ser Ile Gly Gly Leu Tyr Cys Asn
                245                 250                 255
Glu Asp Gly Phe Leu Glu Leu Thr Arg Pro Asp His Pro Lys Leu Cys
            260                 265                 270
Glu Ala Gly Ala Gly Gly Val Thr Ile Lys Asn Asp Leu Asp Asp Ser
        275                 280                 285
```

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

<210> 396
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> predicted protein, partial [Trichoderma reesei
QM6a] 457 aa protein XP_006962014.1 GI:589099983

<400> 396
His Leu Arg Ser His Thr Val Glu Ser Pro Asn Ser Ile Val Lys Arg
1 5 10 15
Gly Thr Cys Ala Phe Pro Thr Asp Asp Pro Asn Leu Val Ala Val Thr
20 25 30
Pro Asp Ala Glu Asn Ala Gly Trp Ala Met Ser Pro Asp Gln Pro Cys
35 40 45
Lys Pro Gly His Tyr Cys Pro Ile Ala Cys Lys Pro Gly Met Val Met
50 55 60
Ala Gln Trp Ser Pro Asp Ser Ser Tyr Ser Tyr Pro Ser Ser Met Asp
65 70 75 80
Gly Gly Leu Tyr Cys Asp Glu Asp Gly Glu Val His Lys Pro Phe Pro
85 90 95
Asn Lys Pro Tyr Cys Val Glu Gly Thr Gly Ala Val Val Ala Val Asn
100 105 110
Lys Cys Gly Glu Pro Met Ser Trp Cys Gln Thr Val Leu Pro Gly Asn
115 120 125
Glu Ala Met Leu Ile Pro Thr Leu Val Glu Asp Gln Ala Thr Ile Ala
130 135 140
Val Pro Asp Thr Ser Tyr Trp Cys Glu Thr Ala Ala His Tyr Tyr Ile
145 150 155 160
Asn Pro Pro Gly Ser Ser Val Ala Asp Cys Val Trp Gly Val Ser Ser
165 170 175

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

<210> 397
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> hypothetical protein M419DRAFT_70331 [Trichoderma reesei RUT C-30] 456 aa protein ETS05514.1 GI:572282500

<400> 397

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Met Lys Val Thr Asp Val Gln Ala Ala Leu Ala Ser Ala Val Val Leu
 1               5                  10                  15
Leu Ser Leu Pro Ala Gly Ser Val Ala Ser Ser His Lys Arg Phe His
            20                  25                  30
Gln Leu Pro Asn Lys Lys His Thr His Leu Arg Ser His Thr Val Glu
```

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

<210> 398
<211> 744
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-D-glucoside glucohydrolase I [Trichoderma
reesei RUT C-30] 744 aa protein ETS03194.1
GI:572280097

<400> 398
Met Arg Tyr Arg Thr Ala Ala Ala Leu Ala Leu Ala Thr Gly Pro Phe
 1               5                  10                  15
Ala Arg Ala Asp Ser His Ser Thr Ser Gly Ala Ser Ala Glu Ala Val
            20                  25                  30
Val Pro Pro Ala Gly Thr Pro Trp Gly Thr Ala Tyr Asp Lys Ala Lys
        35                  40                  45
Ala Ala Leu Ala Lys Leu Asn Leu Gln Asp Lys Val Gly Ile Val Ser
    50                  55                  60
Gly Val Gly Trp Asn Gly Gly Pro Cys Val Gly Asn Thr Ser Pro Ala
65                  70                  75                  80
Ser Lys Ile Ser Tyr Pro Ser Leu Cys Leu Gln Asp Gly Pro Leu Gly
                85                  90                  95
Val Arg Tyr Ser Thr Gly Ser Thr Ala Phe Thr Pro Gly Val Gln Ala
            100                 105                 110
Ala Ser Thr Trp Asp Val Asn Leu Ile Arg Glu Arg Gly Gln Phe Ile
        115                 120                 125
Gly Glu Glu Val Lys Ala Ser Gly Ile His Val Ile Leu Gly Pro Val
    130                 135                 140
Ala Gly Pro Leu Gly Lys Thr Pro Gln Gly Gly Arg Asn Trp Glu Gly
145                 150                 155                 160
Phe Gly Val Asp Pro Tyr Leu Thr Gly Ile Ala Met Gly Gln Thr Ile
                165                 170                 175
Asn Gly Ile Gln Ser Val Gly Val Gln Ala Thr Ala Lys His Tyr Ile
            180                 185                 190
Leu Asn Glu Gln Glu Leu Asn Arg Glu Thr Ile Ser Ser Asn Pro Asp
        195                 200                 205
Asp Arg Thr Leu His Glu Leu Tyr Thr Trp Pro Phe Ala Asp Ala Val
    210                 215                 220
Gln Ala Asn Val Ala Ser Val Met Cys Ser Tyr Asn Lys Val Asn Thr
225                 230                 235                 240
Thr Trp Ala Cys Glu Asp Gln Tyr Thr Leu Gln Thr Val Leu Lys Asp
                245                 250                 255
Gln Leu Gly Phe Pro Gly Tyr Val Met Thr Asp Trp Asn Ala Gln His
            260                 265                 270
Thr Thr Val Gln Ser Ala Asn Ser Gly Leu Asp Met Ser Met Pro Gly
        275                 280                 285
Thr Asp Phe Asn Gly Asn Asn Arg Leu Trp Gly Pro Ala Leu Thr Asn
    290                 295                 300
Ala Val Asn Ser Asn Gln Val Pro Thr Ser Arg Val Asp Asp Met Val
305                 310                 315                 320
Thr Arg Ile Leu Ala Ala Trp Tyr Leu Thr Gly Gln Asp Gln Ala Gly
                325                 330                 335

```
Tyr Pro Ser Phe Asn Ile Ser Arg Asn Val Gln Gly Asn His Lys Thr
            340                 345                 350
Asn Val Arg Ala Ile Ala Arg Asp Gly Ile Val Leu Leu Lys Asn Asp
        355                 360                 365
Ala Asn Ile Leu Pro Leu Lys Lys Pro Ala Ser Ile Ala Val Val Gly
    370                 375                 380
Ser Ala Ala Ile Ile Gly Asn His Ala Arg Asn Ser Pro Ser Cys Asn
385                 390                 395                 400
Asp Lys Gly Cys Asp Asp Gly Ala Leu Gly Met Gly Trp Gly Ser Gly
                405                 410                 415
Ala Val Asn Tyr Pro Tyr Phe Val Ala Pro Tyr Asp Ala Ile Asn Thr
            420                 425                 430
Arg Ala Ser Ser Gln Gly Thr Gln Val Thr Leu Ser Asn Thr Asp Asn
        435                 440                 445
Thr Ser Ser Gly Ala Ser Ala Ala Arg Gly Lys Asp Val Ala Ile Val
    450                 455                 460
Phe Ile Thr Ala Asp Ser Gly Glu Gly Tyr Ile Thr Val Glu Gly Asn
465                 470                 475                 480
Ala Gly Asp Arg Asn Asn Leu Asp Pro Trp His Asn Gly Asn Ala Leu
                485                 490                 495
Val Gln Ala Val Ala Gly Ala Asn Ser Asn Val Ile Val Val Val His
            500                 505                 510
Ser Val Gly Ala Ile Ile Leu Glu Gln Ile Leu Ala Leu Pro Gln Val
        515                 520                 525
Lys Ala Val Val Trp Ala Gly Leu Pro Ser Gln Glu Ser Gly Asn Ala
    530                 535                 540
Leu Val Asp Val Leu Trp Gly Asp Val Ser Pro Ser Gly Lys Leu Val
545                 550                 555                 560
Tyr Thr Ile Ala Lys Ser Pro Asn Asp Tyr Asn Thr Arg Ile Val Ser
                565                 570                 575
Gly Gly Ser Asp Ser Phe Ser Glu Gly Leu Phe Ile Asp Tyr Lys His
            580                 585                 590
Phe Asp Asp Ala Asn Ile Thr Pro Arg Tyr Glu Phe Gly Tyr Gly Leu
        595                 600                 605
Ser Tyr Thr Lys Phe Asn Tyr Ser Arg Leu Ser Val Leu Ser Thr Ala
    610                 615                 620
Lys Ser Gly Pro Ala Thr Gly Ala Val Val Pro Gly Gly Pro Ser Asp
625                 630                 635                 640
Leu Phe Gln Asn Val Ala Thr Val Thr Val Asp Ile Ala Asn Ser Gly
                645                 650                 655
Gln Val Thr Gly Ala Glu Val Ala Gln Leu Tyr Ile Thr Tyr Pro Ser
            660                 665                 670
Ser Ala Pro Arg Thr Pro Pro Lys Gln Leu Arg Gly Phe Ala Lys Leu
        675                 680                 685
Asn Leu Thr Pro Gly Gln Ser Gly Thr Ala Thr Phe Asn Ile Arg Arg
    690                 695                 700
Arg Asp Leu Ser Tyr Trp Asp Thr Ala Ser Gln Lys Trp Val Val Pro
705                 710                 715                 720
Ser Gly Ser Phe Gly Ile Ser Val Gly Ala Ser Ser Arg Asp Ile Arg
                725                 730                 735
Leu Thr Ser Thr Leu Ser Val Ala
            740
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<210> 399
<211> 700
<212> PRT
<213> Artificial Sequence

<220>
<223> hypotheticalprotein M419DRAFT_122639 [Trichoderma
reesei RUT C-30] 700 aa protein ETS03170.1
GI:572280073

<400> 399
Met Ile Leu Gly Cys Glu Ser Thr Gly Val Ile Ser Ala Val Lys His
 1               5                  10                  15
Phe Val Ala Asn Asp Gln Glu His Glu Arg Arg Ala Val Asp Cys Leu
            20                  25                  30
Ile Thr Gln Arg Ala Leu Arg Glu Val Tyr Leu Arg Pro Phe Gln Ile
        35                  40                  45
Val Ala Arg Asp Ala Arg Pro Gly Ala Leu Met Thr Ser Tyr Asn Lys
    50                  55                  60
Val Asn Gly Lys His Val Ala Asp Ser Ala Glu Phe Leu Gln Gly Ile
65                  70                  75                  80
Leu Arg Thr Glu Trp Asn Trp Asp Pro Leu Ile Val Ser Asp Trp Tyr
                85                  90                  95
Gly Thr Tyr Thr Thr Ile Asp Ala Ile Lys Ala Gly Leu Asp Leu Glu
            100                 105                 110
Met Pro Gly Val Ser Arg Tyr Arg Gly Lys Tyr Ile Glu Ser Ala Leu
        115                 120                 125
Gln Ala Arg Leu Leu Lys Gln Ser Thr Ile Asp Glu Arg Ala Arg Arg
    130                 135                 140
Val Leu Arg Phe Ala Gln Lys Ala Ser His Leu Lys Val Ser Glu Val
145                 150                 155                 160
Glu Gln Gly Arg Asp Phe Pro Glu Asp Arg Val Leu Asn Arg Gln Ile
                165                 170                 175
Cys Gly Ser Ser Ile Val Leu Leu Lys Asn Glu Asn Ser Ile Leu Pro
            180                 185                 190
Leu Pro Lys Ser Val Lys Lys Val Ala Leu Val Gly Ser His Val Arg
        195                 200                 205
Leu Pro Ala Ile Ser Gly Gly Gly Ser Ala Ser Leu Val Pro Tyr Tyr
    210                 215                 220
Ala Ile Ser Leu Tyr Asp Ala Val Ser Glu Val Leu Ala Gly Ala Thr
225                 230                 235                 240
Ile Thr His Glu Val Gly Ala Tyr Ala His Gln Met Leu Pro Val Ile
                245                 250                 255
Asp Ala Met Ile Ser Asn Ala Val Ile His Phe Tyr Asn Asp Pro Ile
            260                 265                 270
Asp Val Lys Asp Arg Lys Leu Leu Gly Ser Glu Asn Val Ser Ser Thr
        275                 280                 285
Ser Phe Gln Leu Met Asp Tyr Asn Asn Ile Pro Thr Leu Asn Lys Ala
    290                 295                 300
Met Phe Trp Gly Thr Leu Val Gly Glu Phe Ile Pro Thr Ala Thr Gly
305                 310                 315                 320
Ile Trp Glu Phe Gly Leu Ser Val Phe Gly Thr Ala Asp Leu Tyr Ile
                325                 330                 335
Asp Asn Glu Leu Val Ile Glu Asn Thr Thr His Gln Thr Arg Gly Thr

```
            340                 345                 350
Ala Phe Phe Gly Lys Gly Thr Thr Glu Lys Val Ala Thr Arg Arg Met
        355                 360                 365
Val Ala Gly Ser Thr Tyr Lys Leu Arg Leu Glu Phe Gly Ser Ala Asn
    370                 375                 380
Thr Thr Lys Met Glu Thr Thr Gly Val Val Asn Phe Gly Gly Gly Ala
385                 390                 395                 400
Val His Leu Gly Ala Cys Leu Lys Val Asp Pro Gln Glu Met Ile Ala
                405                 410                 415
Arg Ala Val Lys Ala Ala Ala Asp Ala Asp Tyr Thr Ile Ile Cys Thr
            420                 425                 430
Gly Leu Ser Gly Glu Trp Glu Ser Glu Gly Phe Asp Arg Pro His Met
        435                 440                 445
Asp Leu Pro Pro Gly Val Asp Thr Met Ile Ser Gln Val Leu Asp Ala
    450                 455                 460
Ala Pro Asn Ala Val Val Val Asn Gln Ser Gly Thr Pro Val Thr Met
465                 470                 475                 480
Ser Trp Ala His Lys Ala Lys Ala Ile Val Gln Ala Trp Tyr Gly Gly
                485                 490                 495
Asn Glu Thr Gly His Gly Ile Ser Asp Val Leu Phe Gly Asn Val Asn
            500                 505                 510
Pro Ser Gly Lys Leu Ser Leu Ser Trp Pro Val Asp Val Lys His Asn
        515                 520                 525
Pro Ala Tyr Leu Asn Tyr Ala Ser Val Gly Gly Arg Val Leu Tyr Gly
    530                 535                 540
Glu Asp Val Tyr Val Gly Tyr Lys Phe Tyr Asp Lys Thr Glu Arg Glu
545                 550                 555                 560
Val Leu Phe Pro Phe Gly His Gly Leu Ser Tyr Ala Thr Phe Lys Leu
                565                 570                 575
Pro Asp Ser Thr Val Arg Thr Val Pro Glu Thr Phe His Pro Asp Gln
            580                 585                 590
Pro Thr Val Ala Ile Val Lys Ile Lys Asn Thr Ser Ser Val Pro Gly
        595                 600                 605
Ala Gln Val Leu Gln Leu Tyr Ile Ser Ala Pro Asn Ser Pro Thr His
    610                 615                 620
Arg Pro Val Lys Glu Leu His Gly Phe Glu Lys Val Tyr Leu Glu Ala
625                 630                 635                 640
Gly Glu Glu Lys Glu Val Gln Ile Pro Ile Asp Gln Tyr Ala Thr Ser
                645                 650                 655
Phe Trp Asp Glu Ile Glu Ser Met Trp Lys Ser Glu Arg Gly Ile Tyr
            660                 665                 670
Asp Val Leu Val Gly Phe Ser Ser Gln Glu Ile Ser Gly Lys Gly Lys
        675                 680                 685
Leu Ile Val Pro Glu Thr Arg Phe Trp Met Gly Leu
    690                 695                 700


<210> 400
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> SUN-domain-containing protein [Trichoderma reesei
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RUT C-30] 436 aa protein ETS01671.1 GI:572278501

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

```
                405                 410                 415
Gly Asp Lys Gly Cys Thr Thr Ala Met Pro Ser Gly Gly Lys Ala Val
            420                 425                 430
Ile Arg Tyr Phe
        435
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<210> 401
<211> 874
<212> PRT
<213> Artificial Sequence

<220>
<223> hypotheticalprotein M419DRAFT_25095 [Trichoderma reesei RUT C-30] 874 aa protein ETS01349.1 GI:572278157

<400> 401

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

```
Gln Ala Gln His Thr Gly Val Ala Ser Ala Val Ala Gly Leu Asp Met
    290                 295                 300
Thr Met Pro Gly Asp Thr Ala Phe Asn Thr Gly Ala Ser Tyr Phe Gly
305                 310                 315                 320
Ser Asn Leu Thr Leu Ala Val Leu Asn Gly Thr Val Pro Glu Trp Arg
                325                 330                 335
Ile Asp Asp Met Val Met Arg Ile Met Ala Pro Phe Phe Lys Val Gly
            340                 345                 350
Lys Thr Val Asp Ser Leu Ile Asp Thr Asn Phe Asp Ser Trp Thr Asn
        355                 360                 365
Gly Glu Tyr Gly Tyr Val Gln Ala Ala Val Asn Glu Asn Trp Glu Lys
    370                 375                 380
Val Asn Tyr Gly Val Asp Val Arg Ala Asn His Ala Asn His Ile Arg
385                 390                 395                 400
Glu Val Gly Ala Lys Gly Thr Val Ile Phe Lys Asn Asn Gly Ile Leu
                405                 410                 415
Pro Leu Lys Lys Pro Lys Phe Leu Thr Val Ile Gly Glu Asp Ala Gly
            420                 425                 430
Gly Asn Pro Ala Gly Pro Asn Gly Cys Gly Asp Arg Gly Cys Asp Asp
        435                 440                 445
Gly Thr Leu Ala Met Glu Trp Gly Ser Gly Thr Thr Asn Phe Pro Tyr
    450                 455                 460
Leu Val Thr Pro Asp Ala Ala Leu Gln Ser Gln Ala Leu Gln Asp Gly
465                 470                 475                 480
Thr Arg Tyr Glu Ser Ile Leu Ser Asn Tyr Ala Ile Ser Gln Thr Gln
                485                 490                 495
Ala Leu Val Ser Gln Pro Asp Ala Ile Ala Ile Val Phe Ala Asn Ser
            500                 505                 510
Asp Ser Gly Glu Gly Tyr Ile Asn Val Asp Gly Asn Glu Gly Asp Arg
        515                 520                 525
Lys Asn Leu Thr Leu Trp Lys Asn Gly Asp Asp Leu Ile Lys Thr Val
    530                 535                 540
Ala Ala Val Asn Pro Lys Thr Ile Val Val Ile His Ser Thr Gly Pro
545                 550                 555                 560
Val Ile Leu Lys Asp Tyr Ala Asn His Pro Asn Ile Ser Ala Ile Leu
                565                 570                 575
Trp Ala Gly Ala Pro Gly Gln Glu Ser Gly Asn Ser Leu Val Asp Ile
            580                 585                 590
Leu Tyr Gly Lys Gln Ser Pro Gly Arg Thr Pro Phe Thr Trp Gly Pro
        595                 600                 605
Ser Leu Glu Ser Tyr Gly Val Ser Val Met Thr Thr Pro Asn Asn Gly
    610                 615                 620
Asn Gly Ala Pro Gln Asp Asn Phe Asn Glu Gly Ala Phe Ile Asp Tyr
625                 630                 635                 640
Arg Tyr Phe Asp Lys Val Ala Pro Gly Lys Pro Arg Ser Ser Asp Lys
                645                 650                 655
Ala Pro Thr Tyr Glu Phe Gly Phe Gly Leu Ser Trp Ser Thr Phe Lys
            660                 665                 670
Phe Ser Asn Leu His Ile Gln Lys Asn Asn Val Gly Pro Met Ser Pro
        675                 680                 685
Pro Asn Gly Lys Thr Ile Ala Ala Pro Ser Leu Gly Ser Phe Ser Lys
    690                 695                 700
Asn Leu Lys Asp Tyr Gly Phe Pro Lys Asn Val Arg Arg Ile Lys Glu
705                 710                 715                 720
```

```
Phe Ile Tyr Pro Tyr Leu Ser Thr Thr Thr Ser Gly Lys Glu Ala Ser
                725                 730                 735
Gly Asp Ala His Tyr Gly Gln Thr Ala Lys Glu Phe Leu Pro Ala Gly
            740                 745                 750
Ala Leu Asp Gly Ser Pro Gln Pro Arg Ser Ala Ala Ser Gly Glu Pro
        755                 760                 765
Gly Gly Asn Arg Gln Leu Tyr Asp Ile Leu Tyr Thr Val Thr Ala Thr
    770                 775                 780
Ile Thr Asn Thr Gly Ser Val Met Asp Asp Ala Val Pro Gln Leu Tyr
785                 790                 795                 800
Leu Ser His Gly Gly Pro Asn Glu Pro Pro Lys Val Leu Arg Gly Phe
                805                 810                 815
Asp Arg Ile Glu Arg Ile Ala Pro Gly Gln Ser Val Thr Phe Lys Ala
            820                 825                 830
Asp Leu Thr Arg Arg Asp Leu Ser Asn Trp Asp Thr Lys Lys Gln Gln
        835                 840                 845
Trp Val Ile Thr Asp Tyr Pro Lys Thr Val Tyr Val Gly Ser Ser Ser
    850                 855                 860
Arg Asp Leu Pro Leu Ser Ala Arg Leu Pro
865                 870


<210> 402
<211> 932
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-N-acetylglucosaminidase[Trichoderma reesei
      RUT C-30] 932 aa protein ETS00749.1 GI:572277491

<400> 402
Met Ala Asn Ser Ile Gly Gly Ser Ser Ala Asp Lys Phe Asp Leu Asp
 1               5                  10                  15
Pro Leu Trp Gln Asn Leu Asp Trp Ala Ile Gly Gln Met Met Leu Met
            20                  25                  30
Gly Trp Asp Gly Thr Gln Val Thr Pro Gln Ile Arg Ser Leu Ile Glu
        35                  40                  45
Asp His His Leu Gly Ser Ile Ile Leu Thr Ala Lys Asn Leu Lys Ser
    50                  55                  60
Ala His His Thr Ala Leu Leu Val Gln Glu Leu Gln Met Ile Ala Lys
65                  70                  75                  80
Asn Ser Gly His Pro Gln Pro Leu Leu Ile Ala Val Asp Gln Glu Asn
                85                  90                  95
Gly Gly Val Asn Ser Leu Phe Asp Glu Asp Phe Val Cys Gln Phe Pro
            100                 105                 110
Ser Ala Met Ala Ile Ala Ala Thr Gly Ser Leu Glu Leu Ser Tyr Glu
        115                 120                 125
Val Asn Lys Ala Thr Ala Thr Glu Ile Ser Ala Cys Gly Val Asn Leu
    130                 135                 140
Met Leu Gly Pro Val Leu Asp Val Leu Asn Asn Ala Arg Tyr Gln Val
145                 150                 155                 160
Ile Gly Val Arg Ala Ser Gly Asp Asp Pro Gln Glu Val Ser Gln Tyr
                165                 170                 175
```

```
Gly Leu Ala Ala Leu Ser Gly Ile Arg Asp Ala Gly Val Ala Ser Cys
            180                 185                 190
Gly Lys His Phe Pro Ser Tyr Gly Asn Leu Asp Phe Leu Gly Ser Asn
        195                 200                 205
Leu Asp Val Pro Ile Ile Thr Gln Thr Leu Glu Glu Leu Ser Leu Ser
    210                 215                 220
Ala Leu Val Pro Phe Arg Asn Ala Ile Ala Ser Gly Lys Leu Asp Ala
225                 230                 235                 240
Met Phe Ile Gly Gly Cys Gly Ile Ser Asn Pro Ser Met Asn Val Ser
                245                 250                 255
His Ala Cys Leu Ser Asp Gln Val Val Asp Asp Leu Leu Arg Asn Glu
            260                 265                 270
Leu Gly Phe Lys Gly Val Ala Ile Ser Glu Cys Leu Glu Met Glu Ala
        275                 280                 285
Leu Ser Gln Asp Leu Gly Val Gln Asn Gly Val Val Met Ala Val Glu
    290                 295                 300
Ala Gly Cys Asp Ile Val Leu Leu Cys Arg Ala Tyr Asp Val Gln Leu
305                 310                 315                 320
Glu Ala Ile Lys Gly Leu Lys Leu Gly Tyr Glu Asn Gly Ile Ile Thr
                325                 330                 335
Lys Glu Arg Ile Phe Thr Ser Leu Lys Arg Ile Phe His Leu Lys Ser
            340                 345                 350
Thr Cys Thr Ser Trp Ala Lys Ala Leu Asn Pro Pro Gly Ile Asn Leu
        355                 360                 365
Leu Ser Gln Ile Arg Pro Ser His Leu Ala Leu Ser Arg Arg Ala Tyr
    370                 375                 380
Asp Asp Ser Ile Thr Ile Val Arg Asp Lys Glu Lys Leu Leu Pro Leu
385                 390                 395                 400
Ser Leu Ser Met His Pro Gly Glu Glu Leu Leu Leu Leu Thr Pro Leu
                405                 410                 415
Val Lys Pro Leu Pro Ala Ser Ser Leu Thr Lys Ser Leu Leu Glu Ser
            420                 425                 430
Lys Asn Asp Pro Ser Leu Val Ser Thr Glu His Asp Arg Trp Asn His
        435                 440                 445
Gln Ile Arg Glu Arg Ser Ala Ile Met Ser Gly Glu Gly Val Phe Arg
    450                 455                 460
Glu Phe Gly Lys Thr Leu Ala Arg Tyr Arg Asn Glu Lys Leu Leu His
465                 470                 475                 480
Thr Ser Tyr Thr Ala Asn Gly Val Arg Pro Val His Glu Asn Leu Ile
                485                 490                 495
Asn Arg Ala Ser Cys Ile Ile Ile Phe Thr Ala Asp Ala Asn Arg Asn
            500                 505                 510
Leu Tyr Gln Ala Gly Phe Thr Lys His Val Asp Met Met Cys Ser Met
        515                 520                 525
Leu Arg Ser Arg Gly Gln Lys Lys Gln Leu Ile Val Val Ala Val Ser
    530                 535                 540
Ser Pro Tyr Asp Phe Ala Met Asp Lys Ser Ile Gly Thr Tyr Ile Cys
545                 550                 555                 560
Thr Tyr Asp Phe Thr Glu Asn Ala Met Ala Ala Leu Val Arg Ala Leu
                565                 570                 575
Val Gly Asp Ser Asn Pro Val Gly Thr Met Pro Gly Thr Leu Arg Lys
            580                 585                 590
Ser Lys Lys Val Leu Lys Ser Arg Gln His Trp Leu Val Glu Glu Phe
        595                 600                 605
```

```
Asp Ser Ser Arg Asp Arg Lys Gly Leu Asn Asp Leu Ile Arg Ala Val
    610                 615                 620
His Arg Ala Ser Asp Gln Asp Phe Arg Tyr Leu Gln Thr Ala Thr Ala
625                 630                 635                 640
Asp Thr Phe Leu Leu Ala Asn Gln Asn Ile Lys Glu Thr His Phe Val
                645                 650                 655
Val Arg Asn Ser Ser Thr Gln Ala Leu Tyr Gly Phe Ala Ala Thr Tyr
            660                 665                 670
Phe Val Gln Asn Val Gly Ile Leu Gly Ala Leu Ile Val Asp Pro Thr
        675                 680                 685
Lys Arg Asn Met Ser Ile Gly Arg Ser Leu His Arg Arg Ala Ile Lys
    690                 695                 700
Ser Leu Thr Gln Gln Arg Gly Ile Lys Lys Val Gln Leu Gly Ser Cys
705                 710                 715                 720
Phe Pro Ala Leu Phe Leu Gly Ile Pro Leu Asp Ile Glu Val Thr Thr
                725                 730                 735
Thr Lys Glu Trp Phe Ser Asn Ser Gly Trp Asp Thr Gln Phe Pro Arg
            740                 745                 750
Arg Leu Thr Asn Met Val Ile Gln Asp Leu Ser Ala Trp Tyr Ala Pro
        755                 760                 765
Glu Gly Leu Ser Gln Ser Ile Gln Arg Ala Asn Ile Ser Phe Asp Leu
    770                 775                 780
Ile Tyr Gly Val Glu Ser Gly Asp Thr Val Met His His Val Arg Thr
785                 790                 795                 800
His Ala Asn Pro Glu Val Leu Glu Leu Tyr Arg Thr Ala Leu Glu Glu
                805                 810                 815
Ser Lys Ala Cys Gly Ile Val Arg Ala Lys Asp Ala Ala Gly Asn Leu
            820                 825                 830
Leu Gly Thr Ile Ile Ile Cys Arg Pro Asn Ser Pro Leu Ala Arg Tyr
        835                 840                 845
Val Pro Pro Leu Val Ser Leu Gly Gln Asp Ile Gly Gly Leu Leu Ala
    850                 855                 860
Pro Ile Val Pro Pro Ala Pro Leu Ser Thr Leu Val Leu Gln Gly Leu
865                 870                 875                 880
Ala Leu Met Gly Val Arg Gln Asn Lys Gly His Lys Ala Thr Lys Ser
                885                 890                 895
Val Leu Ser Trp Val Val Asp Asp Ala Tyr Glu Pro Leu Val Ala Met
            900                 905                 910
Gly Phe Asp Val Leu Gln Ala Phe Glu Glu Ile Thr Asn Ser Pro Glu
        915                 920                 925
Thr Phe Gln Thr
    930
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<210> 403
<211> 890
<212> PRT
<213> Artificial Sequence

<220>
<223> hypothetical protein M419DRAFT_86704 [Trichoderma reesei RUT C-30] 890 aa protein ETR99336.1 GI:572275968

<400> 403
Met Leu Pro Arg Arg Met Arg Lys Ser Arg Cys Cys Ile Ala Val Leu
 1               5                  10                  15
Ala Val Ile Ala Ile Ile Val Met Leu Leu Ala Ala Ala Gly Ala Phe
            20                  25                  30
Gly Tyr Lys Lys Leu Lys Ile Thr Pro Leu Asp Gly Lys Ser Pro Pro
        35                  40                  45
Trp Tyr Pro Thr Pro Lys Gly Gly Ser Val Arg Gln Trp Ala Asp Ser
    50                  55                  60
Tyr Gln Lys Ala Ala Glu Met Val Ala Arg Met Thr Leu Pro Glu Lys
65                  70                  75                  80
Val Asn Ile Thr Thr Gly Thr Gly Trp Ser Met Gly Leu Ala Val Gly
                85                  90                  95
Asn Thr Ala Pro Ala Leu Leu Val Gly Phe Pro Ala Leu Ala Leu Gln
            100                 105                 110
Asp Gly Pro Leu Gly Ile Arg Phe Ala Asp Asn Ala Thr Ala Leu Pro
        115                 120                 125
Ala Gly Val Thr Val Gly Ala Thr Trp Asn Arg His Leu Met Tyr Glu
    130                 135                 140
His Gly Arg Val His Ala Leu Glu Ala Arg Gly Lys Gly Ile Asn Ala
145                 150                 155                 160
Leu Leu Gly Pro Cys Val Gly Pro Leu Gly Arg Met Pro Ala Gly Gly
                165                 170                 175
Arg Asn Trp Glu Gly Phe Gly Ala Asp Pro Tyr Leu Gln Gly Val Ala
            180                 185                 190
Gly Tyr Glu Thr Ile Lys Gly Ile Gln Asp Gln Gly Val Met Ala Thr
        195                 200                 205
Ile Lys His Phe Val Ala Asn Glu Gln Glu His Phe Arg Gln Ala Trp
    210                 215                 220
Glu Trp Val Leu Pro Asn Ala Leu Ser Ser Asn Ile Asp Asp Arg Thr
225                 230                 235                 240
Met His Glu Ile Tyr Ala Trp Pro Phe Gly Asp Ala Val Lys Ala Gly
                245                 250                 255
Val Ala Ser Val Met Cys Ser Tyr Asn Met Val Asn Asn Ser Tyr Ala
            260                 265                 270
Cys Gly Asn Ser Lys Leu Leu Asn Gly Ile Leu Lys Asp Glu Leu Gly
        275                 280                 285
Phe Gln Gly Phe Val Met Ser Asp Trp Leu Ala Gln Arg Ser Gly Val
    290                 295                 300
Gly Ser Ala Leu Ala Gly Leu Asp Met Ser Met Pro Gly Asp Gly Leu
305                 310                 315                 320
Arg Trp Gln Asp Gly Asn Ser Leu Trp Gly Pro Asn Leu Ser Arg Ala
                325                 330                 335
Val Leu Asn Gly Ser Leu Pro Leu Glu Arg Leu Asn Asp Met Val Val
            340                 345                 350
Arg Ile Val Ala Ala Trp Tyr Gln Leu Gly Gln Asp Asp Glu Lys Leu
        355                 360                 365
Phe Asp Arg Lys Gly Pro Asn Phe Ser Ser Trp Thr Asn Asp Arg Met
    370                 375                 380
Gly Val Thr Ala Pro Ala Ser Ser Ser Pro Gln Glu Lys Val Val Val
385                 390                 395                 400
Asn Gln Phe Val Asn Val Gln Ala Asn His Ser Ile Leu Ala Arg Gln
                405                 410                 415
Ile Ala Ala Glu Gly Thr Val Leu Leu Lys Asn Glu Gly Val Leu Pro

```
            420                 425                 430
Leu Ser Val Asp Gly Leu Leu Gly Gly Gly Gly Gly Ser Asn Ser Thr
        435                 440                 445
Lys Arg Glu Gly Gln Val Arg Ile Gly Ile Phe Gly Glu Asp Ala Gly
    450                 455                 460
Pro Gly Lys Gly Pro Asn Tyr Cys Glu Asp Arg Ser Cys Asn Gln Gly
465                 470                 475                 480
Thr Leu Ala Ser Gly Trp Gly Ser Gly Ala Val Glu Phe Pro Tyr Leu
                485                 490                 495
Val Ser Pro Ile Glu Ala Leu Arg Lys Lys Phe Asn Lys Asp Lys Val
            500                 505                 510
Lys Leu Thr Glu His Leu Lys Asn Asp Glu Leu Asp Thr Gly Val Ile
        515                 520                 525
Lys Ser Gln Asp Ile Cys Met Val Phe Ile Asn Ser Asp Ser Gly Glu
    530                 535                 540
Gly Tyr Arg Ala Trp Glu Gly Val Arg Gly Asp Arg Asn Asp Leu Lys
545                 550                 555                 560
Pro Gln Lys Gly Gly Val Gly Leu Val Thr His Val Gly Leu Asn Cys
                565                 570                 575
Gly Asn Gly Ser Gly Thr Thr Ile Val Val Leu His Ser Val Gly Pro
            580                 585                 590
Val Val Val Asp Pro Trp Ile Asp Met Pro Gly Ile Lys Ala Leu Ile
        595                 600                 605
Ser Ala Asn Leu Pro Gly Gln Glu Ser Gly Asn Ala Leu Ala Ser Ile
    610                 615                 620
Leu Phe Gly Glu Glu Asn Pro Ser Gly Lys Leu Pro Tyr Thr Val Gly
625                 630                 635                 640
Lys Ser Leu Ser Asp Tyr Gly Pro Gly Gly Gln Val Met Tyr Leu Pro
                645                 650                 655
Asn Gly Ala Val Pro Gln Gln Asp Phe Ser Glu Gly Leu Tyr Ile Asp
            660                 665                 670
Tyr Arg His Phe Asp Lys Phe Asn Ile Glu Pro Arg Tyr Glu Phe Gly
        675                 680                 685
Phe Gly Leu Ser Tyr Thr Asn Phe Asp Tyr Lys Asn Leu Lys Ile Thr
    690                 695                 700
Glu Thr Lys Pro Arg Ser Pro Leu Pro Asp Glu Arg Pro Ala Ala Glu
705                 710                 715                 720
Val Glu Pro Pro Ser Phe Asp Thr Thr Ile Pro Gln Ala Glu Glu Ala
                725                 730                 735
Leu Phe Pro Ser Gly Ile Arg Arg Leu Lys Lys Tyr Val Tyr Pro Tyr
            740                 745                 750
Ile Glu Ser Val Lys Asp Ile Lys Glu Gly Gln Tyr Ser Tyr Pro Asp
        755                 760                 765
Gly Tyr Asp Lys Glu Gln Pro Leu Ser Gly Ala Gly Gly Gly Glu Gly
    770                 775                 780
Gly Asn Pro Ser Leu Trp Asp Ser His Val Ile Val Ser Val Glu Val
785                 790                 795                 800
Thr Asn Thr Gly Lys Leu Gly Gly Lys Ala Val Pro Gln Leu Tyr Leu
                805                 810                 815
Ser Tyr Pro Ala Ser Glu Thr Val Asp Phe Pro Val Arg Val Leu Arg
            820                 825                 830
Gly Phe Asp Lys Val Tyr Ile Gly Lys Gly Glu Thr Lys Thr Val Glu
        835                 840                 845
Phe Ser Leu Thr Arg Arg Asp Leu Ser Tyr Trp Asp Val Glu Arg Gln
```

```
    850                 855                 860
Asn Trp Val Ile Pro Glu Gly Glu Tyr Thr Phe Ala Val Gly Glu Ser
865                 870                 875                 880
Ser Arg Asp Leu Arg Val Ser Gly Thr Trp
                885                 890


<210> 404
<211> 533
<212> PRT
<213> Artificial Sequence

<220>
<223> putative beta-N-acetylglucosaminidase [Trichoderma
      reesei RUT C-30] 533 aa protein ETR97676.1
      GI:572274120

<400> 404
Met Pro Ser Pro Glu Gln Arg Arg Lys Ile Gly Gln Leu Phe Ala Val
 1               5                  10                  15
Gly Phe His Gly Arg Glu Ile Asn Gln Glu Ile Thr Thr Leu Ile Arg
            20                  25                  30
Asp Tyr Gly Val Gly Ala Ile Val Leu Phe Lys Arg Asn Val Leu Asp
        35                  40                  45
Ala Ala Gln Leu Gln Ala Leu Cys Leu Gly Leu Gln Lys Ile Ala Arg
    50                  55                  60
Asp Ala Gly His Asn Gln Pro Leu Phe Ile Gly Ile Asp Gln Glu Asn
65                  70                  75                  80
Gly Leu Val Thr Arg Ile Ser Pro Pro Ile Ala Ser Gln Gln Pro Gly
                85                  90                  95
Pro Met Thr Leu Gly Ala Ala Gly Ser Leu Glu Tyr Ala Tyr Glu Val
            100                 105                 110
Ala Lys Ala Thr Ala Glu Met Leu Arg Tyr Phe Gly Ile Asn Met Asn
        115                 120                 125
Tyr Ala Pro Val Gly Asp Val Asn Ser Glu Pro Leu Asn Pro Val Ile
    130                 135                 140
Gly Val Arg Ser Pro Ser Asp Gln Ala Glu Thr Val Ser Lys Phe Ala
145                 150                 155                 160
Ala Ala Cys Thr Lys Gly Leu Arg Glu His Lys Val Val Pro Cys Ile
                165                 170                 175
Lys His Phe Pro Gly His Gly Asp Thr Ala Val Asp Ser His Tyr Gly
            180                 185                 190
Leu Pro Val Ile Asn Lys Ser Arg Ala Asp Met Glu Lys Leu Glu Leu
        195                 200                 205
Ile Pro Phe Arg Asp Ala Val Ala Asp Asn Ile Glu Met Val Met Thr
    210                 215                 220
Ala His Ile Ser Leu Pro Gln Leu Ala Lys Asp Gly Leu Pro Ala Thr
225                 230                 235                 240
Leu Ser Pro Asp Thr Ile Gly Ile Leu Arg Asn Glu Trp Lys Tyr Glu
                245                 250                 255
Gly Val Ile Met Thr Asp Cys Leu Glu Met Asp Gly Ile Arg Ala Thr
            260                 265                 270
Tyr Gly Thr Val Glu Gly Ser Leu Met Ala Phe Gln Ala Gly Val Asp
        275                 280                 285
```

Asn Val Met Ile Cys His Thr Phe Asp Val Gln Ala Ala Ala Val Asp
290 295 300
Tyr Ile Cys Gly Ala Ile Glu Ser Gly Lys Leu Ser Gln Glu Arg Val
305 310 315 320
Asp Gln Ser Leu Glu Arg Leu Arg Lys Leu Lys Glu Arg Tyr Thr Asn
325 330 335
Trp Asp Ile Ala Leu His Ala Glu Pro Pro Glu Ala Leu Glu Ala Ile
340 345 350
Asn Glu Arg Gly Glu Lys Leu Ala Arg Gln Val Tyr Ala Asp Ala Thr
355 360 365
Thr Leu Val Arg Ala Gln Glu Gly Leu Leu Pro Leu Lys Ala Thr Ala
370 375 380
Lys Ile Ala Phe Val Ser Pro Gly Pro Asp Val Pro Ile Gly Gly Ala
385 390 395 400
Val Asp Ser Gly Thr Leu Pro Thr Arg Val Pro Trp Ile Ala Asp Thr
405 410 415
Phe Gly Glu Gln Ile Arg Lys Arg Ala Pro Glu Met Ser Asp Val Arg
420 425 430
Phe Thr Ser Ser Asn Leu Thr Glu Glu Gln Trp Glu Gln Ile Asp Glu
435 440 445
Ala Asp Val Val Ile Leu Ala Thr Arg Asn Ala Arg Glu Ser Lys Tyr
450 455 460
Gln Lys Glu Leu Gly Leu Glu Val Ala Lys Arg Arg Gly Ser Arg Pro
465 470 475 480
Leu Ile Ser Ile Ala Thr Cys Ala Pro Tyr Asp Phe Leu Asp Asp Glu
485 490 495
Glu Ile Arg Thr Tyr Ile Ala Val Tyr Glu Pro Thr Val Glu Ala Phe
500 505 510
Ser Ala Ala Val Asp Ile Leu Phe Gly Asp Ala Gln Pro Arg Gly Lys
515 520 525
Leu Pro Val Ala His
530

<210> 405
<211> 396
<212> PRT
<213> Artificial Sequence

<220>
<223> UDP-glycotransferase (338)

<400> 405
Met Gly His Lys His Ile Ala Ile Phe Asn Ile Pro Ala His Gly His
1 5 10 15
Ile Asn Pro Thr Leu Ala Leu Thr Ala Ser Leu Val Lys Arg Gly Tyr
20 25 30
Arg Val Thr Tyr Pro Val Thr Asp Glu Phe Val Lys Ala Val Glu Glu
35 40 45
Thr Gly Ala Glu Pro Leu Asn Tyr Arg Ser Thr Leu Asn Ile Asp Pro
50 55 60
Gln Gln Ile Arg Glu Leu Met Lys Asn Lys Lys Asp Met Ser Gln Ala
65 70 75 80
Pro Leu Met Phe Ile Lys Glu Met Glu Glu Val Leu Pro Gln Leu Glu

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

<210> 406
<211> 1191
<212> DNA
<213> Artificial Sequence

<220>
<223> 338 (gDNA, native)

<400> 406
atgggacata aacatatcgc gatttttaat attccggctc acggccatat taatccaacg 60
ctagctttaa cggcaagcct tgtcaaacgc ggttatcggg taacatatcc ggtgacggat 120
gagtttgtga aggctgttga ggaaactggg gcagagccgc tcaactaccg ctcaacttta 180
aatatcgatc cgcagcaaat tcgggagctg atgaaaaata aaaaagatat gtcgcaggct 240

ccgctgatgt ttatcaaaga aatggaggag gttcttcctc agcttgaagc gctctatgag 300
aatgacaagc cagaccttat ccttttttgac tttatggcca tggcgggaaa actgctggct 360
gagaagtttg gaatagaggc ggtccgcctt tgttctacat atgcacagaa cgaacatttt 420
acattcagat ccatttctga agagtttaag atcgagctga cgcctgagca agaggatgct 480
ttgaaaaatt cgaatcttcc gtcatttaac tttgaggata tgttcgagcc tgcaaaattg 540
aacattgtct ttatgcctcg tgcttttcag ccttacggcg aaacgtttga tgagcggttc 600
tcttttgttg gtccttctct tgccaaacgc aagtttcagg aaaaagaaac gccgattatt 660
tcggacagcg gccgtcctgt catgctgata tctttaggga cggcgttcaa tgcctggccg 720
gaattttatc atatgtgcat agaagcattc agggacacga agtggcaggt tatcatggct 780
gttggcacga caatcgatcc tgaaagcttt gatgacatac ctgagaactt ttcgattcat 840
cagcgcgttc ctcagctgga gatcctgaag aaagcggagc tgttcatcac ccatgggggt 900
atgaacagta cgatggaagg gttgaatgcc ggtgtaccgc tcgttgccgt tccgcaaatg 960
cctgaacagg aaatcactgc ccgccgcgtc gaagagcttg ggcttggcaa gcatttgcag 1020
ccggaagaca caacagcagc ttcactgcgg gaagccgtct ctcagacgga tggtgacccg 1080
catgtcctga aacggataca ggacatgcaa aagcacatta aacaagccgg aggggccgag 1140
aaagccgcag atgaaattga ggcattttta gcacccgcag gagtaaaata a 1191

<210> 407
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> 301 UGT98

<400> 407
Met Asp Ala Gln Arg Gly His Thr Thr Thr Ile Leu Met Phe Pro Trp
 1               5                  10                  15
Leu Gly Tyr Gly His Leu Ser Ala Phe Leu Glu Leu Ala Lys Ser Leu
            20                  25                  30
Ser Arg Arg Asn Phe His Ile Tyr Phe Cys Ser Thr Ser Val Asn Leu
        35                  40                  45
Asp Ala Ile Lys Pro Lys Leu Pro Ser Ser Ser Ser Ser Asp Ser Ile
    50                  55                  60
Gln Leu Val Glu Leu Cys Leu Pro Ser Ser Pro Asp Gln Leu Pro Pro
65                  70                  75                  80
His Leu His Thr Thr Asn Ala Leu Pro Pro His Leu Met Pro Thr Leu
                85                  90                  95
His Gln Ala Phe Ser Met Ala Ala Gln His Phe Ala Ala Ile Leu His
            100                 105                 110
Thr Leu Ala Pro His Leu Leu Ile Tyr Asp Ser Phe Gln Pro Trp Ala
        115                 120                 125
Pro Gln Leu Ala Ser Ser Leu Asn Ile Pro Ala Ile Asn Phe Asn Thr
    130                 135                 140
Thr Gly Ala Ser Val Leu Thr Arg Met Leu His Ala Thr His Tyr Pro
145                 150                 155                 160
Ser Ser Lys Phe Pro Ile Ser Glu Phe Val Leu His Asp Tyr Trp Lys
                165                 170                 175
Ala Met Tyr Ser Ala Ala Gly Gly Ala Val Thr Lys Lys Asp His Lys
            180                 185                 190
Ile Gly Glu Thr Leu Ala Asn Cys Leu His Ala Ser Cys Ser Val Ile
        195                 200                 205
Leu Ile Asn Ser Phe Arg Glu Leu Glu Glu Lys Tyr Met Asp Tyr Leu
    210                 215                 220

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

<210> 408
<211> 1419
<212> DNA
<213> Artificial Sequence

<220>
<223> 301(gDNA, native)

<400> 408
ctcgaattca tggatgccca gcgaggtcac accacaacca ttttgatgtt tccatggctc 60
ggctatggcc atctttcggc tttcctagag ttggccaaaa gcctctcaag gaggaacttc 120
catatctact tctgttcaac ctctgttaac ctcgacgcca ttaaaccaaa gcttccttct 180
tcttcctctt ctgattccat ccaacttgtg gaactttgtc ttccatcttc tcctgatcag 240
ctccctcctc atcttcacac aaccaacgcc ctccccccctc acctcatgcc cactctccac 300
caagccttct ccatggctgc ccaacacttt gctgccattt tacacacact tgctccgcat 360
ctcctcattt acgactcttt ccaaccttgg gctcctcaac tagcttcatc cctcaacatt 420
ccagccatca acttcaatac tacgggagct tcagtcctga cccgaatgct tcacgctact 480
cactacccaa gttctaaatt cccaatttca gagtttgttc tccacgatta ttggaaagcc 540
atgtacagcg ccgccggtgg ggctgttaca aaaaaagacc acaaaattgg agaaacactt 600
gcgaattgct tgcatgcttc ttgtagtgta attctaatca atagtttcag agagctcgag 660

gagaaatata tggattatct ctccgttctc ttgaacaaga aagttgttcc ggttggtcct 720
ttggtttacg aaccgaatca agacggggaa gatgaaggtt attcaagcat caaaaattgg 780
cttgacaaaa aggaaccgtc ctccaccgtc ttcgtttcat ttggaagcga atacttcccg 840
tcaaaggaag aaatggaaga gatagcccat gggttagagg cgagcgaggt tcatttcatc 900
tgggtcgtta ggtttcctca aggagacaac accagcgcca ttgaagatgc cttgccgaag 960
gggtttctgg agagggtggg agagagaggg atggtggtga agggttgggc tccccaggcg 1020
aagatactga agcattggag cacaggggga ttcgtgagcc actgtggatg gaactcggtg 1080
atggaaagca tgatgtttgg cgttcccata ataggggttc cgatgcatct ggaccagccc 1140
tttaacgccg gactcgcgga agaagctggc gtcggcgtgg aagccaagcg agattcggac 1200
ggcaaaattc aaagagaaga agttgcaaag tcgatcaaag aagtggtgat tgagaaaacc 1260
agggaagacg tgaggaagaa agcaagagaa atgggtgaga ttttgaggag taaaggagat 1320
gagaaaattg atgagttggt ggctgaaatt tctcttttgc gcaaaaaggc cccatgttca 1380
attgcggccg cactcgagca ccaccaccac caccactga 1419

<210> 409
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> UDP-glycosyltransferases (339)

<400> 409
Met Val Gln Pro Arg Val Leu Leu Phe Pro Phe Pro Ala Leu Gly His
 1               5                  10                  15
Val Lys Pro Phe Leu Ser Leu Ala Glu Leu Leu Ser Asp Ala Gly Ile
            20                  25                  30
Asp Val Val Phe Leu Ser Thr Glu Tyr Asn His Arg Arg Ile Ser Asn
        35                  40                  45
Thr Glu Ala Leu Ala Ser Arg Phe Pro Thr Leu His Phe Glu Thr Ile
    50                  55                  60
Pro Asp Gly Leu Pro Pro Asn Glu Ser Arg Ala Leu Ala Asp Gly Pro
65                  70                  75                  80
Leu Tyr Phe Ser Met Arg Glu Gly Thr Lys Pro Arg Phe Arg Gln Leu
                85                  90                  95
Ile Gln Ser Leu Asn Asp Gly Arg Trp Pro Ile Thr Cys Ile Ile Thr
            100                 105                 110
Asp Ile Met Leu Ser Ser Pro Ile Glu Val Ala Glu Glu Phe Gly Ile
        115                 120                 125
Pro Val Ile Ala Phe Cys Pro Cys Ser Ala Arg Tyr Leu Ser Ile His
    130                 135                 140
Phe Phe Ile Pro Lys Leu Val Glu Glu Gly Gln Ile Pro Tyr Ala Asp
145                 150                 155                 160
Asp Asp Pro Ile Gly Glu Ile Gln Gly Val Pro Leu Phe Glu Gly Leu
                165                 170                 175
Leu Arg Arg Asn His Leu Pro Gly Ser Trp Ser Asp Lys Ser Ala Asp
            180                 185                 190
Ile Ser Phe Ser His Gly Leu Ile Asn Gln Thr Leu Ala Ala Gly Arg
        195                 200                 205
Ala Ser Ala Leu Ile Leu Asn Thr Phe Asp Glu Leu Glu Ala Pro Phe
    210                 215                 220
Leu Thr His Leu Ser Ser Ile Phe Asn Lys Ile Tyr Thr Ile Gly Pro
225                 230                 235                 240
Leu His Ala Leu Ser Lys Ser Arg Leu Gly Asp Ser Ser Ser Ser Ala

```
                245                 250                 255
Ser Ala Leu Ser Gly Phe Trp Lys Glu Asp Arg Ala Cys Met Ser Trp
            260                 265                 270
Leu Asp Cys Gln Pro Pro Arg Ser Val Val Phe Val Ser Phe Gly Ser
        275                 280                 285
Thr Met Lys Met Lys Ala Asp Glu Leu Arg Glu Phe Trp Tyr Gly Leu
    290                 295                 300
Val Ser Ser Gly Lys Pro Phe Leu Cys Val Leu Arg Ser Asp Val Val
305                 310                 315                 320
Ser Gly Gly Glu Ala Ala Glu Leu Ile Glu Gln Met Ala Glu Glu Glu
                325                 330                 335
Gly Ala Gly Gly Lys Leu Gly Met Val Val Glu Trp Ala Ala Gln Glu
            340                 345                 350
Lys Val Leu Ser His Pro Ala Val Gly Gly Phe Leu Thr His Cys Gly
        355                 360                 365
Trp Asn Ser Thr Val Glu Ser Ile Ala Ala Gly Val Pro Met Met Cys
    370                 375                 380
Trp Pro Ile Leu Gly Asp Gln Pro Ser Asn Ala Thr Trp Ile Asp Arg
385                 390                 395                 400
Val Trp Lys Ile Gly Val Glu Arg Asn Asn Arg Glu Trp Asp Arg Leu
                405                 410                 415
Thr Val Glu Lys Met Val Arg Ala Leu Met Glu Gly Gln Lys Arg Val
            420                 425                 430
Glu Ile Gln Arg Ser Met Glu Lys Leu Ser Lys Leu Ala Asn Glu Lys
        435                 440                 445
Val Val Arg Gly Gly Leu Ser Phe Asp Asn Leu Glu Val Leu Val Glu
    450                 455                 460
Asp Ile Lys Lys Leu Lys Pro Tyr Lys Phe
465                 470
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<210> 410
<211> 1425
<212> DNA
<213> Artificial Sequence

<220>
<223> 339 (gDNA)

<400> 410
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atggtgcaac ctcgggtact gctgtttcct ttcccggcac tgggccacgt gaagcccttc 60
ttatcactgg cggagctgct ttccgacgcc ggcatagacg tcgtcttcct cagcaccgag 120
tataaccacc gtcggatctc caacactgaa gccctagcct cccgcttccc gacgcttcat 180
ttcgaaacta taccggatgg cctgccgcct aatgagtcgc gcgctcttgc cgacggccca 240
ctgtatttct ccatgcgtga gggaactaaa ccgagattcc ggcaactgat tcaatctctt 300
aacgacggtc gttggcccat cacctgtatt atcactgaca tcatgttatc ttctccgatt 360
gaagtagcgg aagaatttgg gattccagta attgccttct gcccctgcag tgctcgctac 420
ttatcgattc actttttat accgaagctc gttgaggaag gtcaaattcc atacgcagat 480
gacgatccga ttggagagat ccaggggtg cccttgttcg aaggtctttt gcgacggaat 540
catttgcctg gttcttggtc tgataaatct gcagatatat ctttctcgca tggcttgatt 600
aatcagaccc ttgcagctgg tcgagcctcg gctcttatac tcaacacctt cgacgagctc 660
gaagctccat ttctgaccca tctctcttcc attttcaaca aaatctacac cattggaccc 720
ctccatgctc tgtccaaatc aaggctcggc gactcctcct cctccgcttc tgccctctcc 780
ggattctgga aagaggatag agcctgcatg tcctggctcg actgtcagcc gccgagatct 840
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gtggttttcg tcagtttcgg gagtacgatg aagatgaaag ccgatgaatt gagagagttc 900
tggtatgggt tggtgagcag cgggaaaccg ttcctctgcg tgttgagatc cgacgttgtt 960
tccggcggag aagcggcgga attgatcgaa cagatggcgg aggaggaggg agctggaggg 1020
aagctgggaa tggtagtgga gtgggcagcg caagagaagg tcctgagcca ccctgccgtc 1080
ggtgggtttt tgacgcactg cgggtggaac tcaacggtgg aaagcattgc cgcgggagtt 1140
ccgatgatgt gctggccgat tctcggcgac caacccagca acgccacttg gatcgacaga 1200
gtgtggaaaa ttggggttga aaggaacaat cgtgaatggg acaggttgac ggtggagaag 1260
atggtgagag cattgatgga aggccaaaag agagtggaga ttcagagatc aatggagaag 1320
ctttcaaagt tggcaaatga gaaggttgtc aggggtgggt tgtcttttga taacttggaa 1380
gttctcgttg aagacatcaa aaaattgaaa ccatataaat tttaa 1425

<210> 411
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> 330

<400> 411
Met Asp Thr Arg Lys Arg Ser Ile Arg Ile Leu Met Phe Pro Trp Leu
 1               5                  10                  15
Ala His Gly His Ile Ser Ala Phe Leu Glu Leu Ala Lys Ser Leu Ala
            20                  25                  30
Lys Arg Asn Phe Val Ile Tyr Ile Cys Ser Ser Gln Val Asn Leu Asn
        35                  40                  45
Ser Ile Ser Lys Asn Met Ser Ser Lys Asp Ser Ile Ser Val Lys Leu
    50                  55                  60
Val Glu Leu His Ile Pro Thr Thr Ile Leu Pro Pro Pro Tyr His Thr
65                  70                  75                  80
Thr Asn Gly Leu Pro Pro His Leu Met Ser Thr Leu Lys Arg Ala Leu
                85                  90                  95
Asp Ser Ala Arg Pro Ala Phe Ser Thr Leu Leu Gln Thr Leu Lys Pro
            100                 105                 110
Asp Leu Val Leu Tyr Asp Phe Leu Gln Ser Trp Ala Ser Glu Glu Ala
        115                 120                 125
Glu Ser Gln Asn Ile Pro Ala Met Val Phe Leu Ser Thr Gly Ala Ala
    130                 135                 140
Ala Ile Ser Phe Ile Met Tyr His Trp Phe Glu Thr Arg Pro Glu Glu
145                 150                 155                 160
Tyr Pro Phe Pro Ala Ile Tyr Phe Arg Glu His Glu Tyr Asp Asn Phe
                165                 170                 175
Cys Arg Phe Lys Ser Ser Asp Ser Gly Thr Ser Asp Gln Leu Arg Val
            180                 185                 190
Ser Asp Cys Val Lys Arg Ser His Asp Leu Val Leu Ile Lys Thr Phe
        195                 200                 205
Arg Glu Leu Glu Gly Gln Tyr Val Asp Phe Leu Ser Asp Leu Thr Arg
    210                 215                 220
Lys Arg Phe Val Pro Val Gly Pro Leu Val Gln Glu Val Gly Cys Asp
225                 230                 235                 240
Met Glu Asn Glu Gly Asn Asp Ile Ile Glu Trp Leu Asp Gly Lys Asp
                245                 250                 255
Arg Arg Ser Thr Val Phe Ser Ser Phe Gly Ser Glu Tyr Phe Leu Ser
            260                 265                 270

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Ala Asn Glu Ile Glu Glu Ile Ala Tyr Gly Leu Glu Leu Ser Gly Leu
        275                 280                 285
Asn Phe Ile Trp Val Val Arg Phe Pro His Gly Asp Glu Lys Ile Lys
    290                 295                 300
Ile Glu Glu Lys Leu Pro Glu Gly Phe Leu Glu Arg Val Glu Gly Arg
305                 310                 315                 320
Gly Leu Val Val Glu Gly Trp Ala Gln Gln Arg Arg Ile Leu Ser His
                325                 330                 335
Pro Ser Val Gly Gly Phe Leu Ser His Cys Gly Trp Ser Ser Val Met
            340                 345                 350
Glu Gly Val Tyr Ser Gly Val Pro Ile Ile Ala Val Pro Met His Leu
        355                 360                 365
Asp Gln Pro Phe Asn Ala Arg Leu Val Glu Ala Val Gly Phe Gly Glu
    370                 375                 380
Glu Val Val Arg Ser Arg Gln Gly Asn Leu Asp Arg Gly Glu Val Ala
385                 390                 395                 400
Arg Val Val Lys Lys Leu Val Met Gly Lys Ser Gly Glu Gly Leu Arg
                405                 410                 415
Arg Arg Val Glu Glu Leu Ser Glu Lys Met Arg Glu Lys Gly Glu Glu
            420                 425                 430
Glu Ile Asp Ser Leu Val Glu Glu Leu Val Thr Val Val Arg Arg Arg
        435                 440                 445
Glu Arg Ser Asn Leu Lys Ser Glu Asn Ser Met Lys Lys Leu Asn Val
    450                 455                 460
Met Asp Asp Gly Glu
465
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<210> 412
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> 330 (gDNA, native)

<400> 412
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atggatacaa gaaagagaag catcaggatt ctaatgttcc catggcttgc tcatggccat 60
atctcagcat tcctcgagct ggcgaagtca cttgccaaaa gaaacttcgt catttacatt 120
tgttcttcac aagtaaatct aaattccatc agcaagaaca tgtcatcaaa agactccatt 180
tccgtaaaac ttgttgagct tcacattccc accaccatac ttccccctcc ttaccacacc 240
accaatggcc tcccacccca cctcatgtcc accctcaaga gagccctcga cagtgcccgg 300
cccgccttct ccaccctcct ccaaaccctc aagcccgact tggttttata cgatttcctc 360
cagtcgtggg cctcggagga ggccgagtcg cagaatatac cagccatggt gtttctgagt 420
accggagctg cagcgatttc ttttattatg taccattggt ttgagaccag accggaggag 480
taccctttc cggctatata cttccgggaa cacgagtatg ataacttctg ccgttttaag 540
tcttccgaca gcggtactag tgatcaattg agagtcagcg attgcgttaa acggtcgcac 600
gatttggttc tgatcaagac attccgtgaa ctggaaggac aatacgtaga ttttctctcc 660
gacttgactc ggaagagatt cgtaccagtt ggccccttg ttcaggaggt aggttgtgat 720
atggagaatg aaggaaatga catcatcgaa tggctcgacg ggaaagaccg tcgttcgacg 780
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gagaaaatca agattgagga gaaactgccg gaagggtttc ttgagagagt ggaaggaaga 960
gggttggtgg tggagggatg ggcacagcag aggagaatat tgtcacatcc gagtgttgga 1020
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agggtggtga agaagctggt tatggggaaa agtggggagg ggttacggcg gagggtggag 1260
gagttgagtg agaagatgag agagaaaggg gaggaggaga ttgattcact ggtggaggaa 1320
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<210> 413
<211> 406
<212> PRT
<213> Artificial Sequence

<220>
<223> UDP-glycosyltransferases (328) described in Itkin
et al.

<220>
<221> VARIANT
<222> 153
<223> Xaa = Any Amino Acid

<400> 413
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            20                  25                  30
Leu Ser Arg Arg Asn Phe His Ile Tyr Phe Cys Ser Thr Ser Val Asn
        35                  40                  45
Leu Asp Ala Ile Lys Pro Lys Leu Pro Ser Ser Phe Ser Asp Ser Ile
    50                  55                  60
Gln Phe Val Glu Leu His Leu Pro Ser Ser Pro Glu Phe Pro Pro His
65                  70                  75                  80
Leu His Thr Thr Asn Gly Leu Pro Pro Thr Leu Met Pro Ala Leu His
                85                  90                  95
Gln Ala Phe Ser Met Ala Ala Gln His Phe Glu Ser Ile Leu Gln Thr
            100                 105                 110
Leu Ala Pro His Leu Leu Ile Tyr Asp Ser Leu Gln Pro Trp Ala Pro
        115                 120                 125
Arg Val Ala Ser Ser Leu Lys Ile Pro Ala Ile Asn Phe Asn Thr Thr
    130                 135                 140
Gly Val Phe Val Ile Ser Gln Gly Xaa His Pro Ile His Tyr Pro His
145                 150                 155                 160
Ser Lys Phe Pro Phe Ser Glu Phe Val Leu His Asn His Trp Lys Ala
                165                 170                 175
Met Tyr Ser Thr Ala Asp Gly Ala Ser Thr Glu Arg Thr Arg Lys Arg
            180                 185                 190
Gly Glu Ala Phe Leu Tyr Cys Leu His Ala Ser Cys Ser Val Ile Leu
        195                 200                 205
Ile Asn Ser Phe Arg Glu Leu Glu Gly Lys Tyr Met Asp Tyr Leu Ser
    210                 215                 220
Val Leu Leu Asn Lys Lys Val Val Pro Val Gly Pro Leu Val Tyr Glu
225                 230                 235                 240
Pro Asn Gln Asp Gly Glu Asp Glu Gly Tyr Ser Ser Ile Lys Asn Trp

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                245                 250                 255
Leu Asp Lys Lys Glu Pro Ser Ser Thr Val Phe Val Ser Phe Gly Ser
            260                 265                 270
Glu Tyr Phe Pro Ser Lys Glu Glu Met Glu Glu Ile Ala His Gly Leu
        275                 280                 285
Glu Ala Ser Glu Val Asn Phe Ile Trp Val Val Arg Phe Pro Gln Gly
    290                 295                 300
Asp Asn Thr Ser Gly Ile Glu Asp Ala Leu Pro Lys Gly Phe Leu Glu
305                 310                 315                 320
Arg Ala Gly Glu Arg Gly Met Val Val Lys Gly Trp Ala Pro Gln Ala
                325                 330                 335
Lys Ile Leu Lys His Trp Ser Thr Gly Gly Phe Val Ser His Cys Gly
            340                 345                 350
Trp Asn Ser Val Met Glu Ser Met Met Phe Gly Val Pro Ile Ile Gly
        355                 360                 365
Val Pro Met His Val Asp Gln Pro Phe Asn Ala Gly Leu Val Glu Glu
    370                 375                 380
Ala Gly Val Gly Val Glu Ala Lys Arg Asp Pro Asp Gly Lys Ile Gln
385                 390                 395                 400
Arg Asp Glu Val Ala Lys
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<210> 414
<211> 1359
<212> DNA
<213> Artificial Sequence

<220>
<223> 328 (gDNA, native)

<400> 414

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tacttctgtt caacctctgt taatcttgac gccattaaac caaagcttcc ttcttctttc 180
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atggctgccc agcactttga gtccatttta caaacacttg ccccgcacct tctcatttat 360
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catgcttctt gtagtgtaat tctaatcaat agtttcagag agctcgaggg gaaatatatg 660
gattatctct ctgttctctt gaacaagaaa gttgttccgg ttggtccttt ggtttacgaa 720
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agagacgaag ttgcaaagtt gatcaaagaa gtggtggttg agaaaaccag agaagatgtg 1260
cggaagaaag caagagaaat gagtgagatt ttgaggagca agggagagga gaagtttgat 1320
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gagatggtcg ctgaaatttc tctcttgctt aaaatatga 1359

<210> 415
<211> 828
<212> PRT
<213> Artificial Sequence

<220>
<223> AtSus1

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

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            340                 345                 350
Arg Ile Leu Ile Leu Thr Arg Leu Leu Pro Asp Ala Val Gly Thr Thr
        355                 360                 365
Cys Gly Glu Arg Leu Glu Arg Val Tyr Asp Ser Glu Tyr Cys Asp Ile
    370                 375                 380
Leu Arg Val Pro Phe Arg Thr Glu Lys Gly Ile Val Arg Lys Trp Ile
385                 390                 395                 400
Ser Arg Phe Glu Val Trp Pro Tyr Leu Glu Thr Tyr Thr Glu Asp Ala
                405                 410                 415
Ala Val Glu Leu Ser Lys Glu Leu Asn Gly Lys Pro Asp Leu Ile Ile
            420                 425                 430
Gly Asn Tyr Ser Asp Gly Asn Leu Val Ala Ser Leu Leu Ala His Lys
        435                 440                 445
Leu Gly Val Thr Gln Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys
    450                 455                 460
Tyr Pro Asp Ser Asp Ile Tyr Trp Lys Lys Leu Asp Asp Lys Tyr His
465                 470                 475                 480
Phe Ser Cys Gln Phe Thr Ala Asp Ile Phe Ala Met Asn His Thr Asp
                485                 490                 495
Phe Ile Ile Thr Ser Thr Phe Gln Glu Ile Ala Gly Ser Lys Glu Thr
            500                 505                 510
Val Gly Gln Tyr Glu Ser His Thr Ala Phe Thr Leu Pro Gly Leu Tyr
        515                 520                 525
Arg Val Val His Gly Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val
    530                 535                 540
Ser Pro Gly Ala Asp Met Ser Ile Tyr Phe Pro Tyr Thr Glu Glu Lys
545                 550                 555                 560
Arg Arg Leu Thr Lys Phe His Ser Glu Ile Glu Glu Leu Leu Tyr Ser
                565                 570                 575
Asp Val Glu Asn Lys Glu His Leu Cys Val Leu Lys Asp Lys Lys Lys
            580                 585                 590
Pro Ile Leu Phe Thr Met Ala Arg Leu Asp Arg Val Lys Asn Leu Ser
        595                 600                 605
Gly Leu Val Glu Trp Tyr Gly Lys Asn Thr Arg Leu Arg Glu Leu Ala
    610                 615                 620
Asn Leu Val Val Val Gly Gly Asp Arg Arg Lys Glu Ser Lys Asp Asn
625                 630                 635                 640
Glu Glu Lys Ala Glu Met Lys Lys Met Tyr Asp Leu Ile Glu Glu Tyr
                645                 650                 655
Lys Leu Asn Gly Gln Phe Arg Trp Ile Ser Ser Gln Met Asp Arg Val
            660                 665                 670
Arg Asn Gly Glu Leu Tyr Arg Tyr Ile Cys Asp Thr Lys Gly Ala Phe
        675                 680                 685
Val Gln Pro Ala Leu Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala
    690                 695                 700
Met Thr Cys Gly Leu Pro Thr Phe Ala Thr Cys Lys Gly Gly Pro Ala
705                 710                 715                 720
Glu Ile Ile Val His Gly Lys Ser Gly Phe His Ile Asp Pro Tyr His
                725                 730                 735
Gly Asp Gln Ala Ala Asp Thr Leu Ala Asp Phe Phe Thr Lys Cys Lys
            740                 745                 750
Glu Asp Pro Ser His Trp Asp Glu Ile Ser Lys Gly Gly Leu Gln Arg
        755                 760                 765
Ile Glu Glu Lys Tyr Thr Trp Gln Ile Tyr Ser Gln Arg Leu Leu Thr
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    770                 775                 780
Leu Thr Gly Val Tyr Gly Phe Trp Lys His Val Ser Asn Leu Asp Arg
785                 790                 795                 800
Leu Glu Ala Arg Arg Tyr Leu Glu Met Phe Tyr Ala Leu Lys Tyr Arg
                805                 810                 815
Pro Leu Ala Gln Ala Val Pro Leu Ala Gln Asp Asp
            820                 825
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<210> 416
<211> 2487
<212> DNA
<213> Artificial Sequence

<220>
<223> AtSus1 (gDNA, native)

<400> 416

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acgcttgttt ctgagagaaa cgaagtcctt gccttgcttt ccagggttga agccaaaggt 180
aaaggtattt tacaacaaaa ccagatcatt gctgaattcg aagctttgcc tgaacaaacc 240
cggaagaaac ttgaaggtgg tcctttcttt gaccttctca aatccactca ggaagcaatt 300
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cgagtcaatc tccatgctct tgtcgttgaa gaactccaac ctgctgagtt tcttcatttc 420
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cagaacctca acactctgca acacaccttg aggaaagcag aagagtatct agcagagctt 720
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<210> 417
<211> 759
<212> PRT
<213> Artificial Sequence

<220>
<223> SgCbQ

<400> 417
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            20                  25                  30
Phe Cys Pro Asp Ala Gly Thr Gln Gln Gln Leu Leu Gln Val His Lys
        35                  40                  45
Ala Arg Lys Ala Phe His Asp Asp Arg Phe His Arg Lys Gln Ser Ser
    50                  55                  60
Asp Leu Phe Ile Thr Ile Gln Tyr Gly Lys Glu Val Glu Asn Gly Gly
65                  70                  75                  80
Lys Thr Ala Gly Val Lys Leu Lys Glu Gly Glu Glu Val Arg Lys Glu
                85                  90                  95
Ala Val Glu Ser Ser Leu Glu Arg Ala Leu Ser Phe Tyr Ser Ser Ile
            100                 105                 110
Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro Met Phe
        115                 120                 125
Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val Thr Gly Val Leu Asn
    130                 135                 140
Ser Val Leu Ser Lys His His Arg Gln Glu Met Cys Arg Tyr Val Tyr
145                 150                 155                 160
Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly Pro
                165                 170                 175
Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu Leu
            180                 185                 190
Gly Glu Asp Ala Asn Ala Gly Ala Met Pro Lys Ala Arg Ala Trp Ile
        195                 200                 205
Leu Asp His Gly Gly Ala Thr Gly Ile Thr Ser Trp Gly Lys Leu Trp
    210                 215                 220
Leu Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn Pro Leu Pro
225                 230                 235                 240
Pro Glu Phe Trp Leu Phe Pro Tyr Phe Leu Pro Phe His Pro Gly Arg
                245                 250                 255
Met Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr
            260                 265                 270
Gly Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu Ser Leu Arg
        275                 280                 285
Lys Glu Leu Tyr Ala Val Pro Tyr His Glu Ile Asp Trp Asn Lys Ser
    290                 295                 300

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Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met
305                 310                 315                 320
Gln Asp Ile Leu Trp Gly Ser Leu His His Val Tyr Glu Pro Leu Phe
                325                 330                 335
Thr Arg Trp Pro Ala Lys Arg Leu Arg Glu Lys Ala Leu Gln Thr Ala
            340                 345                 350
Met Gln His Ile His Tyr Glu Asp Glu Asn Thr Arg Tyr Ile Cys Leu
        355                 360                 365
Gly Pro Val Asn Lys Val Leu Asn Leu Leu Cys Cys Trp Val Glu Asp
    370                 375                 380
Pro Tyr Ser Asp Ala Phe Lys Leu His Leu Gln Arg Val His Asp Tyr
385                 390                 395                 400
Leu Trp Val Ala Glu Asp Gly Met Lys Met Gln Gly Tyr Asn Gly Ser
                405                 410                 415
Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Val Ser Thr Lys
            420                 425                 430
Leu Val Asp Asn Tyr Gly Pro Thr Leu Arg Lys Ala His Asp Phe Val
        435                 440                 445
Lys Ser Ser Gln Ile Gln Gln Asp Cys Pro Gly Asp Pro Asn Val Trp
    450                 455                 460
Tyr Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His
465                 470                 475                 480
Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ala Leu
                485                 490                 495
Met Leu Ser Lys Leu Pro Ser Glu Thr Val Gly Glu Ser Leu Glu Arg
            500                 505                 510
Asn Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Asp
        515                 520                 525
Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu
    530                 535                 540
Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr
545                 550                 555                 560
Pro Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Thr Leu Phe
                565                 570                 575
Lys Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Thr Ala Ile
            580                 585                 590
Val Arg Ala Ala Asn Phe Leu Glu Asn Met Gln Arg Thr Asp Gly Ser
        595                 600                 605
Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly
    610                 615                 620
Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Leu Ala
625                 630                 635                 640
Ile Arg Lys Ala Cys Asp Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly
                645                 650                 655
Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn
            660                 665                 670
Leu Glu Gly Asn Arg Pro His Leu Val Asn Thr Ala Trp Val Leu Met
        675                 680                 685
Ala Leu Ile Glu Ala Gly Gln Ala Glu Arg Asp Pro Thr Pro Leu His
    690                 695                 700
Arg Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Asn Gly Asp Phe
705                 710                 715                 720
Pro Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr
                725                 730                 735
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Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr
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Cys His Arg Val Leu Thr Glu
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<210> 418
<211> 2280
<212> DNA
<213> Artificial Sequence

<220>
<223> SgCbQ (gDNA)

<400> 418
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caacagctct tgcaagtcca caaagctcgt aaagctttcc acgatgaccg tttccaccga 180
aagcaatctt ccgatctctt tatcactatt cagtatggaa aggaagtaga aaatggtgga 240
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gggtggtttg gcataaaggg attggtggct gcaggaagga catataataa ttgccttgcc 1920
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agttaccttt catgtcagaa taaggtatac acaaatcttg aaggaaacag accgcacctg 2040
gttaacacgg cctgggtttt aatggccctc atagaagctg gccaggctga gagagaccca 2100
acaccattgc atcgtgcagc aaggttgtta atcaattccc agttggagaa tggtgatttc 2160
ccccaacagg agatcatggg agtctttaat aaaaattgca tgatcacata tgctgcatac 2220
cgaaacattt ttcccatttg ggctcttgga gagtattgcc atcgggtttt gactgaataa 2280

<210> 419
<211> 2280
<212> DNA
<213> Unknown

<220>
<223> Siraitia grosvenorii cucurbitadienol synthase

<400> 419
atgtggaggt taaaggtcgg agcagaaagc gttggggaga atgatgagaa atggttgaag 60
agcataagca atcacttggg acgccaggtg tgggagttct gtccggatgc cggcacccaa 120
caacagctct tgcaagtcca caaagctcgt aaagctttcc acgatgaccg tttccaccga 180
aagcaatctt ccgatctctt tatcactatt cagtatggaa aggaagtaga aaatggtgga 240
aagacagcgg gagtgaaatt gaaagaaggg gaagaggtga ggaaagaggc agtagagagt 300
agcttagaga gggcattaag tttctactca agcatccaga caagcgatgg gaactgggct 360
tcggatcttg gggggcccat gtttttactt ccgggtctgg tgattgccct ctacgttaca 420
ggcgtcttga attctgtttt atccaagcac caccggcaag agatgtgcag atatgtttac 480
aatcaccaga atgaagatgg ggggtggggt ctccacatcg agggcccaag caccatgttt 540
ggttccgcac tgaattatgt tgcactcagg ctgcttggag aagacgccaa cgccggggca 600
atgccaaaag cacgtgcttg gatcttggac cacggtggcg ccaccggaat cacttcctgg 660
ggcaaattgt ggctttctgt acttggagtc tacgaatgga gtggcaataa tcctcttcca 720
cccgaatttt ggttatttcc ttacttccta ccatttcatc caggaagaat gtggtgccat 780
tgtcgaatgg tttatctacc aatgtcatac ttatatggaa agagatttgt tgggccaatc 840
acacccatag ttctgtctct cagaaaagaa ctctacgcag ttccatatca tgaaatagac 900
tggaataaat ctcgcaatac atgtgcaaag gaggatctgt actatccaca tcccaagatg 960
caagatattc tgtggggatc tctccaccac gtgtatgagc ccttgtttac tcgttggcct 1020
gccaaacgcc tgagagaaaa ggctttgcag actgcaatgc aacatattca ctatgaagat 1080
gagaataccc gatatatatg ccttggccct gtcaacaagg tactcaatct gctttgttgt 1140
tgggttgaag atccctactc cgacgccttc aaacttcatc ttcaacgagt ccatgactat 1200
ctctgggttg ctgaagatgg catgaaaatg cagggttata atgggagcca gttgtgggac 1260
actgctttct ccatccaagc aatcgtatcc accaaacttg tagacaacta tggcccaacc 1320
ttaagaaagg cacacgactt cgttaaaagt tctcagattc agcaggactg tcctggggat 1380
cctaatgttt ggtaccgtca cattcataaa ggtgcatggc cattttcaac tcgagatcat 1440
ggatggctca tctctgactg tacagcagag ggattaaagg ctgctttgat gttatccaaa 1500
cttccatccg aaacagttgg ggaatcatta gaacggaatc gcctttgcga tgctgtaaac 1560
gttctccttt ctttgcaaaa cgataatggt ggctttgcat catatgagtt gacaagatca 1620
tacccttggt tggagttgat caaccccgca gaaacgtttg gagatattgt cattgattat 1680
ccgtatgtgg agtgcacctc agccacaatg gaagcactga cgttgtttaa gaaattacat 1740
cccggccata ggaccaaaga aattgatact gctattgtca gggcggccaa cttccttgaa 1800
aatatgcaaa ggacggatgg ctcttggtat ggatgttggg gggtttgctt cacgtatgcg 1860
gggtggtttg gcataaaggg attggtggct gcaggaagga catataataa ttgccttgcc 1920
attcgcaagg cttgcgattt tttactatct aaagagctgc ccggcggtgg atggggagag 1980
agttaccttt catgtcagaa taaggtatac acaaatcttg aaggaaacag accgcacctg 2040
gttaacacgg cctgggtttt aatggccctc atagaagctg gccaggctga gagagaccca 2100
acaccattgc atcgtgcagc aaggttgtta atcaattccc agttggagaa tggtgatttc 2160
ccccaacagg agatcatggg agtctttaat aaaaattgca tgatcacata tgctgcatac 2220
cgaaacattt ttcccatttg ggctcttgga gagtattgcc atcgggtttt gactgaataa 2280


<210> 420
<211> 766
<212> PRT
<213> Artificial Sequence

<220>
<223> Cpep2

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

385 390 395 400
Leu Gln Arg Val His Asp Tyr Leu Trp Val Ala Glu Asp Gly Met Arg
405 410 415
Met Gln Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile
420 425 430
Gln Ala Ile Val Ala Thr Lys Leu Val Asp Ser Tyr Ala Pro Thr Leu
435 440 445
Arg Lys Ala His Asp Phe Val Lys Asp Ser Gln Ile Gln Glu Asp Cys
450 455 460
Pro Gly Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp
465 470 475 480
Pro Phe Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala
485 490 495
Glu Gly Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Thr Met
500 505 510
Val Gly Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val
515 520 525
Leu Leu Ser Leu Gln Asn Asp Asn Gly Gly Phe Ala Ser Tyr Glu Leu
530 535 540
Thr Arg Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe
545 550 555 560
Gly Asp Ile Val Ile Asp Tyr Pro Tyr Val Glu Cys Thr Ala Ala Thr
565 570 575
Met Glu Ala Leu Thr Leu Phe Lys Lys Leu His Pro Gly His Arg Thr
580 585 590
Lys Glu Ile Asp Thr Ala Ile Gly Lys Ala Ala Asn Phe Leu Glu Lys
595 600 605
Met Gln Arg Ala Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe
610 615 620
Thr Tyr Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg
625 630 635 640
Thr Tyr Asn Ser Cys Leu Ala Ile Arg Lys Ala Cys Glu Phe Leu Leu
645 650 655
Ser Lys Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys
660 665 670
Gln Asn Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val
675 680 685
Asn Thr Ala Trp Val Leu Met Ala Leu Ile Glu Ala Gly Gln Gly Glu
690 695 700
Arg Asp Pro Ala Pro Leu His Arg Gly Ala Arg Leu Val Met Asn Ser
705 710 715 720
Gln Leu Glu Asn Gly Asp Phe Val Gln Gln Glu Ile Met Gly Val Phe
725 730 735
Asn Lys Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro
740 745 750
Ile Trp Ala Leu Gly Glu Tyr Cys His Arg Val Leu Thr Glu
755 760 765

<210> 421
<211> 2301
<212> DNA
<213> Artificial Sequence

<220>
<223> Cpep2

<400> 421
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agcgtaagca atcacttggg ccgccaagtt tgggagttct gtgccgccga cgccgccgcc 120
gtcactcctc accagttact acaaattcag aatgctcgca accacttcca tcgcaatcgt 180
ttccaccgga agcagtcttc cgatctcttt ctcgctattc agtatgaaaa ggaaatagcg 240
aagggcggaa aagggaaaga ggcggtgaaa gtgaaagaag gggaggaggt ggggaaagag 300
gcggtgaaga gtacgttaga gagggcacta agtttctaca cagccgtgca gacgagcgat 360
gggaattggg cctcggatct tggagggccc atgtttttac ttccgggtct cgtgattgcc 420
ctttatgtca caggcgtgtt gaattcagtt ttgtccaagc accaccgcgt agagatgtgc 480
agatatattt acaatcacca gaatgaagat ggagggtggg gtctacatat tgagggcaca 540
agcaccatgt ttggttcggc actcaattat gttgcactta ggctgcttgg agaagacgcc 600
gatggcggag acgatggtgc aatgacaaaa gcacgtgctt ggatcttgga gcgcggcggc 660
gccactgcga tcacttcgtg gggaaaattg tggctgtccg tgcttggagt gtacgaatgg 720
agtggcaaca accctcttcc gcctgagttt tggcttctcc cttacagcct accatttcat 780
ccaggacgaa tgtggtgcca ttgtcgaatg gtttatcttc ccatgtctta cttatatggg 840
aagagatttg ttggcccaat cactcccaaa gttctttctc taagacaaga gctctacacg 900
gttccttatc atgaaataga ctggaataaa tcccgcaata catgtgcaaa ggaggatcta 960
tactatccac atcccaagat gcaagacata ctatggggat ctatctacca tgtatatgag 1020
ccattgttca ctcgttggcc tgggaaacgc ctgagggaaa aggctttaca aactgcaatg 1080
aaacatattc actatgaaga tgaaaatagt cgctatatat gtcttggccc agtcaacaag 1140
gtactcaaca tgctttgttg ttgggttgaa gatccctact cagacgcctt caaacttcac 1200
cttcaacgcg tccatgacta tctctgggtt gctgaagatg gcatgagaat gcagggttac 1260
aatggcagcc agttgtggga cactgctttc tccatccaag ccattgtagc taccaaactt 1320
gtagacagct atgccccaac tttaagaaaa gcacatgact ttgttaagga ttctcagatc 1380
caggaggact gtcctgggga tcctaatgtt tggttccgtc atattcataa aggtgcttgg 1440
ccattttcga ctcgagatca tggatggctc atctctgact gcacggctga gggattgaag 1500
gcttctttga tgttatccaa acttccatcc acaatggttg gggagccatt agaaaagaat 1560
cgcctttgtg atgctgttaa tgttctcctt tctttgcaaa atgataacgg tggatttgca 1620
tcatacgagt tgacgagatc ataccttgg ttggagttga tcaacccagc agaaacattc 1680
ggagacattg tcatcgacta tccgtatgtg gagtgcaccg cagcaacaat ggaagcactg 1740
acgttattta agaagctaca tccaggccat aggaccaaag agattgacac agctattggc 1800
aaggcagcca acttccttga gaaaatgcaa agggcggatg gctcttggta tgggtgttgg 1860
ggggtttgtt tcacgtatgc ggggtggttt ggcatcaagg gattggtggc tgcaggaaga 1920
acatataata gctgccttgc catccgcaag gcttgtgagt ttctgctatc taaagagctg 1980
cccggcggtg gatgggggga gagttacctt tcatgtcaga ataaggtgta caccaatctt 2040
gagggaaaca agccacactt ggttaacact gcctgggttt taatggctct cattgaagcc 2100
ggccagggtg agagagaccc agcaccattg caccgtggag caaggttggt aatgaattct 2160
caactggaga atggtgattt cgtgcaacag gagatcatgg gagtgttcaa taagaactgc 2220
atgatcacat atgctgcata ccgaaacatc ttccccattt gggcgcttgg agagtattgc 2280
catcgggttc ttactgaatg a                                          2301

<210> 422
<211> 766
<212> PRT
<213> Artificial Sequence

<220>
<223> Cpep4

<400> 422
Met Trp Arg Leu Lys Val Gly Ala Glu Ser Val Gly Glu Lys Asp Glu

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 1               5                  10                  15
Lys Trp Val Lys Ser Val Ser Asn His Leu Gly Arg Gln Val Trp Glu
            20                  25                  30
Phe Cys Ala Ala Asp Ala Ala Ala Val Thr Pro His Gln Leu Leu Gln
        35                  40                  45
Ile Gln Asn Ala Arg Asn His Phe His Arg Asn Arg Phe His Arg Lys
    50                  55                  60
Gln Ser Ser Asp Leu Phe Leu Ala Ile Gln Tyr Glu Lys Glu Ile Ala
65                  70                  75                  80
Lys Gly Gly Lys Gly Lys Glu Ala Val Lys Val Lys Glu Gly Glu Glu
                85                  90                  95
Val Gly Lys Glu Ala Val Lys Ser Thr Leu Glu Arg Ala Leu Ser Phe
            100                 105                 110
Tyr Thr Ala Val Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu Gly
        115                 120                 125
Gly Pro Met Phe Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val Thr
    130                 135                 140
Gly Val Leu Asn Ser Val Leu Ser Lys His His Arg Val Glu Met Cys
145                 150                 155                 160
Arg Tyr Ile Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His
                165                 170                 175
Ile Glu Gly Thr Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala
            180                 185                 190
Leu Arg Leu Leu Gly Glu Asp Ala Asp Gly Gly Asp Asp Gly Ala Met
        195                 200                 205
Thr Lys Ala Arg Ala Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile
    210                 215                 220
Thr Ser Trp Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp
225                 230                 235                 240
Ser Gly Asn Asn Pro Leu Pro Pro Glu Phe Leu Leu Leu Pro Tyr Ser
                245                 250                 255
Leu Pro Phe His Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr
            260                 265                 270
Leu Pro Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr
        275                 280                 285
Pro Lys Val Leu Ser Leu Arg Gln Glu Leu Tyr Thr Val Pro Tyr His
    290                 295                 300
Glu Ile Asp Trp Asn Lys Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu
305                 310                 315                 320
Tyr Tyr Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr
                325                 330                 335
His Val Tyr Glu Pro Leu Phe Thr Arg Trp Pro Gly Lys Arg Leu Arg
            340                 345                 350
Glu Lys Ala Leu Gln Thr Ala Met Lys His Ile His Tyr Glu Asp Glu
        355                 360                 365
Asn Ser Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met
    370                 375                 380
Leu Cys Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Leu His
385                 390                 395                 400
Leu Gln Arg Val His Asp Tyr Leu Trp Val Ala Glu Asp Gly Met Arg
                405                 410                 415
Met Gln Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile
            420                 425                 430
Gln Ala Ile Val Ala Thr Lys Leu Val Asp Ser Tyr Ala Pro Thr Leu
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        435                 440                 445
Arg Lys Ala His Asp Phe Val Lys Asp Ser Gln Ile Gln Glu Asp Cys
    450                 455                 460
Pro Gly Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp
465                 470                 475                 480
Pro Phe Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala
                485                 490                 495
Glu Gly Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Thr Met
            500                 505                 510
Val Gly Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val
        515                 520                 525
Leu Leu Ser Leu Gln Asn Asp Asn Gly Gly Phe Ala Ser Tyr Glu Leu
    530                 535                 540
Thr Arg Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe
545                 550                 555                 560
Gly Asp Ile Val Ile Asp Tyr Ser Tyr Val Glu Cys Thr Ala Ala Thr
                565                 570                 575
Met Glu Ala Leu Thr Leu Phe Lys Lys Leu His Pro Gly His Arg Thr
            580                 585                 590
Lys Glu Ile Asp Thr Ala Ile Gly Lys Ala Ala Asn Phe Leu Glu Lys
        595                 600                 605
Met Gln Arg Ala Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe
    610                 615                 620
Thr Tyr Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg
625                 630                 635                 640
Thr Tyr Asn Ser Cys Leu Ala Ile Arg Lys Ala Cys Glu Phe Leu Leu
                645                 650                 655
Ser Lys Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys
            660                 665                 670
Gln Asn Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val
        675                 680                 685
Asn Thr Ala Trp Val Leu Met Ala Leu Ile Glu Ala Gly Gln Gly Glu
    690                 695                 700
Arg Asp Pro Ala Pro Leu His Arg Ala Ala Arg Leu Val Met Asn Ser
705                 710                 715                 720
Gln Leu Glu Asn Gly Asp Phe Val Gln Gln Glu Ile Met Gly Val Phe
                725                 730                 735
Asn Lys Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro
            740                 745                 750
Ile Trp Ala Leu Gly Glu Tyr Cys His Arg Val Leu Thr Glu
        755                 760                 765
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<210> 423
<211> 2301
<212> DNA
<213> Artificial Sequence

<220>
<223> Cpep4

<400> 423
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agcgtaagca atcacttggg ccgccaagtt tgggagttct gtgccgccga cgccgccgcc 120

gtcactcctc accagttact acaaattcag aatgctcgca accacttcca tcgcaatcgt 180
ttccaccgga agcagtcttc cgatctcttt ctcgctattc agtatgaaaa ggaaatagcg 240
aagggcggaa aagggaaaga ggcggtgaaa gtgaaagaag gggaggaggt ggggaaagag 300
gcggtgaaga gtacgttaga gagggcacta agtttctaca cagccgtgca gacgagcgat 360
gggaattggg cctcggatct tggagggccc atgtttttac ttccgggtct cgtgattgcc 420
ctttatgtca caggcgtgtt gaattcagtt ttgtccaagc accaccgcgt agagatgtgc 480
agatatattt acaatcacca gaatgaagat ggagggtggg gtctacatat tgagggcaca 540
agcaccatgt ttggttcggc actcaattat gttgcactta ggctgcttgg agaagacgcc 600
gatggcggag acgatggtgc aatgacaaaa gcacgtgctt ggatcttgga gcgcggcggc 660
gccactgcga tcacttcgtg gggaaaattg tggctgtccg tgcttggagt gtacgaatgg 720
agtggcaaca accctcttcc gcctgagttt ttgcttctcc cttacagcct accatttcat 780
ccaggacgaa tgtggtgcca ttgtcgaatg gtttatcttc ccatgtctta cttatatggg 840
aagagatctg ttcgcccaat cactcccaaa gttctttctc taagacaaga gctctacacg 900
gttccttatc atgaaataga ctggaataaa tcccgcaata catgtgcaaa ggaggatcta 960
tactatccac atcccaagat gcaagacata ctatggggat ctatctacca tgtatatgag 1020
ccattgttca ctcgttggcc tgggaaacgc ctgagggaaa aggctttaca aactgcaatg 1080
aaacatattc actatgaaga tgaaaatagt cgctatatat gtcttggccc agtcaacaag 1140
gtactcaaca tgctttgttg ttgggttgaa gatccctact cagacgcctt caaacttcac 1200
cttcaacgcg tccatgacta tctctgggtt gctgaagatg gcatgagaat gcagggttac 1260
aatggcagcc agttgtggga cactgctttc tccatccaag ccattgtagc taccaaactt 1320
gtagacagct atgccccaac tttaagaaaa gcacatgact ttgttaagga ttctcagatc 1380
caggaggact gtcctgggga tcctaatgtt tggttccgtc atattcataa aggtgcttgg 1440
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gcttctttga tgttatccaa acttccatcc acaatggttg gggagccatt agaaaagaat 1560
cgcctttgtg atgctgttaa tgttctcctt tctttgcaaa atgataacgg cggatttgca 1620
tcatacgagt tgacgagatc ataccttgg ttggagttga tcaacccagc agaaacattc 1680
ggagacattg tcatcgacta ttcgtatgtg gagtgcaccg cagcaacaat ggaagcactg 1740
acgttattta agaagctaca tccaggccat aggaccaaag agattgacac agctattggc 1800
aaggcagcca acttccttga gaaaatgcaa agggcggatg gctcttggta tgggtgttgg 1860
ggggtttgtt tcacgtatgc ggggtggttt ggcataaagg gattggtggc tgcaggaaga 1920
acatataata gctgtcttgc catccgcaag gcttgtgagt ttctgctatc taaagagctg 1980
cccggcggtg gatgggggga gagttacctt tcatgtcaga ataaggtgta caccaatctt 2040
gagggaaaca agccacactt ggttaacact gcctgggttt taatggctct cattgaagct 2100
ggccagggtg agagagaccc agcaccattg caccgtgcag caaggttggt aatgaattct 2160
caactggaga atggcgattt cgtgcaacag gagatcatgg gagtgttcaa taagaactgc 2220
atgatcacat atgctgcata ccgaaacatc ttccccattt gggcgcttgg agagtattgc 2280
catcgggttc ttactgaatg a 2301

<210> 424
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Cmax1

<400> 424
Met Trp Arg Leu Lys Val Gly Ala Glu Ser Val Gly Glu Lys Asp Glu
 1               5                  10                  15
Lys Trp Val Lys Ser Val Ser Asn His Leu Gly Arg Gln Val Trp Glu
            20                  25                  30
Phe Cys Ala Asp Ala Ala Ala Asp Thr Pro His Gln Leu Leu Gln Ile
        35                  40                  45
Gln Asn Ala Arg Asn His Phe His His Asn Arg Phe His Arg Lys Gln

```
    50                  55                  60
Ser Ser Asp Leu Phe Leu Ala Ile Gln Tyr Glu Lys Glu Ile Ala Lys
65                  70                  75                  80
Gly Ala Lys Gly Gly Ala Val Lys Val Lys Glu Gly Glu Glu Val Gly
                85                  90                  95
Lys Glu Ala Val Lys Ser Thr Leu Glu Ser Ala Leu Gly Phe Tyr Ser
            100                 105                 110
Ala Val Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro
        115                 120                 125
Met Phe Leu Leu Pro Gly Leu Val Ile Ala Leu His Val Thr Gly Val
    130                 135                 140
Leu Asn Ser Val Leu Ser Lys His His Arg Val Glu Met Cys Arg Tyr
145                 150                 155                 160
Leu Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile Glu
                165                 170                 175
Gly Thr Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg
            180                 185                 190
Leu Leu Gly Glu Asp Ala Asp Gly Gly Asp Gly Gly Ala Met Thr Lys
        195                 200                 205
Ala Arg Ala Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser
    210                 215                 220
Trp Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp Ser Gly
225                 230                 235                 240
Asn Asn Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro
                245                 250                 255
Phe His Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr Leu Pro
            260                 265                 270
Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr Pro Lys
        275                 280                 285
Val Leu Ser Leu Arg Gln Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile
    290                 295                 300
Asp Trp Asn Lys Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr
305                 310                 315                 320
Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His Val
                325                 330                 335
Tyr Glu Pro Leu Phe Thr Arg Trp Pro Gly Lys Arg Leu Arg Glu Lys
            340                 345                 350
Ala Leu Gln Ala Ala Met Lys His Ile His Tyr Glu Asp Glu Asn Ser
        355                 360                 365
Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu Cys
    370                 375                 380
Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Leu His Leu Gln
385                 390                 395                 400
Arg Val His Asp Tyr Leu Trp Val Ala Glu Asp Gly Met Arg Met Gln
                405                 410                 415
Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala
            420                 425                 430
Ile Val Ala Thr Lys Leu Val Asp Ser Tyr Ala Pro Thr Leu Arg Lys
        435                 440                 445
Ala His Asp Phe Val Lys Asp Ser Gln Ile Gln Glu Asp Cys Pro Gly
    450                 455                 460
Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp Pro Phe
465                 470                 475                 480
Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly
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                485                 490                 495
Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Ala Met Val Gly
            500                 505                 510
Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val Leu Leu
        515                 520                 525
Ser Leu Gln Asn Asp Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg
    530                 535                 540
Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp
545                 550                 555                 560
Ile Val Ile Asp Tyr Pro Tyr Val Glu Cys Thr Ala Ala Thr Met Glu
                565                 570                 575
Ala Leu Thr Leu Phe Lys Lys Leu His Pro Gly His Arg Thr Lys Glu
            580                 585                 590
Ile Asp Thr Ala Ile Gly Lys Ala Ala Asn Phe Leu Glu Lys Met Gln
        595                 600                 605
Arg Ala Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr
    610                 615                 620
Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr
625                 630                 635                 640
Asn Ser Cys Leu Ala Ile Arg Lys Ala Cys Glu Phe Leu Leu Ser Lys
                645                 650                 655
Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn
            660                 665                 670
Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val Asn Thr
        675                 680                 685
Ala Trp Val Leu Met Ala Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp
    690                 695                 700
Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu Met Asn Ser Gln Leu
705                 710                 715                 720
Glu Asn Gly Asp Phe Val Gln Gln Glu Ile Met Gly Val Phe Asn Lys
                725                 730                 735
Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp
            740                 745                 750
Ala Leu Gly Glu Tyr Cys His Arg Val Leu Thr Glu
        755                 760
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<210> 425
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Cmax1

<400> 425
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actcctcacc agttactaca aattcagaat gctcgcaacc acttccatca caatcgtttc 180
caccggaagc agtcttccga tctctttctg gctattcaat atgaaaagga aatagcaaag 240
ggcgcaaaag gtggagcggt gaaagtgaaa gaaggggagg aggtggggaa agaggcggtg 300
aagagtacgt tagaaagggc actcggtttc tactcggccg tgcagacaag agatgggaat 360
tgggcctcgg atcttggagg gcccttgttt ttacttccgg gtctcgtgat tgcccttcat 420
gtcacaggcg tcttgaattc agttttgtcc aagcaccacc gcgtagagat gtgcagatat 480

ctttacaatc accagaatga agatggaggg tggggtctac atattgaggg cacaagcacc 540
atgtttggtt cggcactgaa ttacgttgca ctaaggctgc ttggagaaga cgccgatggc 600
ggagacggtg gcgcaatgac aaaagcacgt gcttggatct tggagcgcgg cggcgccact 660
gcgatcactt cgtggggaaa attgtggctg tccgtacttg gagtgtacga atggagtggc 720
aacaaccctc ttccgcctga gttttggctt ctcccttaca gcctaccatt tcatccagga 780
agaatgtggt gccattgtcg aatggtttat cttccaatgt cttacttata tgggaagaga 840
tttgttgggc caatcactcc caaagttctt tctctaaggc aagagctcta cacaattcct 900
tatcatgaaa tagactggaa taaatcccgc aatacatgtg caaaggagga tctgtactat 960
ccacatccca agatgcaaga cattctatgg ggatccatct accatgtata tgagccattg 1020
ttcactcgtt ggcctgggaa acgcctgagg gaaaaggctt tacaagctgc aatgaaacat 1080
attcactatg aagatgaaaa tagtcgatat atatgtcttg gcccagtcaa caaggtactc 1140
aacatgcttt gttgttgggt tgaagatccc tactcagacg ccttcaaact tcaccttcaa 1200
cgcgtccatg actatctctg ggttgctgaa gatggcatga gaatgcaggg ctacaatggc 1260
agccagttgt gggacactgc tttctccatc caagccatcg tagccaccaa acttgtagac 1320
agctatgccc caactttaag aaaagcacat gactttgtta aggattctca gatccaggag 1380
gactgtcctg gggatcctaa tgtttggttc cgtcatattc ataaaggtgc ttggccactt 1440
tcgacacgag atcatggatg gctcatctcc gactgtacag ctgagggatt gaaggcttct 1500
ttgatgttat ccaaacttcc atccacaatg gttggggagc cattagaaaa gaatcgcctt 1560
tgtgatgctg ttaatgttct cctttctttg caaaatgata atggtggatt tgcatcatac 1620
gagttgacga gatcataccc ttggttggag ttgatcaacc cagctgaaac attcggagac 1680
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gccaacttcc ttgagaaaat gcagagggcg gatggctctt ggtacgggtg ttgggggttt 1860
tgttttacgt atgcgggttg gtttggcata aagggattgg tggctgcagg aagaacatat 1920
aatagctgcc ttgccattcg caaggcttgt gagtttctgc tatctaaaga gctgcccggc 1980
ggtggatggg gggagagtta cctttcatgt cagaataagg tgtacaccaa tcttgagggg 2040
aacaagccac acttggttaa cactgcctgg gttttaatgg ctctcattga agctggccag 2100
ggtgagagag acccagcacc attgcaccgt gcagcaaggt tgctaatgaa ttcccaattg 2160
gagaatggcg atttcgtgca acaggagatc atgggagtgt tcaataagaa ctgcatgatc 2220
acatatgctg cataccgaaa catcttcccc atttgggcgc ttggagagta ttgccatcgg 2280
gttcttactg aatga 2295

<210> 426
<211> 765
<212> PRT
<213> Artificial Sequence

<220>
<223> Cmos1

<400> 426
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Lys Trp Val Lys Ser Val Ser Asn His Leu Gly Arg Gln Val Trp Glu
            20                  25                  30
Phe Cys Ala Asp Ala Ala Ala Ala Ala Thr Pro Arg Gln Leu Leu Gln
        35                  40                  45
Ile Gln Asn Ala Arg Asn His Phe His Arg Asn Arg Phe His Arg Lys
    50                  55                  60
Gln Ser Ser Asp Leu Phe Leu Ala Ile Gln Tyr Glu Lys Glu Ile Ala
65                  70                  75                  80
Glu Gly Gly Lys Gly Gly Ala Val Lys Val Lys Glu Glu Glu Glu Val
                85                  90                  95
Gly Lys Glu Ala Val Lys Ser Thr Leu Glu Arg Ala Leu Ser Phe Tyr

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            100                 105                 110
Ser Ala Val Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu Gly Gly
        115                 120                 125
Pro Met Phe Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val Thr Gly
    130                 135                 140
Val Leu Asn Ser Val Leu Ser Lys His His Arg Val Glu Met Cys Arg
145                 150                 155                 160
Tyr Leu Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile
                165                 170                 175
Glu Gly Thr Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu
            180                 185                 190
Arg Leu Leu Gly Glu Asp Ala Asp Gly Gly Asp Asp Gly Ala Met Thr
        195                 200                 205
Lys Ala Arg Ala Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile Thr
    210                 215                 220
Ser Trp Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp Ser
225                 230                 235                 240
Gly Asn Asn Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr Ser Leu
                245                 250                 255
Pro Phe His Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr Leu
            260                 265                 270
Pro Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr Pro
        275                 280                 285
Lys Val Leu Ser Leu Arg Gln Glu Leu Tyr Thr Val Pro Tyr His Glu
    290                 295                 300
Ile Asp Trp Asn Lys Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr
305                 310                 315                 320
Tyr Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His
                325                 330                 335
Val Tyr Glu Pro Leu Phe Thr Arg Trp Pro Gly Lys Arg Leu Arg Glu
            340                 345                 350
Lys Ala Leu Gln Thr Ala Met Lys His Ile His Tyr Glu Asp Glu Asn
        355                 360                 365
Ser Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu
    370                 375                 380
Cys Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Leu His Leu
385                 390                 395                 400
Gln Arg Val His Asp Tyr Leu Trp Val Ala Glu Asp Gly Met Arg Met
                405                 410                 415
Gln Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln
            420                 425                 430
Ala Ile Val Ala Thr Lys Leu Val Asp Ser Tyr Ala Pro Thr Leu Arg
        435                 440                 445
Lys Ala His Asp Phe Val Lys Asp Ser Gln Ile Gln Glu Asp Cys Pro
    450                 455                 460
Gly Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp Pro
465                 470                 475                 480
Phe Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu
                485                 490                 495
Gly Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Ala Met Val
            500                 505                 510
Gly Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val Leu
        515                 520                 525
Leu Ser Leu Gln Asn Asp Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr
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    530                 535                 540
Arg Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly
545                 550                 555                 560
Asp Ile Val Ile Asp Tyr Pro Tyr Val Glu Cys Thr Ala Ala Thr Met
                565                 570                 575
Glu Ala Leu Thr Leu Phe Lys Lys Leu His Pro Gly His Arg Thr Lys
            580                 585                 590
Glu Ile Asp Thr Ala Ile Gly Lys Ala Ala Asn Phe Leu Glu Lys Met
        595                 600                 605
Gln Arg Ala Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr
    610                 615                 620
Tyr Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr
625                 630                 635                 640
Tyr Asn Ser Cys Leu Ala Ile Arg Lys Ala Cys Glu Phe Leu Leu Ser
                645                 650                 655
Lys Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln
            660                 665                 670
Asn Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val Asn
        675                 680                 685
Thr Ala Trp Val Leu Met Ala Leu Ile Glu Ala Gly Gln Gly Glu Arg
    690                 695                 700
Asp Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu Met Asn Ser Gln
705                 710                 715                 720
Leu Glu Asn Gly Asp Phe Val Gln Gln Glu Ile Met Gly Val Phe Asn
                725                 730                 735
Lys Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile
            740                 745                 750
Trp Ala Leu Gly Glu Tyr Cys His Arg Val Leu Thr Glu
        755                 760                 765
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<210> 427
<211> 2296
<212> DNA
<213> Artificial Sequence

<220>
<223> Cmos1

<400> 427
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gccactcctc gccagttact acaaattcag aatgctcgca accacttcca tcgcaatcgt 180
ttccaccgga agcagtcttc cgatctcttt ctcgctattc agtatgaaaa ggaaatagca 240
gagggcggaa aaggtggagc ggtgaaagtg aaagaagagg aggaggtggg gaaagaggcg 300
gtgaagagta cgttagaaag ggcactaagt ttctactcag ccgtgcagac aagcgatggg 360
aattgggcct cggatcttgg agggcccatg tttttacttc cgggtctcgt gattgccctt 420
tatgtcacag gcgtgttgaa ttcagttttg tccaagcacc accgcgtaga gatgtgcaga 480
tatctttaca atcaccagaa tgaagatgga gggtggggtc tacatattga gggcacaagc 540
accatgtttg gttcggcact caattacgtt gcactaaggc tgcttggaga agacgcggat 600
ggcggagacg atggcgcaat gacaaaagca cgtgcttgga tcttggagcg cggcggcgcc 660
actgcgatca cttcgtgggg aaagttgtgg ctgtccgtgc ttggagtgta cgaatggagt 720
ggcaacaacc ctcttccgcc tgagttttgg cttctccctt acagcctacc atttcatcca 780
ggaagaatgt ggtgccattg tcgaatggtt tatcttccca tgtcttactt atatgggaag 840
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agatttgttg ggccaatcac tcccaaagtt ctatcgctaa gacaagagct ttacacggtt 900
ccttatcatg aaatagactg gaacaaatcc cgcaatacat gtgcaaagga ggatctatac 960
tatccacatc ccaagatgca agacattcta tggggatcca tctaccatgt gtatgagcca 1020
ttgttcactc gttggcctgg gaaacgcctg agggaaaagg ctttacaaac tgcaatgaaa 1080
catattcact atgaagatga aaatagtcga tatatatgtc ttggcccagt caacaaggta 1140
ctcaacatgc tttgttgttg ggttgaagat ccctactcag acgccttcaa acttcacctt 1200
caacgcgtcc atgactatct ctgggttgct gaagatggca tgagaatgca gggctacaat 1260
ggcagccagt tgtgggacac tgctttctcc atccaagcca tcgtagccac caaacttgta 1320
gacagctatg ccccaacttt aagaaaagca catgactttg ttaaggattc tcagatccag 1380
gaggactgtc ctggggatcc taatgtttgg ttccgtcata ttcataaagg tgcttggcca 1440
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tctttgatgt tatccaaact tccatccgca atggttgggg agccattaga aaagaatcgc 1560
ctttgtgatg ctgttaatgt tctcctttct ttgcaaaatg ataatggtgg atttgcatca 1620
tacgagttga cgagatcata cccttggttg gagttgatca acccagcaga aacattcgga 1680
gacattgtca tcgactatcc gtatgtggag tgcaccgcag caacaatgga agcactgacg 1740
ttatttaaga agctacatcc aggccatagg accaaagaga ttgacacagc tattggcaag 1800
gcagccaact tccttgagaa aatgcagagg gcggatggct cttggtatgg gtgttggggg 1860
gtttgtttca cgtatgcggg gtggtttggc ataaagggat tggtggctgc aggaagaaca 1920
tataatagct gccttgccat ccgcaaggct tgtgagtttc tgctatctaa agagctgccc 1980
ggcggtggat ggggggagag ttacctttca tgtcagaata aggtgtacac caatcttgag 2040
ggaaacaagc cacacttggt taacactgcc tgggttttaa tggctctcat tgaagctggc 2100
cagggtgaga gagacccagc accattgcac cgtgcagcaa ggttgctaat gaattcccaa 2160
ttggagaatg gcgatttcgt gcaacaggag atcatgggag tgttcaataa gaactgcatg 2220
atcacatatg ctgcataccg aaacatcttc cccatttggg cgcttggaga gtattgccat 2280
cgggttctga ctgaat 2296

<210> 428
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> EPH

<400> 428
Met Glu Lys Ile Glu His Ser Thr Ile Ala Thr Asn Gly Ile Asn Met
 1               5                  10                  15
His Val Ala Ser Ala Gly Ser Gly Pro Ala Val Leu Phe Leu His Gly
            20                  25                  30
Phe Pro Glu Leu Trp Tyr Ser Trp Arg His Gln Leu Leu Tyr Leu Ser
        35                  40                  45
Ser Leu Gly Tyr Arg Ala Ile Ala Pro Asp Leu Arg Gly Phe Gly Asp
    50                  55                  60
Thr Asp Ala Pro Pro Ser Pro Ser Ser Tyr Thr Ala His His Ile Val
65                  70                  75                  80
Gly Asp Leu Val Gly Leu Leu Asp Gln Leu Gly Val Asp Gln Val Phe
                85                  90                  95
Leu Val Gly His Asp Trp Gly Ala Met Met Ala Trp Tyr Phe Cys Leu
            100                 105                 110
Phe Arg Pro Asp Arg Val Lys Ala Leu Val Asn Leu Ser Val His Phe
        115                 120                 125
Thr Pro Arg Asn Pro Ala Ile Ser Pro Leu Asp Gly Phe Arg Leu Met
    130                 135                 140
Leu Gly Asp Asp Phe Tyr Val Cys Lys Phe Gln Glu Pro Gly Val Ala

145 150 155 160
Glu Ala Asp Phe Gly Ser Val Asp Thr Ala Thr Met Phe Lys Lys Phe
165 170 175
Leu Thr Met Arg Asp Pro Arg Pro Pro Ile Ile Pro Asn Gly Phe Arg
180 185 190
Ser Leu Ala Thr Pro Glu Ala Leu Pro Ser Trp Leu Thr Glu Glu Asp
195 200 205
Ile Asp Tyr Phe Ala Ala Lys Phe Ala Lys Thr Gly Phe Thr Gly Gly
210 215 220
Phe Asn Tyr Tyr Arg Ala Ile Asp Leu Thr Trp Glu Leu Thr Ala Pro
225 230 235 240
Trp Ser Gly Ser Glu Ile Lys Val Pro Thr Lys Phe Ile Val Gly Asp
245 250 255
Leu Asp Leu Val Tyr His Phe Pro Gly Val Lys Glu Tyr Ile His Gly
260 265 270
Gly Gly Phe Lys Lys Asp Val Pro Phe Leu Glu Glu Val Val Val Met
275 280 285
Glu Gly Ala Ala His Phe Ile Asn Gln Glu Lys Ala Asp Glu Ile Asn
290 295 300
Ser Leu Ile Tyr Asp Phe Ile Lys Gln Phe
305 310

<210> 429
<211> 945
<212> DNA
<213> Artificial Sequence

<220>
<223> EPH (codon optimized E coli)

<400> 429
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agacaccaat tgttgtactt gtcttctttg ggttacagag ctattgctcc agatttgaga 180
ggtttcggtg acaccgatgc tccaccatct ccatcctcct acaccgccca ccacatcgtt 240
ggtgatttgg tcggtttgtt ggatcaatta ggtgtcgatc aagtcttttt ggttggtcat 300
gattggggtg ctatgatggc ctggtacttc tgtttgttcc gtccagacag agtcaaggcc 360
ttagttaatt tatctgtcca cttcacccca cgtaacccag ctatctctcc attagatggt 420
ttccgtttga tgttgggtga tgatttctac gtttgtaagt ttcaagaacc aggtgtcgct 480
gaagccgatt tcggttctgt tgatactgcc actatgttta aaaagttctt gaccatgaga 540
gatccacgtc cacctattat tccaaacggt ttcagatcct tggccacccc agaagctttg 600
ccatcctggt tgactgaaga ggatatcgat tactttgctg ccaaattcgc taagactggt 660
tttactggtg gtttcaacta ctacagagct atcgacttga cctgggagtt gactgctcca 720
tggtccggtt ctgaaatcaa ggttccaact aagtttattg ttggtgactt agacttggtt 780
taccatttcc caggtgttaa ggaatacatt cacggtggtg gtttcaagaa ggacgttcca 840
ttcttggaag aagttgtcgt catggaaggt gctgctcatt ttatcaacca agaaaaagct 900
gacgaaatta attctttgat ctatgacttc attaaacaat tctag 945

<210> 430
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> CYP87D18

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

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Lys Asp Leu Asp Ser Ile Thr Ile Gln Lys Asn Phe Met Pro Phe Gly
                405                 410                 415
Gly Gly Leu Arg His Cys Ala Gly Ala Glu Tyr Ser Lys Val Tyr Leu
            420                 425                 430
Cys Thr Phe Leu His Ile Leu Cys Thr Lys Tyr Arg Trp Thr Lys Leu
        435                 440                 445
Gly Gly Gly Arg Ile Ala Arg Ala His Ile Leu Ser Phe Glu Asp Gly
    450                 455                 460
Leu His Val Lys Phe Thr Pro Lys Glu
465                 470
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<210> 431
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> CYP87D18

<400> 431
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ctcatcggag agacgattca actgagtcga cccagtgact ccctcgacgt tcacccttc 180
atccagaaaa aagttgaaag atacgggccg atcttcaaaa catgtctggc cggaaggccg 240
gtggtggtgt cggcggacgc agagttcaac aactacataa tgctgcagga aggaagagca 300
gtggaaatgt ggtatttgga tacgctctcc aaatttttcg gcctcgacac cgagtggctc 360
aaagctctgg gcctcatcca caagtacatc agaagcatta ctctcaatca cttcggcgcc 420
gaggccctgc gggagagatt tcttcctttt attgaagcat cctccatgga agcccttcac 480
tcctggtcta ctcaacctag cgtcgaagtc aaaaatgcct ccgctctcat ggtttttagg 540
acctcggtga ataagatgtt cggtgaggat gcgaagaagc tatcgggaaa tatccctggg 600
aagttcacga agcttctagg aggatttctc agtttaccac tgaattttcc cggcaccacc 660
taccacaaat gcttgaagga tatgaaggaa atccagaaga agctaagaga ggttgtagac 720
gatagattgg ctaatgtggg ccctgatgtg gaagatttct tggggcaagc ccttaaagat 780
aaggaatcag agaagttcat ttcagaggag ttcatcatcc aactgttgtt ttctatcagt 840
tttgctagct ttgagtccat ctccaccact cttactttga ttctcaagct ccttgatgaa 900
cacccagaag tagtgaaaga gttggaagct gaacacgagg cgattcgaaa agctagagca 960
gatccagatg gaccaattac ttgggaagaa tacaaatcca tgacttttac attacaagtc 1020
atcaatgaaa ccctaaggtt ggggagtgtc acacctgcct tgttgaggaa aacagttaaa 1080
gatcttcaag taaaaggata cataatcccg gaaggatgga caataatgct tgtcaccgct 1140
tcacgtcaca gagacccaaa agtctataag gaccctcata tcttcaatcc atggcgttgg 1200
aaggacttgg actcaattac catccaaaag aacttcatgc cttttggggg aggcttaagg 1260
cattgtgctg gtgctgagta ctctaaagtc tacttgtgca ccttcttgca catcctctgt 1320
accaaatacc gatggaccaa acttggggga ggaaggattg caagagctca tatattgagt 1380
tttgaagatg ggttacatgt gaagttcaca cccaaggaat ga                    1422

<210> 432
<211> 688
<212> PRT
<213> Artificial Sequence

<220>
<223> AtCPR

<400> 432
Met Thr Ser Ala Leu Tyr Ala Ser Asp Leu Phe Lys Gln Leu Lys Ser
 1               5                  10                  15
Ile Met Gly Thr Asp Ser Leu Ser Asp Asp Val Val Leu Val Ile Ala
            20                  25                  30
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 Asp Asp Tyr Ala Ala Asp Asp Asp Gln Tyr Glu
        115                 120                 125
Glu Lys Leu Lys Lys Glu Thr Leu Ala Phe Phe Cys Val Ala Thr Tyr
    130                 135                 140
Gly Asp Gly Glu Pro Thr Asp Asn Ala Ala Arg Phe Tyr Lys Trp Phe
145                 150                 155                 160
Thr Glu Glu Asn Glu Arg Asp Ile Lys Leu Gln Gln Leu Ala Tyr Gly
                165                 170                 175
Val Phe Ala Leu Gly Asn Arg Gln Tyr Glu His Phe Asn Lys Ile Gly
            180                 185                 190
Ile Val Leu Asp Glu Glu Leu Cys Lys Lys Gly Ala Lys Arg Leu Ile
        195                 200                 205
Glu Val Gly Leu Gly Asp Asp Asp Gln Ser Ile Glu Asp Asp Phe Asn
    210                 215                 220
Ala Trp Lys Glu Ser Leu Trp Ser Glu Leu Asp Lys Leu Leu Lys Asp
225                 230                 235                 240
Glu Asp Asp Lys Ser Val Ala Thr Pro Tyr Thr Ala Val Ile Pro Glu
                245                 250                 255
Tyr Arg Val Val Thr His Asp Pro Arg Phe Thr Thr Gln Lys Ser Met
            260                 265                 270
Glu Ser Asn Val Ala Asn Gly Asn Thr Thr Ile Asp Ile His His Pro
        275                 280                 285
Cys Arg Val Asp Val Ala Val Gln Lys Glu Leu His Thr His Glu Ser
    290                 295                 300
Asp Arg Ser Cys Ile His Leu Glu Phe Asp Ile Ser Arg Thr Gly Ile
305                 310                 315                 320
Thr Tyr Glu Thr Gly Asp His Val Gly Val Tyr Ala Glu Asn His Val
                325                 330                 335
Glu Ile Val Glu Glu Ala Gly Lys Leu Leu Gly His Ser Leu Asp Leu
            340                 345                 350
Val Phe Ser Ile His Ala Asp Lys Glu Asp Gly Ser Pro Leu Glu Ser
        355                 360                 365
Ala Val Pro Pro Pro Phe Pro Gly Pro Cys Thr Leu Gly Thr Gly Leu
    370                 375                 380
Ala Arg Tyr Ala Asp Leu Leu Asn Pro Pro Arg Lys Ser Ala Leu Val
385                 390                 395                 400
Ala Leu Ala Ala Tyr Ala Thr Glu Pro Ser Glu Ala Glu Lys Leu Lys
                405                 410                 415
His Leu Thr Ser Pro Asp Gly Lys Asp Glu Tyr Ser Gln Trp Ile Val

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            420                 425                 430
Ala Ser Gln Arg Ser Leu Leu Glu Val Met Ala Ala Phe Pro Ser Ala
        435                 440                 445
Lys Pro Pro Leu Gly Val Phe Phe Ala Ala Ile Ala Pro Arg Leu Gln
    450                 455                 460
Pro Arg Tyr Tyr Ser Ile Ser Ser Ser Pro Arg Leu Ala Pro Ser Arg
465                 470                 475                 480
Val His Val Thr Ser Ala Leu Val Tyr Gly Pro Thr Pro Thr Gly Arg
                485                 490                 495
Ile His Lys Gly Val Cys Ser Thr Trp Met Lys Asn Ala Val Pro Ala
            500                 505                 510
Glu Lys Ser His Glu Cys Ser Gly Ala Pro Ile Phe Ile Arg Ala Ser
        515                 520                 525
Asn Phe Lys Leu Pro Ser Asn Pro Ser Thr Pro Ile Val Met Val Gly
    530                 535                 540
Pro Gly Thr Gly Leu Ala Pro Phe Arg Gly Phe Leu Gln Glu Arg Met
545                 550                 555                 560
Ala Leu Lys Glu Asp Gly Glu Glu Leu Gly Ser Ser Leu Leu Phe Phe
                565                 570                 575
Gly Cys Arg Asn Arg Gln Met Asp Phe Ile Tyr Glu Asp Glu Leu Asn
            580                 585                 590
Asn Phe Val Asp Gln Gly Val Ile Ser Glu Leu Ile Met Ala Phe Ser
        595                 600                 605
Arg Glu Gly Ala Gln Lys Glu Tyr Val Gln His Lys Met Met Glu Lys
    610                 615                 620
Ala Ala Gln Val Trp Asp Leu Ile Lys Glu Glu Gly Tyr Leu Tyr Val
625                 630                 635                 640
Cys Gly Asp Ala Lys Gly Met Ala Arg Asp Val His Arg Thr Leu His
                645                 650                 655
Thr Ile Val Gln Glu Gln Glu Gly Val Ser Ser Ser Glu Ala Glu Ala
            660                 665                 670
Ile Val Lys Lys Leu Gln Thr Glu Gly Arg Tyr Leu Arg Asp Val Trp
        675                 680                 685
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<210> 433
<211> 2067
<212> DNA
<213> Artificial Sequence

<220>
<223> AtCPR

<400> 433
atgacttctg ctttgtatgc ttccgatttg tttaagcagc tcaagtcaat tatggggaca 60
gattcgttat ccgacgatgt tgtacttgtg attgcaacga cgtctttggc actagtagct 120
ggatttgtgg tgttgttatg gaagaaaacg acggcggatc ggagcgggga gctgaagcct 180
ttgatgatcc ctaagtctct tatggctaag gacgaggatg atgatttgga tttgggatcc 240
gggaagacta gagtctctat cttcttcggt acgcagactg gaacagctga gggatttgct 300
aaggcattat ccgaagaaat caaagcgaga tatgaaaaag cagcagtcaa agatgactat 360
gctgccgatg atgaccagta tgaagagaaa ttgaagaagg aaactttggc atttttctgt 420
gttgctactt atggagatgg agagcctact gacaatgctg ccagatttta caaatggttt 480
acggaggaaa atgaacggga tataaagctt caacaactag catatggtgt gtttgctctt 540
ggtaatcgcc aatatgaaca ttttaataag atcgggatag ttcttgatga agagttatgt 600

aagaaaggtg caaagcgtct tattgaagtc ggtctaggag atgatgatca gagcattgag 660
gatgatttta atgcctggaa agaatcacta tggtctgagc tagacaagct cctcaaagac 720
gaggatgata aaagtgtggc aactccttat acagctgtta ttcctgaata ccgggtggtg 780
actcatgatc ctcggtttac aactcaaaaa tcaatggaat caaatgtggc caatggaaat 840
actactattg acattcatca tccctgcaga gttgatgttg ctgtgcagaa ggagcttcac 900
acacatgaat ctgatcggtc ttgcattcat ctcgagttcg acatatccag gacgggtatt 960
acatatgaaa caggtgacca tgtaggtgta tatgctgaaa atcatgttga aatagttgaa 1020
gaagctggaa aattgcttgg ccactcttta gatttagtat tttccataca tgctgacaag 1080
gaagatggct ccccattgga aagcgcagtg ccgcctcctt tccctggtcc atgcacactt 1140
gggactggtt tggcaagata cgcagacctt ttgaaccctc ctcgaaagtc tgcgttagtt 1200
gccttggcgg cctatgccac tgaaccaagt gaagccgaga aacttaagca cctgacatca 1260
cctgatggaa aggatgagta ctcacaatgg attgttgcaa gtcagagaag tcttttagag 1320
gtgatggctg cttttccatc tgcaaaaccc ccactaggtg tatttttgc tgcaatagct 1380
cctcgtctac aacctcgtta ctactccatc tcatcctcgc caagattggc gccaagtaga 1440
gttcatgtta catccgcact agtatatggt ccaactccta ctggtagaat ccacaagggt 1500
gtgtgttcta cgtggatgaa gaatgcagtt cctgcggaga aaagtcatga atgtagtgga 1560
gccccaatct ttattcgagc atctaatttc aagttaccat ccaacccttc aactccaatc 1620
gttatggtgg gacctgggac tgggctggca ccttttagag gttttctgca ggaaaggatg 1680
gcactaaaag aagatggaga agaactaggt tcatctttgc tcttctttgg gtgtagaaat 1740
cgacagatgg actttatata cgaggatgag ctcaataatt ttgttgatca aggcgtaata 1800
tctgagctca tcatggcatt ctcccgtgaa ggagctcaga aggagtatgt tcaacataag 1860
atgatggaga aggcagcaca agtttgggat ctaataaagg aagaaggata tctctatgta 1920
tgcggtgatg ctaagggcat ggcgagggac gtccaccgaa ctctacacac cattgttcag 1980
gagcaggaag gtgtgagttc gtcagaggca gaggctatag ttaagaaact tcaaaccgaa 2040
ggaagatacc tcagagatgt ctggtga 2067

<210> 434
<211> 767
<212> PRT
<213> Artificial Sequence

<220>
<223> AGY15763.1

<400> 434
Met Trp Lys Val Pro Lys Phe Ile Lys Gln Ser Tyr Leu Val Phe Leu
 1               5                  10                  15
Leu Ala Leu Leu Leu Tyr Ser Ser Phe Gly Phe Ser Phe Ser Arg Thr
            20                  25                  30
Glu Ala Thr Thr Ser Thr Gly Ala Leu Gly Pro Val Thr Pro Lys Asp
        35                  40                  45
Thr Ile Tyr Gln Ile Val Thr Asp Arg Phe Phe Asp Gly Asp Pro Ser
    50                  55                  60
Asn Asn Lys Pro Pro Gly Phe Asp Pro Thr Leu Phe Asp Asp Pro Asp
65                  70                  75                  80
Gly Asn Asn Gln Gly Asn Gly Lys Asp Leu Lys Leu Tyr Gln Gly Gly
                85                  90                  95
Asp Phe Gln Gly Ile Ile Asp Lys Ile Pro Tyr Leu Lys Asn Met Gly
            100                 105                 110
Ile Thr Ala Val Trp Ile Ser Ala Pro Tyr Glu Asn Arg Asp Thr Val
        115                 120                 125
Ile Glu Asp Tyr Gln Ser Asp Gly Ser Ile Asn Arg Trp Thr Ser Phe
    130                 135                 140
His Gly Tyr His Ala Arg Asn Tyr Phe Ala Thr Asn Lys His Phe Gly

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145                 150                 155                 160
Thr Met Lys Asp Phe Ile Arg Leu Arg Asp Ala Leu His Gln Asn Gly
                165                 170                 175
Ile Lys Leu Val Ile Asp Phe Val Ser Asn His Ser Ser Arg Trp Gln
            180                 185                 190
Asn Pro Thr Leu Asn Phe Ala Pro Glu Asp Gly Lys Leu Tyr Glu Pro
        195                 200                 205
Asp Lys Asp Ala Asn Gly Asn Tyr Val Phe Asp Ala Asn Gly Glu Pro
    210                 215                 220
Ala Asp Tyr Asn Gly Asp Gly Lys Val Glu Asn Leu Leu Ala Asp Pro
225                 230                 235                 240
His Asn Asp Val Asn Gly Phe Phe His Gly Leu Gly Asp Arg Gly Asn
                245                 250                 255
Asp Thr Ser Arg Phe Gly Tyr Arg Tyr Lys Asp Leu Gly Ser Leu Ala
            260                 265                 270
Asp Tyr Ser Gln Glu Asn Ala Leu Val Val Glu His Leu Glu Lys Ala
        275                 280                 285
Ala Lys Phe Trp Lys Ser Lys Gly Ile Asp Gly Phe Arg His Asp Ala
    290                 295                 300
Thr Leu His Met Asn Pro Ala Phe Val Lys Gly Phe Lys Asp Ala Ile
305                 310                 315                 320
Asp Ser Asp Ala Gly Gly Pro Val Thr His Phe Gly Glu Phe Phe Ile
                325                 330                 335
Gly Arg Pro Asp Pro Lys Tyr Asp Glu Tyr Arg Thr Phe Pro Glu Arg
            340                 345                 350
Thr Gly Val Asn Asn Leu Asp Phe Glu Tyr Phe Arg Ala Ala Thr Asn
        355                 360                 365
Ala Phe Gly Asn Phe Ser Glu Thr Met Ser Ser Phe Gly Asp Met Met
    370                 375                 380
Ile Lys Thr Ser Asn Asp Tyr Ile Tyr Glu Asn Gln Thr Val Thr Phe
385                 390                 395                 400
Leu Asp Asn His Asp Val Thr Arg Phe Arg Tyr Ile Gln Pro Asn Asp
                405                 410                 415
Lys Pro Tyr His Ala Ala Leu Ala Val Leu Met Thr Ser Arg Gly Ile
            420                 425                 430
Pro Asn Ile Tyr Tyr Gly Thr Glu Gln Tyr Leu Met Pro Ser Asp Ser
        435                 440                 445
Ser Asp Ile Ala Gly Arg Met Phe Met Gln Thr Ser Thr Asn Phe Asp
    450                 455                 460
Glu Asn Thr Thr Ala Tyr Lys Val Ile Gln Lys Leu Ser Asn Leu Arg
465                 470                 475                 480
Lys Asn Asn Glu Ala Ile Ala Tyr Gly Thr Thr Glu Ile Leu Tyr Ser
                485                 490                 495
Thr Asn Asp Val Leu Val Phe Lys Arg Gln Phe Tyr Asp Lys Gln Val
            500                 505                 510
Ile Val Ala Val Asn Arg Gln Pro Asp Gln Thr Phe Thr Ile Pro Glu
        515                 520                 525
Leu Asp Thr Thr Leu Pro Val Gly Thr Tyr Ser Asp Val Leu Gly Gly
    530                 535                 540
Leu Leu Tyr Gly Ser Ser Met Ser Val Asn Asn Val Asn Gly Gln Asn
545                 550                 555                 560
Lys Ile Ser Ser Phe Thr Leu Ser Gly Gly Glu Val Asn Val Trp Ser
                565                 570                 575
Tyr Asn Pro Ser Leu Gly Thr Leu Thr Pro Arg Ile Gly Asp Val Ile
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            580                 585                 590
Ser Thr Met Gly Arg Pro Gly Asn Thr Val Tyr Ile Tyr Gly Thr Gly
        595                 600                 605
Leu Gly Gly Ser Val Thr Val Lys Phe Gly Ser Thr Val Ala Thr Val
    610                 615                 620
Val Ser Asn Ser Asp Gln Met Ile Glu Ala Ile Val Pro Asn Thr Asn
625                 630                 635                 640
Pro Gly Ile Gln Asn Ile Thr Val Thr Lys Gly Ser Val Thr Ser Asp
                645                 650                 655
Pro Phe Arg Tyr Glu Val Leu Ser Gly Asp Gln Val Gln Val Ile Phe
            660                 665                 670
His Val Asn Ala Thr Thr Asn Trp Gly Glu Asn Ile Tyr Val Val Gly
        675                 680                 685
Asn Ile Pro Glu Leu Gly Ser Trp Asp Pro Asn Gln Ser Ser Glu Ala
    690                 695                 700
Met Leu Asn Pro Asn Tyr Pro Glu Trp Phe Leu Pro Val Ser Val Pro
705                 710                 715                 720
Lys Gly Ala Thr Phe Glu Phe Lys Phe Ile Lys Lys Asp Asn Asn Gly
                725                 730                 735
Asn Val Ile Trp Glu Ser Arg Ser Asn Arg Val Phe Thr Ala Pro Asn
            740                 745                 750
Ser Ser Thr Gly Thr Ile Asp Thr Pro Leu Tyr Phe Trp Asp Asn
        755                 760                 765


<210> 435
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<223> AGY15764.1

<400> 435
Thr Thr Ser Thr Gly Ala Leu Gly Pro Val Thr Pro Lys Asp Thr Ile
 1               5                  10                  15
Tyr Gln Ile Val Thr Asp Arg Phe Phe Asp Gly Asp Pro Ser Asn Asn
            20                  25                  30
Lys Pro Pro Gly Phe Asp Pro Thr Leu Phe Asp Asp Pro Asp Gly Asn
        35                  40                  45
Asn Gln Gly Asn Gly Lys Asp Leu Lys Leu Tyr Gln Gly Gly Asp Phe
    50                  55                  60
Gln Gly Ile Ile Asp Lys Ile Pro Tyr Leu Lys Asn Met Gly Ile Thr
65                  70                  75                  80
Ala Val Trp Ile Ser Ala Pro Tyr Glu Asn Arg Asp Thr Val Ile Glu
                85                  90                  95
Asp Tyr Gln Ser Asp Gly Ser Ile Asn Arg Trp Thr Ser Phe His Gly
            100                 105                 110
Tyr His Ala Arg Asn Tyr Phe Ala Thr Asn Lys His Phe Gly Thr Met
        115                 120                 125
Lys Asp Phe Ile Arg Leu Arg Asp Ala Leu His Gln Asn Gly Ile Lys
    130                 135                 140
Leu Val Ile Asp Phe Val Ser Asn His Ser Ser Arg Trp Gln Asn Pro
145                 150                 155                 160
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Thr Leu Asn Phe Ala Pro Glu Asp Gly Lys Leu Tyr Glu Pro Asp Lys
                165                 170                 175
Asp Ala Asn Gly Asn Tyr Val Phe Asp Ala Asn Gly Glu Pro Ala Asp
            180                 185                 190
Tyr Asn Gly Asp Gly Lys Val Glu Asn Leu Leu Ala Asp Pro His Asn
        195                 200                 205
Asp Val Asn Gly Phe Phe His Gly Leu Gly Asp Arg Gly Asn Asp Thr
    210                 215                 220
Ser Arg Phe Gly Tyr Arg Tyr Lys Asp Leu Gly Ser Leu Ala Asp Tyr
225                 230                 235                 240
Ser Gln Glu Asn Ala Leu Val Val Glu His Leu Glu Lys Ala Ala Lys
                245                 250                 255
Phe Trp Lys Ser Lys Gly Ile Asp Gly Phe Arg His Asp Ala Thr Leu
            260                 265                 270
His Met Asn Pro Ala Phe Val Lys Gly Phe Lys Asp Ala Ile Asp Ser
        275                 280                 285
Asp Ala Gly Gly Pro Val Thr His Phe Gly Glu Phe Phe Ile Gly Arg
    290                 295                 300
Pro Asp Pro Lys Tyr Asp Glu Tyr Arg Thr Phe Pro Glu Arg Thr Gly
305                 310                 315                 320
Val Asn Asn Leu Asp Phe Glu Tyr Phe Arg Ala Ala Thr Asn Ala Phe
                325                 330                 335
Gly Asn Phe Ser Glu Thr Met Ser Ser Phe Gly Asp Met Met Ile Lys
            340                 345                 350
Thr Ser Asn Asp Tyr Ile Tyr Glu Asn Gln Thr Val Thr Phe Leu Asp
        355                 360                 365
Asn His Asp Val Thr Arg Phe Arg Tyr Ile Gln Pro Asn Asp Lys Pro
    370                 375                 380
Tyr His Ala Ala Leu Ala Val Leu Met Thr Ser Arg Gly Ile Pro Asn
385                 390                 395                 400
Ile Tyr Tyr Gly Thr Glu Gln Tyr Leu Met Pro Ser Asp Ser Ser Asp
                405                 410                 415
Ile Ala Gly Arg Met Phe Met Gln Thr Ser Thr Asn Phe Asp Glu Asn
            420                 425                 430
Thr Thr Ala Tyr Lys Val Ile Gln Lys Leu Ser Asn Leu Arg Lys Asn
        435                 440                 445
Asn Glu Ala Ile Ala Tyr Gly Thr Thr Glu Ile Leu Tyr Ser Thr Asn
    450                 455                 460
Asp Val Leu Val Phe Lys Arg Gln Phe Tyr Asp Lys Gln Val Ile Val
465                 470                 475                 480
Ala Val Asn Arg Gln Pro Asp Gln Thr Phe Thr Ile Pro Glu Leu Asp
                485                 490                 495
Thr Thr Leu Pro Val Gly Thr Tyr Ser Asp Val Leu Gly Gly Leu Leu
            500                 505                 510
Tyr Gly Ser Ser Met Ser Val Asn Asn Val Asn Gly Gln Asn Lys Ile
        515                 520                 525
Ser Ser Phe Thr Leu Ser Gly Gly Glu Val Asn Val Trp Ser Tyr Asn
    530                 535                 540
Pro Ser Leu Gly Thr Leu Thr Pro Arg Ile Gly Asp Val Ile Ser Thr
545                 550                 555                 560
Met Gly Arg Pro Gly Asn Thr Val Tyr Ile Tyr Gly Thr Gly Leu Gly
                565                 570                 575
Gly Ser Val Thr Val Lys Phe Gly Ser Thr Val Ala Thr Val Val Ser
            580                 585                 590
```

Asn Ser Asp Gln Met Ile Glu Ala Ile Val Pro Asn Thr Asn Pro Gly
595 600 605
Ile Gln Asn Ile Thr Val Thr Lys Gly Ser Val Thr Ser Asp Pro Phe
610 615 620
Arg Tyr Glu Val Leu Ser Gly Asp Gln Val Gln Val Ile Phe His Val
625 630 635 640
Asn Ala Thr Thr Asn Trp Gly Glu Asn Ile Tyr Val Val Gly Asn Ile
645 650 655
Pro Glu Leu Gly Ser Trp Asp Pro Asn Gln Ser Ser Glu Ala Met Leu
660 665 670
Asn Pro Asn Tyr Pro Glu Trp Phe Leu Pro Val Ser Val Pro Lys Gly
675 680 685
Ala Thr Phe Glu Phe Lys Phe Ile Lys Lys Asp Asn Asn Gly Asn Val
690 695 700
Ile Trp Glu Ser Arg Ser Asn Arg Val Phe Thr Ala Pro Asn Ser Ser
705 710 715 720
Thr Gly Thr Ile Asp Thr Pro Leu Tyr Phe Trp Asp Asn
725 730

<210> 436
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> 311

<400> 436
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

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        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 Ala Ala
    450                 455                 460
Ala Leu Glu His His His His His His
465                 470
```

<210> 437
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> 311(gDNA native)

<400> 437
atggactccg gctactcctc ctcctacgcc gccgccgccg ggatgcacgt cgtgatctgc 60
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> 438
<211> 1386
<212> DNA
<213> Artificial Sequence

<220>
<223> 311(gDNA codon opt Ecoli)

<400> 438
atggatagcg gttatagcag cagctatgca gcagcagccg gtatgcatgt tgttatttgt 60
ccgtggctgg catttggtca tctgctgccg tgtctggatc tggcacagcg tctggcaagc 120
cgtggtcatc gtgttagctt tgttagcaca ccgcgtaata ttagccgtct gcctccggtt 180
cgtccggcac tggcaccgct ggttgcattt gttgcactgc cgctgcctcg tgttgaaggt 240
ctgccggatg gtgcagaaag caccaatgat gttccgcatg atcgtccgga tatggttgaa 300
ctgcatcgtc gtgcatttga tggtctggca gcaccgttta gcgaatttct gggcaccgca 360
tgtgcagatt gggttattgt tgatgttttt catcattggg cagccgcagc agcactggaa 420
cataaagttc cgtgtgcaat gatgctgctg ggtagcgcac atatgattgc aagcattgca 480
gatcgtcgtc tggaacgtgc agaaaccgaa agtcctgcgg cagcaggtca gggtcgtcct 540
gcagccgcac cgacctttga agttgcacgt atgaaactga ttcgtaccaa aggtagcagc 600
ggtatgagcc tggcagaacg ttttagtctg accctgagcc gtagcagcct ggttgttggt 660
cgtagctgtg ttgaatttga accggaaacc gttccgctgc tgagcaccct gcgtggtaaa 720
ccgattacct ttctgggtct gatgcctccg ctgcatgaag gtcgtcgcga agatggtgaa 780
gatgcaaccg ttcgttggct ggatgcacag cctgcaaaaa gcgttgttta tgttgccctg 840
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gatcagggtc cgaatgcacg tctgattgaa gcaaaaaatg caggtctgca ggttgcccgt 1200
aatgatggtg atggtagctt tgatcgtgaa ggtgttgcag cagccattcg tgcagttgca 1260
gttgaagaag aaagcagcaa agtttttcag gccaaagcca aaaaactgca agaaattgtt 1320
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aaagat 1386

<210> 439
<211> 458
<212> PRT

<213> Artificial Sequence

<220>
<223> UGT76G1

<400> 439
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            20                  25                  30
Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr
        35                  40                  45
Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg
    50                  55                  60
Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro
65                  70                  75                  80
Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His
                85                  90                  95
Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser
            100                 105                 110
Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr
        115                 120                 125
Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu
    130                 135                 140
Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln
145                 150                 155                 160
Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu
                165                 170                 175
Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser
            180                 185                 190
Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile
        195                 200                 205
Lys Gln Thr 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

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Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn
385                 390                 395                 400
Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val
                405                 410                 415
Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln
            420                 425                 430
Lys Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu
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Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu
    450                 455
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<210> 440
<211> 1377
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT76G1 (DNA, native)

<400> 440
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ttcagtatca ccatctttca caccaacttc aacaaaccca aaacatctaa ttaccctcac 180
ttcactttca gattcatcct cgacaacgac ccacaagacg aacgcatttc caatctaccg 240
actcatggtc cgctcgctgg tatgcggatt ccgattatca acgaacacgg agctgacgaa 300
ttacgacgcg aactggaact gttgatgtta gcttctgaag aagatgaaga ggtatcgtgt 360
ttaatcacgg atgctctttg gtacttcgcg caatctgttg ctgacagtct taacctccga 420
cggcttgttt tgatgacaag cagcttgttt aattttcatg cacatgtttc acttcctcag 480
tttgatgagc ttggttacct cgatcctgat gacaaaaccc gtttggaaga acaagcgagt 540
gggtttccta tgctaaaagt gaaagacatc aagtctgcgt attcgaactg gcaaatactc 600
aaagagatat tagggaagat gataaaacaa acaaaagcat cttcaggagt catctggaac 660
tcatttaagg aactcgaaga gtctgagctc gaaactgtta tccgtgagat cccggctcca 720
agtttcttga taccactccc caagcatttg acagcctctt ccagcagctt actagaccac 780
gatcgaaccg tttttcaatg gttagaccaa caaccgccaa gttcggtact gtatgttagt 840
tttggtagta ctagtgaagt ggatgagaaa gatttcttgg aaatagctcg tgggttggtt 900
gatagcaagc agtcgttttt atgggtggtt cgacctgggt ttgtcaaggg ttcgacgtgg 960
gtcgaaccgt tgccagatgg gttcttgggt gaaagaggac gtattgtgaa atgggttcca 1020
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tctacgttgg aaagcgtttg tgaaggtgtt cctatgattt tctcggattt tgggctcgat 1140
caaccgttga atgctagata catgagtgat gttttgaagg taggggtgta tttggaaaat 1200
gggtgggaaa gaggagagat agcaaatgca ataagaagag ttatggtgga tgaagaagga 1260
gaatacatta gacagaatgc aagagttttg aaacaaaagg cagatgtttc tttgatgaag 1320
ggtggttcgt cttacgaatc attagagtct ctagtttctt acatttcatc gttgtaa    1377
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<210> 441
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT73C5

<400> 441

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 1               5                  10                  15
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            20                  25                  30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
        35                  40                  45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
    50                  55                  60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65                  70                  75                  80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
                85                  90                  95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
            100                 105                 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
        115                 120                 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
    130                 135                 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145                 150                 155                 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
                165                 170                 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
            180                 185                 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
        195                 200                 205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
    210                 215                 220
Gly Ser Val Ser Glu Thr Thr Lys Ser Ser Pro Leu His Phe Val Leu
225                 230                 235                 240
Phe Pro Phe Met Ala Gln Gly His Met Ile Pro Met Val Asp Ile Ala
                245                 250                 255
Arg Leu Leu Ala Gln Arg Gly Val Ile Ile Thr Ile Val Thr Thr Pro
            260                 265                 270
His Asn Ala Ala Arg Phe Lys Asn Val Leu Asn Arg Ala Ile Glu Ser
        275                 280                 285
Gly Leu Pro Ile Asn Leu Val Gln Val Lys Phe Pro Tyr Leu Glu Ala
    290                 295                 300
Gly Leu Gln Glu Gly Gln Glu Asn Ile Asp Ser Leu Asp Thr Met Glu
305                 310                 315                 320
Arg Met Ile Pro Phe Phe Lys Ala Val Asn Phe Leu Glu Glu Pro Val
                325                 330                 335
Gln Lys Leu Ile Glu Glu Met Asn Pro Arg Pro Ser Cys Leu Ile Ser
            340                 345                 350
Asp Phe Cys Leu Pro Tyr Thr Ser Lys Ile Ala Lys Lys Phe Asn Ile
        355                 360                 365
Pro Lys Ile Leu Phe His Gly Met Gly Cys Phe Cys Leu Leu Cys Met
    370                 375                 380
His Val Leu Arg Lys Asn Arg Glu Ile Leu Asp Asn Leu Lys Ser Asp
385                 390                 395                 400
Lys Glu Leu Phe Thr Val Pro Asp Phe Pro Asp Arg Val Glu Phe Thr
                405                 410                 415
Arg Thr Gln Val Pro Val Glu Thr Tyr Val Pro Ala Gly Asp Trp Lys
            420                 425                 430
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Asp Ile Phe Asp Gly Met Val Glu Ala Asn Glu Thr Ser Tyr Gly Val
435 440 445
Ile Val Asn Ser Phe Gln Glu Leu Glu Pro Ala Tyr Ala Lys Asp Tyr
450 455 460
Lys Glu Val Arg Ser Gly Lys Ala Trp Thr Ile Gly Pro Val Ser Leu
465 470 475 480
Cys Asn Lys Val Gly Ala Asp Lys Ala Glu Arg Gly Asn Lys Ser Asp
485 490 495
Ile Asp Gln Asp Glu Cys Leu Lys Trp Leu Asp Ser Lys Lys His Gly
500 505 510
Ser Val Leu Tyr Val Cys Leu Gly Ser Ile Cys Asn Leu Pro Leu Ser
515 520 525
Gln Leu Lys Glu Leu Gly Leu Gly Leu Glu Glu Ser Gln Arg Pro Phe
530 535 540
Ile Trp Val Ile Arg Gly Trp Glu Lys Tyr Lys Glu Leu Val Glu Trp
545 550 555 560
Phe Ser Glu Ser Gly Phe Glu Asp Arg Ile Gln Asp Arg Gly Leu Leu
565 570 575
Ile Lys Gly Trp Ser Pro Gln Met Leu Ile Leu Ser His Pro Ser Val
580 585 590
Gly Gly Phe Leu Thr His Cys Gly Trp Asn Ser Thr Leu Glu Gly Ile
595 600 605
Thr Ala Gly Leu Pro Leu Leu Thr Trp Pro Leu Phe Ala Asp Gln Phe
610 615 620
Cys Asn Glu Lys Leu Val Val Glu Val Leu Lys Ala Gly Val Arg Ser
625 630 635 640
Gly Val Glu Gln Pro Met Lys Trp Gly Glu Glu Glu Lys Ile Gly Val
645 650 655
Leu Val Asp Lys Glu Gly Val Lys Lys Ala Val Glu Glu Leu Met Gly
660 665 670
Glu Ser Asp Asp Ala Lys Glu Arg Arg Arg Arg Ala Lys Glu Leu Gly
675 680 685
Asp Ser Ala His Lys Ala Val Glu Glu Gly Gly Ser Ser His Ser Asn
690 695 700
Ile Ser Phe Leu Leu Gln Asp Ile Met Glu Leu Ala Glu Pro Asn Asn
705 710 715 720
Ala Ala Ala Ser

<210> 442
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT73C5 (DNA, native)

<400> 442
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tggcgaaaca aaaagtttga attgggtttg gagtttccca atcttcctta ttatattgat 180
ggtgatgtta aattaacaca gtctatggcc atcatacgtt atatagctga caagcacaac 240
atgttgggtg gttgtccaaa agagcgtgca gagatttcaa tgcttgaagg agcggttttg 300

gatattagat acggtgtttc gagaattgca tatagtaaag actttgaaac tctcaaagtt 360
gattttctta gcaagctacc tgaaatgctg aaaatgttcg aagatcgttt atgtcataaa 420
acatatttaa atggtgatca tgtaacccat cctgacttca tgttgtatga cgctcttgat 480
gttgttttat acatggaccc aatgtgcctg gatgcgttcc caaaattagt ttgttttaaa 540
aaacgtattg aagctatccc acaaattgat aagtacttga aatccagcaa gtatatagca 600
tggcctttgc agggctggca agccacgttt ggtggtggcg accatcctcc aaaatcggat 660
ctggttccgc gtggatccgt ttccgaaaca accaaatctt ctccacttca ctttgttctc 720
ttccctttca tggctcaagg ccacatgatt cccatggttg atattgcaag gctcttggct 780
cagcgtggtg tgatcataac aattgtcacg acgcctcaca atgcagcgag gttcaagaat 840
gtcctaaacc gtgccattga gtctggcttg cccatcaact tagtgcaagt caagtttcca 900
tatctagaag ctggtttgca agaaggacaa gagaatatcg attctcttga cacaatggag 960
cggatgatac ctttctttaa agcggttaac tttctcgaag aaccagtcca gaagctcatt 1020
gaagagatga accctcgacc aagctgtcta atttctgatt tttgtttgcc ttatacaagc 1080
aaaatcgcca agaagttcaa tatcccaaag atcctcttcc atggcatggg ttgcttttgt 1140
cttctgtgta tgcatgtttt acgcaagaac cgtgagatct tggacaattt aaagtcagat 1200
aaggagcttt tcactgttcc tgattttcct gatagagttg aattcacaag aacgcaagtt 1260
ccggtagaaa catatgttcc agctggagac tggaaagata tctttgatgg tatggtagaa 1320
gcgaatgaga catcttatgg tgtgatcgtc aactcatttc aagagctcga gcctgcttat 1380
gccaaagact acaaggaggt aaggtccggt aaagcatgga ccattggacc cgtttccttg 1440
tgcaacaagg taggagccga caaagcagag aggggaaaca aatcagacat tgatcaagat 1500
gagtgcctta aatggctcga ttctaagaaa catggctcgg tgctttacgt ttgtcttgga 1560
agtatctgta atcttccttt gtctcaactc aaggagctgg gactaggcct agaggaatcc 1620
caaagacctt tcatttgggt cataagaggt tgggagaagt acaaagagtt agttgagtgg 1680
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tcccctcaaa tgcttatcct ttcacatcca tcagttggag ggttcctaac acactgtggt 1800
tggaactcga ctcttgaggg gataactgct ggtctaccgc tacttacatg gccgctattc 1860
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agaagaagag ccaaagagct tggagattca gctcacaagg ctgtggaaga aggaggctct 2100
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gcggccgcat cgtga 2175

<210> 443
<211> 1512
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT73C5 (Codon optimized Ecoli)

<400> 443
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cgtggtgtga ttattaccat tgttaccaca ccgcataatg cagcacgctt taaaaacgtt 180
ctgaatcgtg caattgaaag cggtctgccg attaatctgg ttcaggttaa atttccgtat 240
ctggaagcag gtctgcaaga aggtcaagaa aatattgata gcctggatac catggaacgc 300
atgattccgt ttttcaaagc cgtgaatttt ctggaagaac cggtgcagaa actgatcgaa 360
gaaatgaatc cgcgtccgag ctgtctgatt agcgattttt gtctgccgta taccagcaaa 420
atcgccaaaa aattcaacat cccgaaaatc ctgtttcatg gtatgggttg tttttgcctg 480
ctgtgtatgc atgttctgcg taaaaatcgt gaaatcctgg ataacctgaa aagcgataaa 540
gaactgttta ccgttccgga ttttccggat cgtgtggaat ttacccgtac acaggttccg 600
gttgaaacct atgttccggc aggcgattgg aaagatattt ttgatggtat ggtggaagcc 660
aacgaaacca gctatggtgt tattgtgaat agctttcaag aactggaacc ggcatatgcg 720

aaagattaca aagaagttcg tagcggtaaa gcatggacca ttggtccggt tagcctgtgt 780
aataaagttg gtgcagataa agcagaacgc ggtaataaaa gtgatatcga tcaggatgaa 840
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cgtccgttta tttgggttat tcgtggttgg gagaaataca aagaactggt tgaatggttt 1020
agcgaaagcg gttttgaaga tcgtattcag gatcgtggcc tgctgattaa aggttggagt 1080
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aatagcaccc tggaaggtat tacagctggc ctgccgctgc tgacctggcc tctgtttgca 1200
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ggtgttaaaa aagccgtgga agaactgatg ggtgaaagtg atgatgcaaa agaacgtcgt 1380
cgtcgtgcaa aagagctggg cgatagcgca cataaagcag ttgaagaagg tggtagcagc 1440
catagcaata ttagctttct gctgcaggat attatggaac tggcagaacc gaataactaa 1500
gcggccgctg aa 1512

<210> 444
<211> 495
<212> PRT
<213> Artificial Sequence

<220>
<223> UGT73C6

<400> 444
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Phe Pro Phe Met Ala Gln Gly His Met Ile Pro Met Val Asp Ile Ala
            20                  25                  30
Arg Leu Leu Ala Gln Arg Gly Val Leu Ile Thr Ile Val Thr Thr Pro
        35                  40                  45
His Asn Ala Ala Arg Phe Lys Asn Val Leu Asn Arg Ala Ile Glu Ser
    50                  55                  60
Gly Leu Pro Ile Asn Leu Val Gln Val Lys Phe Pro Tyr Gln Glu Ala
65                  70                  75                  80
Gly Leu Gln Glu Gly Gln Glu Asn Met Asp Leu Leu Thr Thr Met Glu
                85                  90                  95
Gln Ile Thr Ser Phe Phe Lys Ala Val Asn Leu Leu Lys Glu Pro Val
            100                 105                 110
Gln Asn Leu Ile Glu Glu Met Ser Pro Arg Pro Ser Cys Leu Ile Ser
        115                 120                 125
Asp Met Cys Leu Ser Tyr Thr Ser Glu Ile Ala Lys Lys Phe Lys Ile
    130                 135                 140
Pro Lys Ile Leu Phe His Gly Met Gly Cys Phe Cys Leu Leu Cys Val
145                 150                 155                 160
Asn Val Leu Arg Lys Asn Arg Glu Ile Leu Asp Asn Leu Lys Ser Asp
                165                 170                 175
Lys Glu Tyr Phe Ile Val Pro Tyr Phe Pro Asp Arg Val Glu Phe Thr
            180                 185                 190
Arg Pro Gln Val Pro Val Glu Thr Tyr Val Pro Ala Gly Trp Lys Glu
        195                 200                 205
Ile Leu Glu Asp Met Val Glu Ala Asp Lys Thr Ser Tyr Gly Val Ile
    210                 215                 220
Val Asn Ser Phe Gln Glu Leu Glu Pro Ala Tyr Ala Lys Asp Phe Lys
225                 230                 235                 240

Glu Ala Arg Ser Gly Lys Ala Trp Thr Ile Gly Pro Val Ser Leu Cys
245 250 255
Asn Lys Val Gly Val Asp Lys Ala Glu Arg Gly Asn Lys Ser Asp Ile
260 265 270
Asp Gln Asp Glu Cys Leu Glu Trp Leu Asp Ser Lys Glu Pro Gly Ser
275 280 285
Val Leu Tyr Val Cys Leu Gly Ser Ile Cys Asn Leu Pro Leu Ser Gln
290 295 300
Leu Leu Glu Leu Gly Leu Gly Leu Glu Glu Ser Gln Arg Pro Phe Ile
305 310 315 320
Trp Val Ile Arg Gly Trp Glu Lys Tyr Lys Glu Leu Val Glu Trp Phe
325 330 335
Ser Glu Ser Gly Phe Glu Asp Arg Ile Gln Asp Arg Gly Leu Leu Ile
340 345 350
Lys Gly Trp Ser Pro Gln Met Leu Ile Leu Ser His Pro Ser Val Gly
355 360 365
Gly Phe Leu Thr His Cys Gly Trp Asn Ser Thr Leu Glu Gly Ile Thr
370 375 380
Ala Gly Leu Pro Met Leu Thr Trp Pro Leu Phe Ala Asp Gln Phe Cys
385 390 395 400
Asn Glu Lys Leu Val Val Gln Ile Leu Lys Val Gly Val Ser Ala Glu
405 410 415
Val Lys Glu Val Met Lys Trp Gly Glu Glu Glu Lys Ile Gly Val Leu
420 425 430
Val Asp Lys Glu Gly Val Lys Lys Ala Val Glu Glu Leu Met Gly Glu
435 440 445
Ser Asp Asp Ala Lys Glu Arg Arg Arg Arg Ala Lys Glu Leu Gly Glu
450 455 460
Ser Ala His Lys Ala Val Glu Glu Gly Gly Ser Ser His Ser Asn Ile
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485 490 495

<210> 445
<211> 1485
<212> DNA
<213> Artificial Sequence

<220>
<223> UGT73C6 (gDNA, native)

<400> 445
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cttataacaa ttgtcacgac gcctcacaat gcagcaaggt tcaagaatgt cctaaaccgt 180
gccattgagt ctggtttgcc catcaaccta gtgcaagtca agtttccata tcaagaagct 240
ggtctgcaag aaggacaaga aaatatggat ttgcttacca cgatggagca gataacatct 300
ttctttaaag cggttaactt actcaaagaa ccagtccaga accttattga agagatgagc 360
ccgcgaccaa gctgtctaat ctctgatatg tgtttgtcgt atacaagcga aatcgccaag 420
aagttcaaaa taccaaagat cctcttccat ggcatgggtt gcttttgtct tctgtgtgtt 480
aacgttctgc gcaagaaccg tgagatcttg gacaatttaa agtctgataa ggagtacttc 540
attgttcctt attttcctga tagagttgaa ttcacaagac ctcaagttcc ggtggaaaca 600
tatgttcctg caggctggaa agagatcttg gaggatatgg tagaagcgga taagacatct 660

tatggtgtta tagtcaactc atttcaagag ctcgaacctg cgtatgccaa agacttcaag 720
gaggcaaggt ctggtaaagc atggaccatt ggacctgttt ccttgtgcaa caaggtagga 780
gtagacaaag cagagagggg aaacaaatca gatattgatc aagatgagtg ccttgaatgg 840
ctcgattcta aggaaccggg atctgtgctc tacgtttgcc ttggaagtat ttgtaatctt 900
cctctgtctc agctccttga gctgggacta ggcctagagg aatcccaaag acctttcatc 960
tgggtcataa gaggttggga gaaatacaaa gagttagttg agtggttctc ggaaagcggc 1020
tttgaagata gaatccaaga tagaggactt ctcatcaaag gatggtcccc tcaaatgctt 1080
atcctttcac atccttctgt tggagggttc ttaacgcact gcggatggaa ctcgactctt 1140
gaggggataa ctgctggtct accaatgctt acatggccac tatttgcaga ccaattctgc 1200
aacgagaaac tggtcgtaca aatactaaaa gtcggtgtaa gtgccgaggt taaagaggtc 1260
atgaaatggg gagaagaaga gaagatagga gtgttggtgg ataaagaagg agtgaagaag 1320
gcagtggaag aactaatggg tgagagtgat gatgcaaaag agagaagaag aagagccaaa 1380
gagcttggag aatcagctca caaggctgtg gaagaaggag gctcctctca ttctaatatc 1440
actttcttgc tacaagacat aatgcaacta gcacagtcca ataat 1485

<210> 446
<211> 759
<212> PRT
<213> Artificial Sequence

<220>
<223> SgCbQ

<400> 446
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 1               5                  10                  15
Lys Trp Leu Lys Ser Ile Ser Asn His Leu Gly Arg Gln Val Trp Glu
            20                  25                  30
Phe Cys Pro Asp Ala Gly Thr Gln Gln Gln Leu Leu Gln Val His Lys
        35                  40                  45
Ala Arg Lys Ala Phe His Asp Asp Arg Phe His Arg Lys Gln Ser Ser
    50                  55                  60
Asp Leu Phe Ile Thr Ile Gln Tyr Gly Lys Glu Val Glu Asn Gly Gly
65                  70                  75                  80
Lys Thr Ala Gly Val Lys Leu Lys Glu Gly Glu Glu Val Arg Lys Glu
                85                  90                  95
Ala Val Glu Ser Ser Leu Glu Arg Ala Leu Ser Phe Tyr Ser Ser Ile
            100                 105                 110
Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro Met Phe
        115                 120                 125
Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val Thr Gly Val Leu Asn
    130                 135                 140
Ser Val Leu Ser Lys His His Arg Gln Glu Met Cys Arg Tyr Val Tyr
145                 150                 155                 160
Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly Pro
                165                 170                 175
Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu Leu
            180                 185                 190
Gly Glu Asp Ala Asn Ala Gly Ala Met Pro Lys Ala Arg Ala Trp Ile
        195                 200                 205
Leu Asp His Gly Gly Ala Thr Gly Ile Thr Ser Trp Gly Lys Leu Trp
    210                 215                 220
Leu Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn Pro Leu Pro
225                 230                 235                 240

```
Pro Glu Phe Trp Leu Phe Pro Tyr Phe Leu Pro Phe His Pro Gly Arg
                245                 250                 255
Met Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr
            260                 265                 270
Gly Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu Ser Leu Arg
        275                 280                 285
Lys Glu Leu Tyr Ala Val Pro Tyr His Glu Ile Asp Trp Asn Lys Ser
    290                 295                 300
Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met
305                 310                 315                 320
Gln Asp Ile Leu Trp Gly Ser Leu His His Val Tyr Glu Pro Leu Phe
                325                 330                 335
Thr Arg Trp Pro Ala Lys Arg Leu Arg Glu Lys Ala Leu Gln Thr Ala
            340                 345                 350
Met Gln His Ile His Tyr Glu Asp Glu Asn Thr Arg Tyr Ile Cys Leu
        355                 360                 365
Gly Pro Val Asn Lys Val Leu Asn Leu Leu Cys Cys Trp Val Glu Asp
    370                 375                 380
Pro Tyr Ser Asp Ala Phe Lys Leu His Leu Gln Arg Val His Asp Tyr
385                 390                 395                 400
Leu Trp Val Ala Glu Asp Gly Met Lys Met Gln Gly Tyr Asn Gly Ser
                405                 410                 415
Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Val Ser Thr Lys
            420                 425                 430
Leu Val Asp Asn Tyr Gly Pro Thr Leu Arg Lys Ala His Asp Phe Val
        435                 440                 445
Lys Ser Ser Gln Ile Gln Gln Asp Cys Pro Gly Asp Pro Asn Val Trp
    450                 455                 460
Tyr Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His
465                 470                 475                 480
Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ala Leu
                485                 490                 495
Met Leu Ser Lys Leu Pro Ser Glu Thr Val Gly Glu Ser Leu Glu Arg
            500                 505                 510
Asn Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Asp
        515                 520                 525
Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu
    530                 535                 540
Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr
545                 550                 555                 560
Pro Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Thr Leu Phe
                565                 570                 575
Lys Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Thr Ala Ile
            580                 585                 590
Val Arg Ala Ala Asn Phe Leu Glu Asn Met Gln Arg Thr Asp Gly Ser
        595                 600                 605
Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly
    610                 615                 620
Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Leu Ala
625                 630                 635                 640
Ile Arg Lys Ala Cys Asp Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly
                645                 650                 655
Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn
            660                 665                 670
```

Leu Glu Gly Asn Arg Pro His Leu Val Asn Thr Ala Trp Val Leu Met
675 680 685
Ala Leu Ile Glu Ala Gly Gln Ala Glu Arg Asp Pro Thr Pro Leu His
690 695 700
Arg Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Asn Gly Asp Phe
705 710 715 720
Pro Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr
725 730 735
Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr
740 745 750
Cys His Arg Val Leu Thr Glu
755

<210> 447
<211> 418
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 5 [Trichoderma reesei QM6a] GenBank: EGR512.1

<400> 447
Met Asn Lys Ser Val Ala Pro Leu Leu Leu Ala Ala Ser Ile Leu Tyr
1 5 10 15
Gly Gly Ala Ala Ala Gln Gln Thr Val Trp Gly Gln Cys Gly Gly Ile
20 25 30
Gly Trp Ser Gly Pro Thr Asn Cys Ala Pro Gly Ser Ala Cys Ser Thr
35 40 45
Leu Asn Pro Tyr Tyr Ala Gln Cys Ile Pro Gly Ala Thr Thr Ile Thr
50 55 60
Thr Ser Thr Arg Pro Pro Ser Gly Pro Thr Thr Thr Thr Arg Ala Thr
65 70 75 80
Ser Thr Ser Ser Ser Thr Pro Pro Thr Ser Ser Gly Val Arg Phe Ala
85 90 95
Gly Val Asn Ile Ala Gly Phe Asp Phe Gly Cys Thr Thr Asp Gly Thr
100 105 110
Cys Val Thr Ser Lys Val Tyr Pro Pro Leu Lys Asn Phe Thr Gly Ser
115 120 125
Asn Asn Tyr Pro Asp Gly Ile Gly Gln Met Gln His Phe Val Asn Asp
130 135 140
Asp Gly Met Thr Ile Phe Arg Leu Pro Val Gly Trp Gln Tyr Leu Val
145 150 155 160
Asn Asn Asn Leu Gly Gly Asn Leu Asp Ser Thr Ser Ile Ser Lys Tyr
165 170 175
Asp Gln Leu Val Gln Gly Cys Leu Ser Leu Gly Ala Tyr Cys Ile Val
180 185 190
Asp Ile His Asn Tyr Ala Arg Trp Asn Gly Gly Ile Ile Gly Gln Gly
195 200 205
Gly Pro Thr Asn Ala Gln Phe Thr Ser Leu Trp Ser Gln Leu Ala Ser
210 215 220
Lys Tyr Ala Ser Gln Ser Arg Val Trp Phe Gly Ile Met Asn Glu Pro
225 230 235 240

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

<210> 448
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 61 [Trichoderma reesei QM6a] 249 aa protein EGR50392.1 GI:340520155

<400> 448

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

Asn Thr Gln Val Trp Ala Gln Gln Asp Leu Ile Asn Gln Gly Asn Lys
145 150 155 160
Trp Thr Val Lys Ile Pro Ser Ser Leu Arg Pro Gly Asn Tyr Val Phe
165 170 175
Arg His Glu Leu Leu Ala Ala His Gly Ala Ser Ser Ala Asn Gly Met
180 185 190
Gln Asn Tyr Pro Gln Cys Val Asn Ile Ala Val Thr Gly Ser Gly Thr
195 200 205
Lys Ala Leu Pro Ala Gly Thr Pro Ala Thr Gln Leu Tyr Lys Pro Thr
210 215 220
Asp Pro Gly Ile Leu Phe Asn Pro Tyr Thr Thr Ile Thr Ser Tyr Thr
225 230 235 240
Ile Pro Gly Pro Ala Leu Trp Gln Gly
245

<210> 449
<211> 326
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 61, partial
[Trichoderma reesei QM6a] 326 aa protein
EGR49821.1 GI:340519583

<400> 449
Ser Ala His Thr Thr Phe Thr Thr Leu Phe Ile Asp Lys Lys Asn Gln
1 5 10 15
Gly Asp Gly Thr Cys Val Arg Met Pro Tyr Asp Asp Lys Thr Ala Thr
20 25 30
Asn Pro Val Lys Pro Ile Thr Ser Ser Asp Met Ala Cys Gly Arg Asn
35 40 45
Gly Gly Asp Pro Val Pro Phe Ile Cys Ser Ala Lys Lys Gly Ser Leu
50 55 60
Leu Thr Phe Glu Phe Arg Leu Trp Pro Asp Ala Gln Gln Pro Gly Ser
65 70 75 80
Ile Asp Pro Gly His Leu Gly Pro Cys Ala Val Tyr Leu Lys Lys Val
85 90 95
Asp Asn Met Phe Ser Asp Ser Ala Ala Gly Gly Gly Trp Phe Lys Ile
100 105 110
Trp Glu Asp Gly Tyr Asp Ser Lys Thr Gln Lys Trp Cys Val Asp Arg
115 120 125
Leu Val Lys Asn Asn Gly Leu Leu Ser Val Arg Leu Pro Arg Gly Leu
130 135 140
Pro Ala Gly Tyr Tyr Ile Val Arg Pro Glu Ile Leu Ala Leu His Trp
145 150 155 160
Ala Ala His Arg Asp Asp Pro Gln Phe Tyr Leu Gly Cys Ala Gln Ile
165 170 175
Phe Val Asp Ser Asp Val Arg Gly Pro Leu Glu Ile Pro Arg Arg Gln
180 185 190
Gln Ala Thr Ile Pro Gly Tyr Val Asn Ala Lys Thr Pro Gly Leu Thr
195 200 205
Phe Asp Ile Tyr Gln Asp Lys Leu Pro Pro Tyr Pro Met Pro Gly Pro

```
    210                 215                 220
Lys Val Tyr Ile Pro Pro Ala Lys Gly Asn Lys Pro Asn Gln Asp Leu
225                 230                 235                 240
Asn Ala Gly Arg Leu Val Gln Thr Asp Gly Leu Ile Pro Lys Asp Cys
                245                 250                 255
Leu Ile Lys Lys Ala Asn Trp Cys Gly Arg Pro Val Glu Pro Tyr Ser
            260                 265                 270
Ser Ala Arg Met Cys Trp Arg Ala Val Asn Asp Cys Tyr Ala Gln Ser
        275                 280                 285
Lys Lys Cys Arg Glu Ser Ser Pro Pro Ile Gly Leu Thr Asn Cys Asp
    290                 295                 300
Arg Trp Ser Asp His Cys Gly Lys Met Asp Ala Leu Cys Glu Gln Glu
305                 310                 315                 320
Lys Tyr Lys Gly Pro Pro
                325
```

<210> 450
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 7 [Trichoderma reesei QM6a] 459 aa protein EGR48251.1 GI:340518009

<400> 450

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

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

<210> 451
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 45 [Trichoderma reesei QM6a] 242 aa protein EGR47058.1 GI:340516811

<400> 451

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

```
                85                  90                  95
Ala Gly Gln Ser Ile Ile Val Met Val Thr Asn Leu Cys Pro Asn Asn
            100                 105                 110
Gly Asn Ala Gln Trp Cys Pro Val Val Gly Gly Thr Asn Gln Tyr Gly
        115                 120                 125
Tyr Ser Tyr His Phe Asp Ile Met Ala Gln Asn Glu Ile Phe Gly Asp
    130                 135                 140
Asn Val Val Val Asp Phe Glu Pro Ile Ala Cys Pro Gly Gln Ala Ala
145                 150                 155                 160
Ser Asp Trp Gly Thr Cys Leu Cys Val Gly Gln Gln Glu Thr Asp Pro
                165                 170                 175
Thr Pro Val Leu Gly Asn Asp Thr Gly Ser Thr Pro Pro Gly Ser Ser
            180                 185                 190
Pro Pro Ala Thr Ser Ser Ser Pro Pro Ser Gly Gly Gly Gln Gln Thr
        195                 200                 205
Leu Tyr Gly Gln Cys Gly Gly Ala Gly Trp Thr Gly Pro Thr Thr Cys
    210                 215                 220
Gln Ala Pro Gly Thr Cys Lys Val Gln Asn Gln Trp Tyr Ser Gln Cys
225                 230                 235                 240
Leu Pro
```

<210> 452
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 5 [Trichoderma reesei QM6a] 438 aa protein EGR44174.1 GI:340513898

<400> 452

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

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

<210> 453
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 45 [Trichoderma reesei QM6a] 242 aa protein XP_006967072.1 GI:589110099

<400> 453

```
Met Lys Ala Thr Leu Val Leu Gly Ser Leu Ile Val Gly Ala Val Ser
 1               5                  10                  15
Ala Tyr Lys Ala Thr Thr Thr Arg Tyr Tyr Asp Gly Gln Glu Gly Ala
            20                  25                  30
Cys Gly Cys Gly Ser Ser Ser Gly Ala Phe Pro Trp Gln Leu Gly Ile
        35                  40                  45
Gly Asn Gly Val Tyr Thr Ala Ala Gly Ser Gln Ala Leu Phe Asp Thr
```

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

<210> 454
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 7 [Trichoderma reesei QM6a] 459 aa protein XP_006965674.1 GI:589107303

<400> 454

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

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


<210> 455
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 61, partial
      [Trichoderma reesei QM6a] 326 aa protein
      XP_006964038.1 GI:589104031

<400> 455
```

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

Gly Ile Gly Tyr Ser Gly Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys
        435                 440                 445
Gln Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu
    450                 455


<210> 456
<211> 326
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 61, partial
      [Trichoderma reesei QM6a] 326 aa protein
      XP_006964038.1 GI:589104031

<400> 456
Ser Ala His Thr Thr Phe Thr Thr Leu Phe Ile Asp Lys Lys Asn Gln
 1               5                  10                  15
Gly Asp Gly Thr Cys Val Arg Met Pro Tyr Asp Asp Lys Thr Ala Thr
            20                  25                  30
Asn Pro Val Lys Pro Ile Thr Ser Ser Asp Met Ala Cys Gly Arg Asn
        35                  40                  45
Gly Gly Asp Pro Val Pro Phe Ile Cys Ser Ala Lys Lys Gly Ser Leu
    50                  55                  60
Leu Thr Phe Glu Phe Arg Leu Trp Pro Asp Ala Gln Gln Pro Gly Ser
65                  70                  75                  80
Ile Asp Pro Gly His Leu Gly Pro Cys Ala Val Tyr Leu Lys Lys Val
                85                  90                  95
Asp Asn Met Phe Ser Asp Ser Ala Ala Gly Gly Gly Trp Phe Lys Ile
            100                 105                 110
Trp Glu Asp Gly Tyr Asp Ser Lys Thr Gln Lys Trp Cys Val Asp Arg
        115                 120                 125
Leu Val Lys Asn Asn Gly Leu Leu Ser Val Arg Leu Pro Arg Gly Leu
    130                 135                 140
Pro Ala Gly Tyr Tyr Ile Val Arg Pro Glu Ile Leu Ala Leu His Trp
145                 150                 155                 160
Ala Ala His Arg Asp Asp Pro Gln Phe Tyr Leu Gly Cys Ala Gln Ile
                165                 170                 175
Phe Val Asp Ser Asp Val Arg Gly Pro Leu Glu Ile Pro Arg Arg Gln
            180                 185                 190
Gln Ala Thr Ile Pro Gly Tyr Val Asn Ala Lys Thr Pro Gly Leu Thr
        195                 200                 205
Phe Asp Ile Tyr Gln Asp Lys Leu Pro Pro Tyr Pro Met Pro Gly Pro
    210                 215                 220
Lys Val Tyr Ile Pro Pro Ala Lys Gly Asn Lys Pro Asn Gln Asp Leu
225                 230                 235                 240
Asn Ala Gly Arg Leu Val Gln Thr Asp Gly Leu Ile Pro Lys Asp Cys
                245                 250                 255
Leu Ile Lys Lys Ala Asn Trp Cys Gly Arg Pro Val Glu Pro Tyr Ser
            260                 265                 270
Ser Ala Arg Met Cys Trp Arg Ala Val Asn Asp Cys Tyr Ala Gln Ser
        275                 280                 285
Lys Lys Cys Arg Glu Ser Ser Pro Pro Ile Gly Leu Thr Asn Cys Asp

```
    290                 295                 300
Arg Trp Ser Asp His Cys Gly Lys Met Asp Ala Leu Cys Glu Gln Glu
305                 310                 315                 320
Lys Tyr Lys Gly Pro Pro
                325
```

<210> 457
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 61 [Trichoderma reesei QM6a] 249 aa protein XP_006963879.1 GI:589103713

<400> 457

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

<210> 458
<211> 418
<212> PRT

<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 5 [Trichoderma reesei QM6a] 418 aa protein XP_006962583.1 GI:589101121

<400> 458
Met Asn Lys Ser Val Ala Pro Leu Leu Leu Ala Ala Ser Ile Leu Tyr
 1               5                  10                  15
Gly Gly Ala Ala Ala Gln Gln Thr Val Trp Gly Gln Cys Gly Gly Ile
            20                  25                  30
Gly Trp Ser Gly Pro Thr Asn Cys Ala Pro Gly Ser Ala Cys Ser Thr
        35                  40                  45
Leu Asn Pro Tyr Tyr Ala Gln Cys Ile Pro Gly Ala Thr Thr Ile Thr
    50                  55                  60
Thr Ser Thr Arg Pro Pro Ser Gly Pro Thr Thr Thr Thr Arg Ala Thr
65                  70                  75                  80
Ser Thr Ser Ser Ser Thr Pro Pro Thr Ser Ser Gly Val Arg Phe Ala
                85                  90                  95
Gly Val Asn Ile Ala Gly Phe Asp Phe Gly Cys Thr Thr Asp Gly Thr
            100                 105                 110
Cys Val Thr Ser Lys Val Tyr Pro Pro Leu Lys Asn Phe Thr Gly Ser
        115                 120                 125
Asn Asn Tyr Pro Asp Gly Ile Gly Gln Met Gln His Phe Val Asn Asp
    130                 135                 140
Asp Gly Met Thr Ile Phe Arg Leu Pro Val Gly Trp Gln Tyr Leu Val
145                 150                 155                 160
Asn Asn Asn Leu Gly Gly Asn Leu Asp Ser Thr Ser Ile Ser Lys Tyr
                165                 170                 175
Asp Gln Leu Val Gln Gly Cys Leu Ser Leu Gly Ala Tyr Cys Ile Val
            180                 185                 190
Asp Ile His Asn Tyr Ala Arg Trp Asn Gly Gly Ile Ile Gly Gln Gly
        195                 200                 205
Gly Pro Thr Asn Ala Gln Phe Thr Ser Leu Trp Ser Gln Leu Ala Ser
    210                 215                 220
Lys Tyr Ala Ser Gln Ser Arg Val Trp Phe Gly Ile Met Asn Glu Pro
225                 230                 235                 240
His Asp Val Asn Ile Asn Thr Trp Ala Ala Thr Val Gln Glu Val Val
                245                 250                 255
Thr Ala Ile Arg Asn Ala Gly Ala Thr Ser Gln Phe Ile Ser Leu Pro
            260                 265                 270
Gly Asn Asp Trp Gln Ser Ala Gly Ala Phe Ile Ser Asp Gly Ser Ala
        275                 280                 285
Ala Ala Leu Ser Gln Val Thr Asn Pro Asp Gly Ser Thr Thr Asn Leu
    290                 295                 300
Ile Phe Asp Val His Lys Tyr Leu Asp Ser Asp Asn Ser Gly Thr His
305                 310                 315                 320
Ala Glu Cys Thr Thr Asn Asn Ile Asp Gly Ala Phe Ser Pro Leu Ala
                325                 330                 335
Thr Trp Leu Arg Gln Asn Asn Arg Gln Ala Ile Leu Thr Glu Thr Gly
            340                 345                 350
Gly Gly Asn Val Gln Ser Cys Ile Gln Asp Met Cys Gln Gln Ile Gln
        355                 360                 365
Tyr Leu Asn Gln Asn Ser Asp Val Tyr Leu Gly Tyr Val Gly Trp Gly

    370                 375                 380
Ala Gly Ser Phe Asp Ser Thr Tyr Val Leu Thr Glu Thr Pro Thr Gly
385                 390                 395                 400
Ser Gly Asn Ser Trp Thr Asp Thr Ser Leu Val Ser Ser Cys Leu Ala
                405                 410                 415
Arg Lys



<210> 459
<211> 344
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 61 [Trichoderma reesei
      QM6a] 344 aa protein  XP_006961567.1 GI:589099089

<400> 459
Met Ile Gln Lys Leu Ser Asn Leu Leu Val Thr Ala Leu Ala Val Ala
 1               5                  10                  15
Thr Gly Val Val Gly His Gly His Ile Asn Asp Ile Val Ile Asn Gly
            20                  25                  30
Val Trp Tyr Gln Ala Tyr Asp Pro Thr Thr Phe Pro Tyr Glu Ser Asn
        35                  40                  45
Pro Pro Ile Val Val Gly Trp Thr Ala Ala Asp Leu Asp Asn Gly Phe
    50                  55                  60
Val Ser Pro Asp Ala Tyr Gln Asn Pro Asp Ile Ile Cys His Lys Asn
65                  70                  75                  80
Ala Thr Asn Ala Lys Gly His Ala Ser Val Lys Ala Gly Asp Thr Ile
                85                  90                  95
Leu Phe Gln Trp Val Pro Val Pro Trp Pro His Pro Gly Pro Ile Val
            100                 105                 110
Asp Tyr Leu Ala Asn Cys Asn Gly Asp Cys Glu Thr Val Asp Lys Thr
        115                 120                 125
Thr Leu Glu Phe Phe Lys Ile Asp Gly Val Gly Leu Leu Ser Gly Gly
    130                 135                 140
Asp Pro Gly Thr Trp Ala Ser Asp Val Leu Ile Ser Asn Asn Asn Thr
145                 150                 155                 160
Trp Val Val Lys Ile Pro Asp Asn Leu Ala Pro Gly Asn Tyr Val Leu
                165                 170                 175
Arg His Glu Ile Ile Ala Leu His Ser Ala Gly Gln Ala Asn Gly Ala
            180                 185                 190
Gln Asn Tyr Pro Gln Cys Phe Asn Ile Ala Val Ser Gly Ser Gly Ser
        195                 200                 205
Leu Gln Pro Ser Gly Val Leu Gly Thr Asp Leu Tyr His Ala Thr Asp
    210                 215                 220
Pro Gly Val Leu Ile Asn Ile Tyr Thr Ser Pro Leu Asn Tyr Ile Ile
225                 230                 235                 240
Pro Gly Pro Thr Val Val Ser Gly Leu Pro Thr Ser Val Ala Gln Gly
                245                 250                 255
Ser Ser Ala Ala Thr Ala Thr Ala Ser Ala Thr Val Pro Gly Gly Gly
            260                 265                 270
Ser Gly Pro Thr Ser Arg Thr Thr Thr Thr Ala Arg Thr Thr Gln Ala

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        275                 280                 285
Ser Ser Arg Pro Ser Ser Thr Pro Pro Ala Thr Thr Ser Ala Pro Ala
    290                 295                 300
Gly Gly Pro Thr Gln Thr Leu Tyr Gly Gln Cys Gly Gly Ser Gly Tyr
305                 310                 315                 320
Ser Gly Pro Thr Arg Cys Ala Pro Pro Ala Thr Cys Ser Thr Leu Asn
                325                 330                 335
Pro Tyr Tyr Ala Gln Cys Leu Asn
            340


<210> 460
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Endoglucanase 249 aa protein Q7Z9M7.3 GI:43314396

<400> 460
Met Lys Ser Cys Ala Ile Leu Ala Ala Leu Gly Cys Leu Ala Gly Ser
 1               5                  10                  15
Val Leu Gly His Gly Gln Val Gln Asn Phe Thr Ile Asn Gly Gln Tyr
            20                  25                  30
Asn Gln Gly Phe Ile Leu Asp Tyr Tyr Tyr Gln Lys Gln Asn Thr Gly
        35                  40                  45
His Phe Pro Asn Val Ala Gly Trp Tyr Ala Glu Asp Leu Asp Leu Gly
    50                  55                  60
Phe Ile Ser Pro Asp Gln Tyr Thr Thr Pro Asp Ile Val Cys His Lys
65                  70                  75                  80
Asn Ala Ala Pro Gly Ala Ile Ser Ala Thr Ala Ala Ala Gly Ser Asn
                85                  90                  95
Ile Val Phe Gln Trp Gly Pro Gly Val Trp Pro His Pro Tyr Gly Pro
            100                 105                 110
Ile Val Thr Tyr Val Val Glu Cys Ser Gly Ser Cys Thr Thr Val Asn
        115                 120                 125
Lys Asn Asn Leu Arg Trp Val Lys Ile Gln Glu Ala Gly Ile Asn Tyr
    130                 135                 140
Asn Thr Gln Val Trp Ala Gln Gln Asp Leu Ile Asn Gln Gly Asn Lys
145                 150                 155                 160
Trp Thr Val Lys Ile Pro Ser Ser Leu Arg Pro Gly Asn Tyr Val Phe
                165                 170                 175
Arg His Glu Leu Leu Ala Ala His Gly Ala Ser Ser Ala Asn Gly Met
            180                 185                 190
Gln Asn Tyr Pro Gln Cys Val Asn Ile Ala Val Thr Gly Ser Gly Thr
        195                 200                 205
Lys Ala Leu Pro Ala Gly Thr Pro Ala Thr Gln Leu Tyr Lys Pro Thr
    210                 215                 220
Asp Pro Gly Ile Leu Phe Asn Pro Tyr Thr Thr Ile Thr Ser Tyr Thr
225                 230                 235                 240
Ile Pro Gly Pro Ala Leu Trp Gln Gly
                245
```

<210> 461
<211> 222
<212> PRT
<213> Artificial Sequence

<220>
<223> xylanase [Trichoderma reesei] 222 aa protein
CAA49293.1 GI:396564

<400> 461
```
Met Val Ser Phe Thr Ser Leu Leu Ala Ala Ser Pro Pro Ser Arg Ala
 1               5                  10                  15
Ser Cys Arg Pro Ala Ala Glu Val Glu Ser Val Ala Val Glu Lys Arg
            20                  25                  30
Gln Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
        35                  40                  45
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
    50                  55                  60
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
65                  70                  75                  80
Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
                85                  90                  95
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
            100                 105                 110
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
        115                 120                 125
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
    130                 135                 140
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
145                 150                 155                 160
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
                165                 170                 175
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
            180                 185                 190
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
        195                 200                 205
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
    210                 215                 220
```

<210> 462
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> xylanase [Trichoderma reesei] 229 aa protein
CAA49294.1 GI:396566

<400> 462
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Met Val Ala Phe Ser Ser Leu Ile Cys Ala Leu Thr Ser Ile Ala Ser
 1               5                  10                  15
Thr Leu Ala Met Pro Thr Gly Leu Glu Pro Glu Ser Ser Val Asn Val
            20                  25                  30
```

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


<210> 463
<211> 223
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-xylanase precursor [Trichoderma reesei] 223
      aa protein AAB5278.1 GI:78816

<400> 463
Met Val Ser Phe Thr Ser Leu Leu Ala Gly Val Ala Ala Ile Ser Gly
 1               5                  10                  15
Val Leu Ala Ala Pro Ala Ala Glu Val Glu Pro Val Ala Val Glu Lys
            20                  25                  30
Arg Gln Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe His
        35                  40                  45
Ser Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro
    50                  55                  60
Gly Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly
65                  70                  75                  80
Gly Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser
                85                  90                  95
Gly Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp
            100                 105                 110
Ser Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Gly Asn Phe Gly Thr
        115                 120                 125
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Tyr Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp
    130                 135                 140
Gly Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser
145                 150                 155                 160
Ile Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn
                165                 170                 175
His Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp
            180                 185                 190
Ala Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala
        195                 200                 205
Val Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
    210                 215                 220


<210> 464
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Structural Comparison Of Two Major
      Endo-1,4-Beta-Xylanases From Trichodrema Reesei 19
      aa protein 1XYP_A GI:112721

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 464
Xaa Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
 1               5                  10                  15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
            20                  25                  30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
        35                  40                  45
Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
    50                  55                  60
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65                  70                  75                  80
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
                85                  90                  95
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
            100                 105                 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
        115                 120                 125
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
    130                 135                 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145                 150                 155                 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
                165                 170                 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185                 190
```

<210> 465
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, Structural Comparison Of Two Major
Endo-1,4-Beta-Xylanases From Trichodrema Reesei 19
aa protein 1XYP_B GI:1127211

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 465
Xaa Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
1 5 10 15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
20 25 30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
35 40 45
Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
50 55 60
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65 70 75 80
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
85 90 95
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
100 105 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
115 120 125
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
130 135 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145 150 155 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
165 170 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
180 185 190

<210> 466
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Structural Comparison Of Two Major
Endo-1,4-Beta-Xylanases From Trichodrema Reesei 19
aa protein 1XYO_A GI:1127212

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 466
Xaa Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
 1               5                  10                  15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
            20                  25                  30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
        35                  40                  45
Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
    50                  55                  60
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65                  70                  75                  80
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
                85                  90                  95
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
            100                 105                 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
        115                 120                 125
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
    130                 135                 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145                 150                 155                 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
                165                 170                 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185                 190


<210> 467
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, Structural Comparison Of Two Major
      Endo-1,4-Beta-Xylanases From Trichodrema Reesei 19
      aa protein 1XYO_B GI:1127213

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 467
Xaa Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
 1               5                  10                  15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
            20                  25                  30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
        35                  40                  45

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Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
    50                  55                  60
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65                  70                  75                  80
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
                85                  90                  95
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
            100                 105                 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
        115                 120                 125
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
    130                 135                 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145                 150                 155                 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
                165                 170                 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185                 190


<210> 468
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Structural Comparison Of Two Major
      Endo-1,4-Beta-Xylanases From Trichodrema Reesei
      19 aa protein 1ENX_A GI:1127272

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 468
Xaa Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
 1               5                  10                  15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
            20                  25                  30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
        35                  40                  45
Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
    50                  55                  60
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65                  70                  75                  80
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
                85                  90                  95
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
            100                 105                 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
        115                 120                 125
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
    130                 135                 140
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Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145                 150                 155                 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
                165                 170                 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185                 190


<210> 469
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, Structural Comparison Of Two Major
      Endo-1,4-Beta-Xylanases From Trichodrema Reesei 19
      aa protein 1ENX_B GI:1127273

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 469
Xaa Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
 1               5                  10                  15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
            20                  25                  30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
        35                  40                  45
Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
    50                  55                  60
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65                  70                  75                  80
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
                85                  90                  95
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
            100                 105                 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
        115                 120                 125
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
    130                 135                 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145                 150                 155                 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
                165                 170                 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185                 190


<210> 470
<211> 190
<212> PRT
<213> Artificial Sequence
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<220>
<223> Chain A, Endo-1,4-beta-xylanase Ii Complex With
4,5-epoxypentyl-beta- D-xyloside 190 aa protein
1RED_A GI:1942592

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 470
Xaa Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
 1               5                  10                  15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
            20                  25                  30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
        35                  40                  45
Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
    50                  55                  60
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65                  70                  75                  80
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
                85                  90                  95
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
            100                 105                 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
        115                 120                 125
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
    130                 135                 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145                 150                 155                 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
                165                 170                 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185                 190


<210> 471
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> ChainB, Endo-1,4-beta-xylanase Ii Complex With
4,5-epoxypentyl-beta- D-xyloside 190 aa protein
1RED_B GI:1942593

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 471

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

<210> 472
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Endo-1,4-Beta-Xylanase Ii Complex With
3,4-Epoxybutyl-Beta- D-Xyloside 190 aa protein
1REE_A GI:1942594

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 472

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

```
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
            100                 105                 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
        115                 120                 125
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
    130                 135                 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145                 150                 155                 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
                165                 170                 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185                 190


<210> 473
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, Endo-1,4-Beta-Xylanase Ii Complex With
      3,4-Epoxybutyl-Beta- D-Xyloside190 aa protein
      1REE_B GI:1942595

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 473
Xaa Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
 1               5                  10                  15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
            20                  25                  30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
        35                  40                  45
Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
    50                  55                  60
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65                  70                  75                  80
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
                85                  90                  95
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
            100                 105                 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
        115                 120                 125
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
    130                 135                 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145                 150                 155                 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
                165                 170                 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185                 190
```

<210> 474
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Endo-1,4-Beta-Xylanase Ii Complex With
2,3-Epoxypropyl-Beta- D-Xyloside 190 aa protein
1REF_A GI:1942596

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 474
Xaa Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
1 5 10 15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
20 25 30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
35 40 45
Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
50 55 60
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65 70 75 80
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
85 90 95
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
100 105 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
115 120 125
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
130 135 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145 150 155 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
165 170 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
180 185 190

<210> 475
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, Endo-1,4-Beta-Xylanase Ii Complex With
2,3-Epoxypropyl-Beta-D-Xyloside 1REF_B GI:1942597
xylanase III [Trichoderma reesei] 347 aa protein
BAA89465.2 GI:7328936

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 475
Xaa Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
 1               5                  10                  15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
            20                  25                  30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
        35                  40                  45
Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
    50                  55                  60
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65                  70                  75                  80
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
                85                  90                  95
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
            100                 105                 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
        115                 120                 125
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
    130                 135                 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145                 150                 155                 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
                165                 170                 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185                 190


<210> 476
<211> 71
<212> PRT
<213> Artificial Sequence

<220>
<223> xylanase, partial [Trichoderma reesei] 71 aa
      protein AAG01167.1 GI:9858850

<220>
<221> VARIANT
<222> 9
<223> Xaa = Any Amino Acid

<400> 476
Ser Tyr Leu Ser Val Tyr Gly Trp Xaa Thr Asp Pro Leu Ile Glu Tyr
 1               5                  10                  15
Tyr Ile Val Glu Ser Tyr Gly Asp Tyr Asn Pro Gly Ser Gly Gly Thr
            20                  25                  30
Tyr Lys Gly Thr Val Thr Ser Asp Gly Ser Val Tyr Asp Ile Tyr Thr
        35                  40                  45

```
Ala Thr Arg Thr Asn Ala Ala Ser Ile Gln Gly Thr Ala Thr Phe Thr
    50                  55                  60
Gln Tyr Trp Ser Val Arg Arg
65                  70


<210> 477
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> transcription factor ACEII [Trichoderma reesei]
      341 aa protein AAK69383.1 GI:14581734

<400> 477
Met Asp Leu Arg Gln Ala Cys Asp Arg Cys His Asp Lys Lys Leu Arg
 1               5                  10                  15
Cys Pro Arg Ile Ser Gly Ser Pro Cys Cys Ser Arg Cys Ala Lys Ala
            20                  25                  30
Asn Val Ala Cys Val Phe Ser Pro Pro Ser Arg Pro Phe Arg Pro His
        35                  40                  45
Glu Pro Leu Asn His Ser His Glu His Ser His Ser His Ser His Asn
    50                  55                  60
His Asn Gly Val Gly Val Ser Phe Asp Trp Leu Asp Leu Met Ser Leu
65                  70                  75                  80
Glu Gln Gln Gln Glu Gln Gln Gln Gly Gln Pro Gln His Pro Pro Pro
                85                  90                  95
Pro Val Gln Thr Leu Ser Glu Arg Leu Ala Ala Leu Leu Cys Ala Leu
            100                 105                 110
Asp Arg Met Leu Gln Ala Val Pro Ser Ser Leu Asp Met His His Val
        115                 120                 125
Ser Arg Gln Gln Leu Arg Glu Tyr Ala Asp Thr Val Gly Thr Gly Phe
    130                 135                 140
Asp Leu Gln Ser Thr Leu Asp Ser Leu Leu His His Ala Gln Asp Leu
145                 150                 155                 160
Ala Ser Leu Tyr Ser Glu Ala Val Pro Ala Ser Phe Asn Lys Arg Thr
                165                 170                 175
Thr Ala Ala Glu Ala Asp Ala Leu Cys Ala Val Pro Asp Cys Val His
            180                 185                 190
Gln Asp Arg Thr Ser Leu His Thr Thr Pro Leu Pro Lys Leu Asp His
        195                 200                 205
Ala Leu Leu Asn Leu Val Met Ala Cys His Ile Arg Leu Leu Asp Val
    210                 215                 220
Met Asp Thr Leu Ala Glu His Gly Arg Met Cys Ala Phe Met Val Ala
225                 230                 235                 240
Thr Leu Pro Pro Asp Tyr Asp Pro Lys Phe Ala Val Pro Glu Ile Arg
                245                 250                 255
Val Gly Thr Phe Val Ala Pro Thr Asp Thr Ala Ala Ser Met Leu Leu
            260                 265                 270
Ser Val Val Val Glu Leu Gln Thr Val Leu Val Ala Arg Val Lys Asp
        275                 280                 285
Leu Val Ala Met Val Asp Gln Val Lys Asp Asp Ala Arg Ala Ala Arg
    290                 295                 300
```

```
Glu Ala Lys Val Val Arg Leu Gln Cys Gly Ile Leu Leu Glu Arg Ala
305                 310                 315                 320
Glu Ser Thr Leu Gly Glu Trp Ser Arg Phe Lys Asp Gly Leu Val Ser
                325                 330                 335
Ala Arg Leu Leu Lys
            340


<210> 478
<211> 934
<212> PRT
<213> Artificial Sequence

<220>
<223> xylanase regulator 1, partial [Trichoderma reesei]
      934 aa protein AAO33577.1 GI:28194501

<400> 478
Met Leu Ser Asn Pro Leu Arg Arg Tyr Ser Ala Tyr Pro Asp Ile Ser
 1               5                  10                  15
Ser Ala Ser Phe Asp Pro Asn Tyr His Gly Ser Gln Ser His Leu His
            20                  25                  30
Ser Ile Asn Val Asn Thr Phe Gly Asn Ser His Pro Tyr Pro Met Gln
        35                  40                  45
His Leu Ala Gln His Ala Glu Leu Ser Ser Ser Arg Met Ile Arg Ala
    50                  55                  60
Ser Pro Val Gln Pro Lys Gln Arg Gln Gly Ser Leu Ile Ala Ala Arg
65                  70                  75                  80
Lys Asn Ser Thr Gly Thr Ala Gly Pro Ile Arg Arg Arg Ile Ser Arg
                85                  90                  95
Ala Cys Asp Gln Cys Asn Gln Leu Arg Thr Lys Cys Asp Gly Leu His
            100                 105                 110
Pro Cys Ala His Cys Ile Glu Phe Gly Leu Gly Cys Glu Tyr Val Arg
        115                 120                 125
Glu Arg Lys Lys Arg Gly Lys Ala Ser Arg Lys Asp Ile Ala Ala Gln
    130                 135                 140
Gln Ala Ala Ala Ala Ala Ala Gln His Ser Gly Gln Val Gln Asp Gly
145                 150                 155                 160
Pro Glu Asp Gln His Arg Lys Leu Ser Arg Gln Gln Ser Glu Ser Ser
                165                 170                 175
Arg Gly Ser Ala Glu Leu Ala Gln Pro Ala His Asp Pro Pro His Gly
            180                 185                 190
His Ile Glu Gly Ser Val Ser Ser Phe Ser Asp Asn Gly Leu Ser Gln
        195                 200                 205
His Ala Ala Met Gly Gly Met Asp Gly Leu Glu Asp His His Gly His
    210                 215                 220
Val Gly Val Asp Pro Ala Leu Gly Arg Thr Gln Leu Glu Ala Ser Ser
225                 230                 235                 240
Ala Met Gly Leu Gly Ala Tyr Gly Glu Val His Pro Gly Tyr Glu Ser
                245                 250                 255
Pro Gly Met Asn Gly His Val Met Val Pro Pro Ser Tyr Gly Ala Gln
            260                 265                 270
Thr Thr Met Ala Gly Tyr Ser Gly Ile Ser Tyr Ala Ala Gln Ala Pro
        275                 280                 285
```

```
Ser Pro Ala Thr Tyr Ser Ser Asp Gly Asn Phe Arg Leu Thr Gly His
    290                 295                 300
Ile His Asp Tyr Pro Leu Ala Asn Gly Ser Ser Pro Ser Trp Gly Val
305                 310                 315                 320
Ser Leu Ala Ser Pro Ser Leu Arg Tyr His Val Leu Arg Pro Val Leu
                325                 330                 335
Leu Asp Val Arg Asn Ile Tyr Pro Val Ser Leu Ala Cys Asp Gln Met
            340                 345                 350
Asp Met Tyr Phe Ser Ser Ser Ser Ser Ala Gln Met Arg Pro Met Ser
        355                 360                 365
Pro Tyr Val Glu Gly Phe Val Phe Arg Lys Arg Ser Phe Leu His Pro
    370                 375                 380
Thr Asp Pro Arg Arg Cys Gln Pro Ala Leu Leu Ala Ser Met Leu Trp
385                 390                 395                 400
Val Ala Ala Gln Thr Ser Glu Ala Ser Phe Leu Thr Ser Leu Pro Ser
                405                 410                 415
Ala Arg Ser Lys Val Cys Gln Lys Leu Leu Glu Leu Thr Val Gly Leu
            420                 425                 430
Leu Gln Pro Leu Ile His Thr Gly Thr Asn Ser Pro Ser Pro Lys Thr
        435                 440                 445
Ser Pro Val Val Gly Ala Ala Ala Leu Gly Val Leu Gly Val Ala Met
    450                 455                 460
Pro Gly Ser Leu Asn Met Asp Ser Leu Ala Gly Glu Thr Gly Ala Phe
465                 470                 475                 480
Gly Ala Ile Gly Ser Leu Asp Asp Val Ile Ala Tyr Val Arg Leu Ala
                485                 490                 495
Thr Val Val Ser Ala Ser Glu Tyr Lys Gly Ala Ser Leu Arg Trp Trp
            500                 505                 510
Gly Ala Ala Trp Ser Leu Ala Arg Glu Leu Lys Leu Gly Arg Glu Leu
        515                 520                 525
Pro Pro Gly Asn Pro Pro Ala Asn Gln Glu Asp Gly Glu Gly Leu Ser
    530                 535                 540
Glu Asp Val Asp Glu His Asp Leu Asn Arg Asn Asn Thr Arg Leu Gly
545                 550                 555                 560
Arg Lys Arg Ser Ala Lys Ser Asp Ala Ile Thr Glu Glu Glu Arg Glu
                565                 570                 575
Glu Arg Arg Arg Ala Trp Trp Leu Val Tyr Ile Val Asp Arg His Leu
            580                 585                 590
Ala Leu Cys Tyr Asn Arg Pro Leu Phe Leu Leu Asp Ser Glu Cys Ser
        595                 600                 605
Asp Leu Tyr His Pro Met Asp Asp Ile Lys Trp Gln Ala Gly Lys Phe
    610                 615                 620
Arg Ser His Asp Ala Gly Asn Ser Ser Ile Asn Ile Asp Ser Ser Met
625                 630                 635                 640
Thr Asp Glu Phe Gly Asp Ser Pro Arg Ala Ala Arg Gly Ala His Tyr
                645                 650                 655
Glu Cys Arg Gly Arg Ser Ile Phe Gly Tyr Phe Leu Ser Leu Met Thr
            660                 665                 670
Ile Leu Gly Glu Ile Val Asp Val His His Ala Lys Ser His Pro Arg
        675                 680                 685
Phe Gly Val Gly Phe Arg Ser Ala Arg Asp Trp Asp Glu Gln Val Ala
    690                 695                 700
Glu Ile Thr Arg His Leu Asp Met Tyr Glu Glu Ser Leu Lys Arg Phe
705                 710                 715                 720
```

Val Ala Lys His Leu Pro Leu Ser Ser Lys Asp Lys Glu Gln His Glu
                725                 730                 735
Met His Asp Ser Gly Ala Val Thr Asp Met Gln Ser Pro Leu Ser Val
            740                 745                 750
Arg Thr Asn Ala Ser Ser Arg Met Thr Glu Ser Glu Ile Gln Ala Ser
        755                 760                 765
Ile Val Val Ala Tyr Ser Thr His Val Met His Val Leu His Ile Leu
    770                 775                 780
Leu Ala Asp Lys Trp Asp Pro Ile Asn Leu Leu Asp Asp Asp Asp Leu
785                 790                 795                 800
Trp Ile Ser Ser Glu Gly Phe Val Thr Ala Thr Ser His Ala Val Ser
                805                 810                 815
Ala Ala Glu Ala Ile Ser Gln Ile Leu Glu Phe Asp Pro Gly Leu Glu
            820                 825                 830
Phe Met Pro Phe Phe Phe Gly Ile Tyr Leu Leu Gln Gly Ser Phe Leu
        835                 840                 845
Leu Leu Leu Ile Ala Asp Lys Leu Gln Ala Glu Ala Ser Pro Ser Val
    850                 855                 860
Ile Lys Ala Cys Glu Thr Ile Val Arg Ala His Glu Ala Cys Val Val
865                 870                 875                 880
Thr Leu Ser Thr Glu Tyr Gln Arg Asn Phe Ser Lys Val Met Arg Ser
                885                 890                 895
Ala Leu Ala Leu Ile Arg Gly Arg Val Pro Glu Asp Leu Ala Glu Gln
            900                 905                 910
Gln Gln Arg Arg Arg Glu Leu Leu Ala Leu Tyr Arg Trp Thr Gly Asn
        915                 920                 925
Gly Thr Gly Leu Ala Leu
    930

<210> 479
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Transcription factor ACEII 341 aa
      protein Q96WN6.1 GI:50400614

<400> 479
Met Asp Leu Arg Gln Ala Cys Asp Arg Cys His Asp Lys Lys Leu Arg
 1               5                  10                  15
Cys Pro Arg Ile Ser Gly Ser Pro Cys Cys Ser Arg Cys Ala Lys Ala
            20                  25                  30
Asn Val Ala Cys Val Phe Ser Pro Pro Ser Arg Pro Phe Arg Pro His
        35                  40                  45
Glu Pro Leu Asn His Ser His Glu His Ser His Ser His Ser His Asn
    50                  55                  60
His Asn Gly Val Gly Val Ser Phe Asp Trp Leu Asp Leu Met Ser Leu
65                  70                  75                  80
Glu Gln Gln Gln Glu Gln Gln Gln Gly Gln Pro Gln His Pro Pro Pro
                85                  90                  95
Pro Val Gln Thr Leu Ser Glu Arg Leu Ala Ala Leu Leu Cys Ala Leu
            100                 105                 110

```
Asp Arg Met Leu Gln Ala Val Pro Ser Ser Leu Asp Met His His Val
        115                 120                 125
Ser Arg Gln Gln Leu Arg Glu Tyr Ala Asp Thr Val Gly Thr Gly Phe
    130                 135                 140
Asp Leu Gln Ser Thr Leu Asp Ser Leu Leu His His Ala Gln Asp Leu
145                 150                 155                 160
Ala Ser Leu Tyr Ser Glu Ala Val Pro Ala Ser Phe Asn Lys Arg Thr
                165                 170                 175
Thr Ala Ala Glu Ala Asp Ala Leu Cys Ala Val Pro Asp Cys Val His
            180                 185                 190
Gln Asp Arg Thr Ser Leu His Thr Thr Pro Leu Pro Lys Leu Asp His
        195                 200                 205
Ala Leu Leu Asn Leu Val Met Ala Cys His Ile Arg Leu Leu Asp Val
    210                 215                 220
Met Asp Thr Leu Ala Glu His Gly Arg Met Cys Ala Phe Met Val Ala
225                 230                 235                 240
Thr Leu Pro Pro Asp Tyr Asp Pro Lys Phe Ala Val Pro Glu Ile Arg
                245                 250                 255
Val Gly Thr Phe Val Ala Pro Thr Asp Thr Ala Ala Ser Met Leu Leu
            260                 265                 270
Ser Val Val Val Glu Leu Gln Thr Val Leu Val Ala Arg Val Lys Asp
        275                 280                 285
Leu Val Ala Met Val Asp Gln Val Lys Asp Asp Ala Arg Ala Ala Arg
    290                 295                 300
Glu Ala Lys Val Val Arg Leu Gln Cys Gly Ile Leu Leu Glu Arg Ala
305                 310                 315                 320
Glu Ser Thr Leu Gly Glu Trp Ser Arg Phe Lys Asp Gly Leu Val Ser
                325                 330                 335
Ala Arg Leu Leu Lys
            340
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<210> 480
<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Structure Of Vil-Xylanase 189 aa protein
2D97_A GI:112490431

<220>
<221> VARIANT
<222> 8, 72, 134, 178
<223> Xaa = Any Amino Acid

<400> 480

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Thr Ile Gln Pro Gly Thr Gly Xaa Asn Asn Gly Tyr Phe Tyr Ser Tyr
 1               5                  10                  15
Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly Gly
            20                  25                  30
Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly Lys
        35                  40                  45
Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly Ser
```

```
    50                  55                  60
Tyr Asn Pro Asn Gly Asn Ser Xaa Leu Ser Val Tyr Gly Trp Ser Arg
65                  70                  75                  80
Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr Asn
                85                  90                  95
Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly Ser
            100                 105                 110
Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile
        115                 120                 125
Gly Thr Ala Thr Phe Xaa Gln Tyr Trp Ser Val Arg Arg Asn His Arg
    130                 135                 140
Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala Gln
145                 150                 155                 160
Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val Glu
                165                 170                 175
Gly Xaa Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185


<210> 481
<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Structure Of Vil (Extra KiI2
      ADDED)-Xylanase
      189 aa protein 2D98_A GI:112490433

<220>
<221> VARIANT
<222> 8, 72, 95, 134, 170, 178
<223> Xaa = Any Amino Acid

<400> 481
Thr Ile Gln Pro Gly Thr Gly Xaa Asn Asn Gly Tyr Phe Tyr Ser Tyr
 1               5                  10                  15
Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly Gly
            20                  25                  30
Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly Lys
        35                  40                  45
Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly Ser
    50                  55                  60
Tyr Asn Pro Asn Gly Asn Ser Xaa Leu Ser Val Tyr Gly Trp Ser Arg
65                  70                  75                  80
Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Xaa Asn
                85                  90                  95
Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly Ser
            100                 105                 110
Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile
        115                 120                 125
Gly Thr Ala Thr Phe Xaa Gln Tyr Trp Ser Val Arg Arg Asn His Arg
    130                 135                 140
Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala Gln
```

145 150 155 160
Gln Gly Leu Thr Leu Gly Thr Met Asp Xaa Gln Ile Val Ala Val Glu
165 170 175
Gly Xaa Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
180 185

<210> 482
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Xylanase Ii From Tricoderma Reesei At
100k 190 aa protein 2DFB_A GI:112490475

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 482
Xaa Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
1 5 10 15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
20 25 30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
35 40 45
Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
50 55 60
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65 70 75 80
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
85 90 95
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
100 105 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
115 120 125
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
130 135 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145 150 155 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
165 170 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
180 185 190

<210> 483
<211> 190
<212> PRT
<213> Artificial Sequence

<220>

<223> Chain A, Xylanase Ii From Tricoderma Reesei At
293k 190 aa protein 2DFC_A GI:112490477

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 483
Xaa Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
 1               5                  10                  15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
            20                  25                  30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
        35                  40                  45
Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
    50                  55                  60
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65                  70                  75                  80
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
                85                  90                  95
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
            100                 105                 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
        115                 120                 125
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
    130                 135                 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145                 150                 155                 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
                165                 170                 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185                 190


<210> 484
<211> 324
<212> PRT
<213> Artificial Sequence

<220>
<223> TPA_inf: chitinase 18-12 [Trichoderma reesei] 324
aa protein DAA05860.1 GI:126032263

<400> 484
Met Pro Ser Leu Thr Ala Leu Ala Gly Leu Leu Ala Leu Val Pro Ser
 1               5                  10                  15
Ala Leu Ala Gly Trp Asn Pro Asp Ser Lys Gln Asn Ile Ala Val Tyr
            20                  25                  30
Trp Gly Gln Asn Ser Ala Asn Ser Gln Ser Thr Gln Gln Arg Leu Ser
        35                  40                  45
Phe Tyr Cys Asn Asp Asp Asn Ile Asn Val Ile Glu Ile Ala Phe Leu
    50                  55                  60
Asn Gly Ile Asn Pro Pro Met Thr Asn Phe Ala Asn Ala Gly Asp Arg

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

<210> 485
<211> 324
<212> PRT
<213> Artificial Sequence

<220>
<223> TPA_inf: chitinase 18-12 [Trichoderma reesei] 324
aa protein DAA05860.1 GI:126032263

<400> 485
Met Pro Ser Leu Thr Ala Leu Ala Gly Leu Leu Ala Leu Val Pro Ser
1 5 10 15
Ala Leu Ala Gly Trp Asn Pro Asp Ser Lys Gln Asn Ile Ala Val Tyr
20 25 30
Trp Gly Gln Asn Ser Ala Asn Ser Gln Ser Thr Gln Gln Arg Leu Ser
35 40 45
Phe Tyr Cys Asn Asp Asp Asn Ile Asn Val Ile Glu Ile Ala Phe Leu
50 55 60
Asn Gly Ile Asn Pro Pro Met Thr Asn Phe Ala Asn Ala Gly Asp Arg

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

<210> 486
<211> 401
<212> PRT
<213> Artificial Sequence

<220>
<223> TPA_inf: chitinase 18-13 [Trichoderma reesei] 401
aa protein DAA5861.1 GI:126032265

<400> 486
Met Phe Phe Ser Lys Ala Leu Ala Ala Ala Gly Leu Leu Ala Thr Ala
1 5 10 15
Ala Tyr Ala Ala Pro Thr Met Glu Lys Arg Ala Ala Gly Gly Lys Leu
20 25 30
Val Val Tyr Trp Gly Ala Glu Asp Asp Ser Thr Thr Leu Ala Asn Val
35 40 45
Cys Ala Asp Ser Ser Tyr Asp Ile Val Asn Leu Ala Phe Leu Ser Arg
50 55 60
Phe Phe Ala Gly Gly Gly Tyr Pro Glu Leu Ser Leu Ser Thr Leu Gly

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

<210> 487
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> TPA_inf: chitinase 18-14 [Trichoderma reesei] 411
aa protein DAA05862.1 GI:126032267

<400> 487
Met Phe Phe Thr Lys Ala Val Gly Gly Leu Gly Leu Leu Ala Ser Leu
 1               5                  10                  15
Ala Ser Ser Ala Pro Asn Pro Ile Ala Arg Arg Gln Ala Pro Gly Ala
            20                  25                  30
Gln Asn Val Val Tyr Trp Gly Gln Asn Gly Gly Gly Thr Val Glu Asn
        35                  40                  45
Asn Asp Leu Ser Ala Tyr Cys Thr Pro Thr Ser Gly Ile Asp Ile Ile
    50                  55                  60
Val Leu Ser Phe Leu Tyr Gln Trp Gly Gln Gly Ser Ser Ala Leu Gly
65                  70                  75                  80
Gly Thr Ile Gly Gln Ser Cys Gly Ile Thr Thr Ser Gly Glu Pro Gln
                85                  90                  95
Asn Cys Asp Ala Leu Thr Ala Ala Ile Thr Lys Cys Lys Thr Ala Gly
            100                 105                 110
Val Lys Ile Ile Leu Ser Leu Gly Gly Ala Ser Ala Phe Ser Ser Phe
        115                 120                 125
Gln Thr Ala Asp Gln Ala Ala Gln Ala Gly Gln Tyr Leu Trp Asn Ala
    130                 135                 140
Tyr Gly Gly Gly Ser Gly Val Thr Arg Pro Leu Gly Asn Asn Val Met
145                 150                 155                 160
Asp Gly Phe Asp Leu Asp Ile Glu Ser Asn Pro Gly Thr Asn Glu Asn
                165                 170                 175
Tyr Ala Ala Leu Val Ser Ala Leu Arg Ser Asn Phe Ala Ser Asp Pro
            180                 185                 190
Ser Arg Gln Tyr Val Ile Ser Gly Ala Pro Gln Cys Pro Leu Pro Glu
        195                 200                 205
Pro Asn Met Gly Val Ile Ile Gln Asn Ala Gln Phe Asp Tyr Leu Trp
    210                 215                 220
Val Gln Phe Tyr Asn Asn Asn Glu Tyr Pro Gly Asp Pro Cys Ser Leu
225                 230                 235                 240
Gly Leu Pro Gly Asp Ala Pro Phe Asn Phe Asn Asn Trp Thr Thr Phe
                245                 250                 255
Ile Gln Ser Thr Pro Ser Lys Asp Ala Lys Val Phe Val Gly Val Pro
            260                 265                 270
Ala Ala Pro Leu Ala Ala Asn Gly Ala Pro Ser Gly Glu Val Tyr Tyr
        275                 280                 285
Ala Thr Pro Ser Gln Leu Ala Asp Ile Val Asn Asp Val Lys Ser Asn
    290                 295                 300
Pro Ala Phe Gly Gly Ile Met Met Trp Ser Ala Gly Phe Ser Asp Thr
305                 310                 315                 320
Asn Val Asn Asp Gly Cys Asn Tyr Ala Gln Glu Ala Lys Asn Ile Leu
                325                 330                 335
Leu Thr Gly Ser Pro Cys Ser Ser Gly Pro Val Ser Val Ser Arg Pro
            340                 345                 350
Pro Val Ser Ser Pro Thr Ile Thr Ser Ser Pro Pro Gly Thr Ser Pro
        355                 360                 365
Ala Pro Pro Ser Gln Thr Gly Ser Val Pro Gln Trp Gly Gln Cys Gly
    370                 375                 380
Gly Asn Gly Tyr Thr Gly Pro Thr Gln Cys Val Ala Pro Phe Lys Cys
385                 390                 395                 400
Val Ala Thr Ser Glu Trp Trp Ser Gln Cys Glu
                405                 410

<210> 488
<211> 401
<212> PRT
<213> Artificial Sequence

<220>
<223> TPA_inf: chitinase 18-16 [Trichoderma reesei] 401
aa protein DAA05864.1 GI:126032269

<400> 488
Met Leu Ser Arg Thr Leu Leu Thr Ala Leu Gly Leu Thr Thr Ile Ala
 1               5                  10                  15
Ala Ala Ala Pro Ser Gln Thr Val Lys Thr Arg Gln Ala Pro Gly Gly
            20                  25                  30
Gln Asn Ala Val Tyr Trp Gly Ala Thr Asn Asn Glu Asn Asp Asn Leu
        35                  40                  45
Ser Thr Tyr Cys Thr Ala Ser Ser Gly Ile Asp Ile Val Ile Leu Ser
    50                  55                  60
Phe Leu Asp Ile Tyr Gly Ala Thr Gly Asn Phe Pro Ser Gly Asn Met
65                  70                  75                  80
Gly Asn Ser Cys Tyr Val Gly Thr Asn Gly Val Pro Gln Leu Cys Asp
                85                  90                  95
Asp Leu Ala Ser Ser Ile Ala Thr Cys Gln Ala Ala Gly Ile Lys Val
            100                 105                 110
Ile Ile Ser Leu Gly Gly Ala Ala Ser Ser Tyr Ser Leu Gln Ser Gln
        115                 120                 125
Ser Gln Ala Val Ala Ile Gly Gln Tyr Leu Trp Asn Ala Tyr Gly Asn
    130                 135                 140
Ser Gly Asn Thr Thr Val Gln Arg Pro Phe Gly Asn Val Phe Val Asn
145                 150                 155                 160
Gly Phe Asp Phe Asp Ile Glu Leu Asn Ala Gly Ser Gln Tyr Tyr Gln
                165                 170                 175
Tyr Leu Ile Ser Thr Leu Arg Ser Asn Phe Ala Asn Asp Pro Lys Asn
            180                 185                 190
Thr Tyr Tyr Ile Thr Gly Ala Pro Gln Cys Pro Ile Pro Glu Pro Asn
        195                 200                 205
Met Gly Glu Ile Ile Ser Thr Ser Gln Phe Asp Tyr Leu Trp Val Gln
    210                 215                 220
Phe Tyr Asn Asn Asn Pro Val Cys Ser Leu Gly Leu Pro Gly Asp Ala
225                 230                 235                 240
Pro Phe Asn Phe Asn Asp Trp Val Ser Phe Ile Ser Thr Thr Pro Ser
                245                 250                 255
Lys Asn Ala Lys Leu Phe Val Gly Ala Pro Ala Ser Thr Leu Gly Ala
            260                 265                 270
Asn Gly Asn Ala Gly Gly Ala Lys Tyr Tyr Ala Thr Pro Glu Gln Leu
        275                 280                 285
Ala Gly Ile Val Asn Ser Val Lys Ser Ser Pro Phe Phe Gly Gly Ile
    290                 295                 300
Met Leu Trp Asp Ala Gly Tyr Ser Asp Ser Asn Val Asn Asn Gly Cys
305                 310                 315                 320
Asn Tyr Ala Gln Glu Ala Lys Asn Ile Leu Leu Thr Gly Thr Ala Cys
                325                 330                 335
Gly Gly Glu Ser Ser Pro Pro Pro Ser Thr Thr Thr Thr Ala Val Pro

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            340                 345                 350
Pro Pro Ala Ser Ser Thr Pro Ser Asn Pro Ser Gly Gly Ser Val Pro
        355                 360                 365
Gln Trp Gly Gln Cys Gly Gly Asp Gly Tyr Thr Gly Pro Thr Gln Cys
    370                 375                 380
Val Ala Pro Tyr Lys Cys Val Ala Thr Ser Glu Trp Trp Ser Ser Cys
385                 390                 395                 400
Gln
```

<210> 489
<211> 1034
<212> PRT
<213> Artificial Sequence

<220>
<223> TPA_inf: chitinase 18-18 [Trichoderma reesei] 1034
aa protein DAA05866.1 GI:126032275

<400> 489

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Met Val Ser Ala Ser Ala Gly Leu Ala Ala Val Gly Leu Leu Asn Gly
 1               5                  10                  15
Tyr Trp Gly Gln Tyr Thr Thr Thr Glu Gly Leu Arg Pro His Cys Asp
            20                  25                  30
Ser Gly Val Asp Ser Ile Thr Leu Gly Phe Val Asn Gly Ala Pro Asp
        35                  40                  45
Ala Ser Gly Tyr Pro Ser Leu Asn Phe Gly Pro Asn Cys Trp Ala Glu
    50                  55                  60
Ser Tyr Pro Gly Asn Leu Gly Leu Pro Ser Lys Leu Leu Ser His Cys
65                  70                  75                  80
Met Ser Leu Gln Ser Asp Ile Pro Tyr Cys Arg Ser Lys Gly Val Lys
                85                  90                  95
Val Ile Leu Ser Ile Gly Gly Val Tyr Asn Ala Leu Thr Ser Asn Tyr
            100                 105                 110
Phe Val Gly Asp Asn Gly Thr Ala Thr Asp Phe Ala Thr Phe Leu Tyr
        115                 120                 125
Asn Ala Phe Gly Pro Tyr Asn Ala Ser Tyr Thr Gly Pro Arg Pro Phe
    130                 135                 140
Asp Asp Ile Thr Thr Gly Leu Pro Thr Ser Val Asp Gly Phe Asp Phe
145                 150                 155                 160
Asp Ile Glu Ala Asp Phe Pro Asn Gly Pro Tyr Ile Lys Met Ile Glu
                165                 170                 175
Thr Phe Arg Ser Leu Asp Ser Ser Met Leu Ile Thr Gly Ala Pro Gln
            180                 185                 190
Cys Pro Thr Asn Pro Gln Tyr Phe Val Met Lys Asp Met Ile Gln Gln
        195                 200                 205
Ala Ala Phe Asp Lys Leu Phe Ile Gln Phe Tyr Asn Asn Pro Val Cys
    210                 215                 220
Asp Ala Ile Pro Gly Asn Thr Ala Gly Asp Lys Phe Asn Tyr Asp Asp
225                 230                 235                 240
Trp Glu Ala Val Ile Ala Gly Ser Ala Lys Ser Lys Ser Ala Lys Leu
                245                 250                 255
Tyr Ile Gly Leu Pro Ala Ile Gln Glu Pro Asn Glu Ser Gly Tyr Ile
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            260                 265                 270
Asp Pro Ile Ala Met Lys Asn Leu Val Cys Gln Tyr Lys Asp Arg Pro
        275                 280                 285
His Phe Gly Gly Leu Ser Leu Trp Asp Leu Ser Arg Gly Leu Val Asn
    290                 295                 300
Asn Ile Asn Gly Thr Ser Phe Asn Gln Trp Ala Leu Asp Ala Leu Gln
305                 310                 315                 320
Tyr Gly Cys Asn Pro Ile Pro Thr Thr Thr Thr Thr Thr Ser Thr Val
                325                 330                 335
Ser Ser Thr Thr Ala Ala Ser Ser Thr Thr Ala Ser Ser Thr Thr Ala
            340                 345                 350
Ser Thr Thr Lys Ala Ser Ser Thr Ser Lys Ala Ser Ser Thr Ser Lys
        355                 360                 365
Ala Ser Ser Thr Ser Lys Ala Ser Ser Thr Ser Lys Ala Ser Ser Thr
    370                 375                 380
Ser Lys Ala Ser Ser Thr Ser Lys Ala Ser Ser Thr Ser Lys Ala Ser
385                 390                 395                 400
Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys Val Ser Thr Thr Ser Lys
                405                 410                 415
Ala Ser Ser Thr Ser Lys Ala Ser Ser Ser Thr Lys Ala Ser Thr Thr
            420                 425                 430
Ser Lys Ala Ser Ser Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser
        435                 440                 445
Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys
    450                 455                 460
Ala Ser Thr Thr Ser Lys Ala Ser Ser Thr Ser Lys Ala Ser Ser Ser
465                 470                 475                 480
Thr Lys Ala Ser Thr Thr Ser Lys Ala Ser Ser Thr Ser Lys Ala Ser
                485                 490                 495
Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys
            500                 505                 510
Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser Ser Thr
        515                 520                 525
Ser Lys Ala Ser Ser Ser Thr Lys Ala Ser Thr Thr Ser Lys Ala Ser
    530                 535                 540
Ser Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys
545                 550                 555                 560
Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr
                565                 570                 575
Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser
            580                 585                 590
Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys
        595                 600                 605
Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys Val Ser Thr Thr
    610                 615                 620
Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser
625                 630                 635                 640
Ser Thr Ser Lys Val Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys
                645                 650                 655
Val Ser Ala Lys Ala Thr Thr Ser Thr Lys Ala Ser Thr Thr Val Lys
            660                 665                 670
Pro Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr
        675                 680                 685
Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser
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    690                 695                 700
Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys
705                 710                 715                 720
Ala Ala Thr Thr Ser Val Lys Pro Thr Ser Lys Thr Ser Thr Ser Ser
                725                 730                 735
Lys Pro Asn Val Ser Ala Ser Ser Ser Asn Val Gly Arg Asp Ala Thr
            740                 745                 750
Ser Leu Val Glu Ala Ser Thr Ser Thr Ser Ala Ala Val Leu Tyr Pro
        755                 760                 765
Thr Thr Thr Ser Arg Trp Ser Asn Ser Thr Ile Thr Arg Ser Ser Ser
    770                 775                 780
Leu Thr Thr Pro Ile Val Ser Asp Pro Ala Ser Leu Thr Thr Ser Val
785                 790                 795                 800
Val Tyr Thr Thr Ser Val His Thr Val Thr Lys Cys Pro Ala Tyr Val
                805                 810                 815
Thr Asp Cys Pro Ala Gly Gly Tyr Val Thr Thr Glu Thr Ile Pro Leu
            820                 825                 830
Tyr Thr Thr Val Cys Pro Ile Ser Glu Ala Thr Gln Thr Ala Ala Pro
        835                 840                 845
Thr Val Thr Thr Glu Ala Pro Gln Pro Trp Thr Thr Ser Thr Val Tyr
    850                 855                 860
Thr Thr Arg Val Tyr Thr Ile Thr Ser Cys Ala Pro Gly Val Val Asp
865                 870                 875                 880
Cys Pro Ala Asn Gln Val Thr Thr Glu Thr Ile Pro Trp Tyr Thr Thr
                885                 890                 895
Val Cys Pro Val Thr Ala Thr Ala Thr Pro Val Gly Pro Gly Ser Val
            900                 905                 910
Val Phe Pro Gln Asn Thr Glu Val Gly Gln Pro Ser Leu Val Gly Pro
        915                 920                 925
Val Val Glu Ala Ala Tyr Pro Thr Ala Ser Ser Ser Leu Gln Thr Leu
    930                 935                 940
Val Lys Pro Ala Thr Ser Val Gly Val Pro Gln Gly Ser Pro Ala Gly
945                 950                 955                 960
Ser Ser Val Ala Pro Gly Ser Ser Ser Lys Pro Thr Ala Pro Ala Gly
                965                 970                 975
Pro Pro Ser Tyr Pro Thr Gly Gly Ser Gly Asn Ala Ser Pro Ser Gly
            980                 985                 990
Ser Trp Ser Gly Val Pro Val Gly Pro Ser Ser Val Pro Gly Ile Pro
        995                 1000                1005
Glu Ala Asn Ala Ala Ser Val Met Ser Ala Ser Leu Phe Gly Leu Val
    1010                1015                1020
Ile Val Met Ala Ala Gln Val Phe Val Leu
1025                1030


<210> 490
<211> 178
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Structural Comparison Of Two Major
      Endo-1,4-Beta-Xylanases From Trichodrema Reesei
      178 aa protein 1XYN_A GI:157834272
```

<400> 490
Ala Ser Ile Asn Tyr Asp Gln Asn Tyr Gln Thr Gly Gly Gln Val Ser
 1               5                  10                  15
Tyr Ser Pro Ser Asn Thr Gly Phe Ser Val Asn Trp Asn Thr Gln Asp
            20                  25                  30
Asp Phe Val Val Gly Val Gly Trp Thr Thr Gly Ser Ser Ala Pro Ile
        35                  40                  45
Asn Phe Gly Gly Ser Phe Ser Val Asn Ser Gly Thr Gly Leu Leu Ser
    50                  55                  60
Val Tyr Gly Trp Ser Thr Asn Pro Leu Val Glu Tyr Tyr Ile Met Glu
65                  70                  75                  80
Asp Asn His Asn Tyr Pro Ala Gln Gly Thr Val Lys Gly Thr Val Thr
                85                  90                  95
Ser Asp Gly Ala Thr Tyr Thr Ile Trp Glu Asn Thr Arg Val Asn Glu
            100                 105                 110
Pro Ser Ile Gln Gly Thr Ala Thr Phe Asn Gln Tyr Ile Ser Val Arg
        115                 120                 125
Asn Ser Pro Arg Thr Ser Gly Thr Val Thr Val Gln Asn His Phe Asn
    130                 135                 140
Ala Trp Ala Ser Leu Gly Leu His Leu Gly Gln Met Asn Tyr Gln Val
145                 150                 155                 160
Val Ala Val Glu Gly Trp Gly Gly Ser Gly Ser Ala Ser Gln Ser Val
                165                 170                 175
Ser Asn



<210> 491
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> xylanase, partial [Trichoderma reesei]
      ACB38137.1 GI:170786291

<400> 491
Gln Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
 1               5                  10                  15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
            20                  25                  30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
        35                  40                  45
Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
    50                  55                  60
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65                  70                  75                  80
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
                85                  90                  95
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
            100                 105                 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
        115                 120                 125

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Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
    130                 135                 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145                 150                 155                 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
                165                 170                 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185                 190


<210> 492
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Xylanase Ii From Trichoderma Reesei
      Cocrystallized With Tris- Dipicolinate Europium
      190 aa protein 3LGR_A GI:319443539

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 492
Xaa Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
 1               5                  10                  15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
            20                  25                  30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
        35                  40                  45
Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
    50                  55                  60
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65                  70                  75                  80
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
                85                  90                  95
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
            100                 105                 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
        115                 120                 125
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
    130                 135                 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145                 150                 155                 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
                165                 170                 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185                 190


<210> 493
<211> 189
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<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Crystal Structures Of Mutant Endo-
-1,4-xylanase Ii Complexed With Substrate (1.15 A)
And Products (1.6 A) 189 aa protein 4HK8_A
GI:572153255

<400> 493
Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser Tyr
 1               5                  10                  15
Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly Gly
            20                  25                  30
Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly Lys
        35                  40                  45
Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly Ser
    50                  55                  60
Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser Arg
65                  70                  75                  80
Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr Asn
                85                  90                  95
Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly Ser
            100                 105                 110
Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile
        115                 120                 125
Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His Arg
    130                 135                 140
Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala Gln
145                 150                 155                 160
Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val Gln
                165                 170                 175
Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185


<210> 494
<211> 188
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Crystal Structures Of Mutant
Endo-beta-1,4-xylanase Ii Complexed With Substrate
(1.15 A) And Products (1.6 A) 188 aa protein
4HK9_A GI:572153256

<400> 494
Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser Tyr Trp
 1               5                  10                  15
Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly Gly Gln
            20                  25                  30
Phe Ser Val Asn Trp Ser Asn Ser Gly His Phe Val Gly Gly Lys Gly
        35                  40                  45

```
Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly Ser Tyr
    50                  55                  60
Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser Arg Asn
65                  70                  75                  80
Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr Asn Pro
                85                  90                  95
Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly Ser Val
            100                 105                 110
Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile Gly
        115                 120                 125
Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His Arg Ser
    130                 135                 140
Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala Gln Gln
145                 150                 155                 160
Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val Glu Gly
                165                 170                 175
Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185


<210> 495
<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Crystal Structures Of Mutant
      Endo-beta-1,4-xylanase Ii Complexed With Substrate
      (1.15 A) And Products (1.6 A) 189 aa protein
      4HKL_A GI:572153257

<400> 495
Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser Tyr
 1               5                  10                  15
Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly Gly
            20                  25                  30
Gln Phe Ser Val Asn Trp Ser Asn Ser Gly His Phe Val Gly Gly Lys
        35                  40                  45
Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly Ser
    50                  55                  60
Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser Arg
65                  70                  75                  80
Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr Asn
                85                  90                  95
Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly Ser
            100                 105                 110
Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile
        115                 120                 125
Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His Arg
    130                 135                 140
Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala Gln
145                 150                 155                 160
Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val Glu
                165                 170                 175
```

Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185


<210> 496
<211> 169
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Crystal Structures Of Mutant
      Endo-beta-1,4-xylanase Ii (e177q) In The Apo Form
      189 aa protein 4HKO_A GI:572153258

<400> 496
Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser Tyr
 1               5                  10                  15
Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly Gly
            20                  25                  30
Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly Lys
        35                  40                  45
Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Asn Pro Leu Ile
    50                  55                  60
Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr Asn Pro Ser Thr Gly
65                  70                  75                  80
Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly Ser Val Tyr Asp Ile
                85                  90                  95
Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile Gly Thr Ala Thr
            100                 105                 110
Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His Arg Ser Ser Gly Ser
        115                 120                 125
Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala Gln Gln Gly Leu Thr
    130                 135                 140
Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val Gln Gly Tyr Phe Ser
145                 150                 155                 160
Ser Gly Ser Ala Ser Ile Thr Val Ser
                165


<210> 497
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Crystal Structures Of Mutant
      Endo-beta-1,4-xylanase Ii Complexed With Substrate
      And Products 190 aa protein 4HKW_A GI:572153259

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 497
Xaa Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
 1               5                  10                  15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
            20                  25                  30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
        35                  40                  45
Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
    50                  55                  60
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65                  70                  75                  80
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
                85                  90                  95
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
            100                 105                 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
        115                 120                 125
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
    130                 135                 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145                 150                 155                 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
                165                 170                 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185                 190


<210> 498
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Joint X-ray/neutron Structure Of
      Trichoderma Reesei Xylanase Ii In Complex With Mes
      At Ph 5.7 190 aa protein 4S2D_A GI:929984639

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 498
Xaa Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
 1               5                  10                  15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
            20                  25                  30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
        35                  40                  45
Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
    50                  55                  60
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65                  70                  75                  80
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr

```
                85                  90                  95
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
            100                 105                 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
        115                 120                 125
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
    130                 135                 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145                 150                 155                 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
                165                 170                 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185                 190


<210> 499
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Joint X-ray/neutron Structure Of
      Trichoderma Reesei Xylanase Ii At Ph 4.4 190 aa
      protein 4S2F_A GI:929984640

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 499
Xaa Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
 1               5                  10                  15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
            20                  25                  30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
        35                  40                  45
Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
    50                  55                  60
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65                  70                  75                  80
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
                85                  90                  95
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
            100                 105                 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
        115                 120                 125
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
    130                 135                 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145                 150                 155                 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
                165                 170                 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
```

180 185 190

<210> 500
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Joint X-ray/neutron Structure Of
Trichoderma Reesei Xylanase Ii At Ph 5.8 190 aa
protein 4S2G_A GI:929984641

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 500
Xaa Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
1 5 10 15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
20 25 30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
35 40 45
Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
50 55 60
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65 70 75 80
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
85 90 95
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
100 105 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
115 120 125
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
130 135 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145 150 155 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
165 170 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
180 185 190

<210> 501
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Joint X-ray/neutron Structure Of
Trichoderma Reesei Xylanase Ii At Ph 8.5 190 aa
protein 4S2H_A GI:929984642

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 501
Xaa Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
 1               5                  10                  15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
            20                  25                  30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
        35                  40                  45
Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
    50                  55                  60
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65                  70                  75                  80
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
                85                  90                  95
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
            100                 105                 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
        115                 120                 125
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
    130                 135                 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145                 150                 155                 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
                165                 170                 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185                 190


<210> 502
<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, X-ray Structure Analysis Of Xylanase -
      N44d
      189 aa protein 4XQ4_A GI:929984784

<400> 502
Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser Tyr
 1               5                  10                  15
Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly Gly
            20                  25                  30
Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asp Phe Val Gly Gly Lys
        35                  40                  45
Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly Ser
    50                  55                  60
Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser Arg
65                  70                  75                  80

Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr Asn
85 90 95
Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly Ser
100 105 110
Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile
115 120 125
Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His Arg
130 135 140
Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala Gln
145 150 155 160
Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val Glu
165 170 175
Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
180 185

<210> 503
<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, X-ray Structure Analysis Of Xylanase -
N44d 189 aa protein 4XQ4_B GI:929984785

<400> 503
Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser Tyr
1 5 10 15
Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly Gly
20 25 30
Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asp Phe Val Gly Gly Lys
35 40 45
Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly Ser
50 55 60
Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser Arg
65 70 75 80
Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr Asn
85 90 95
Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly Ser
100 105 110
Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile
115 120 125
Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His Arg
130 135 140
Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala Gln
145 150 155 160
Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val Glu
165 170 175
Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
180 185

<210> 504
<211> 189

<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, X-ray Structure Analysis Of Xylanase-wt
At Ph4.0 189 aa protein 4XQD_A GI:929984786

<400> 504
Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser Tyr
 1               5                  10                  15
Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly Gly
            20                  25                  30
Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly Lys
        35                  40                  45
Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly Ser
    50                  55                  60
Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser Arg
65                  70                  75                  80
Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr Asn
                85                  90                  95
Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly Ser
            100                 105                 110
Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile
        115                 120                 125
Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His Arg
    130                 135                 140
Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala Gln
145                 150                 155                 160
Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val Glu
                165                 170                 175
Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185


<210> 505
<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, X-ray Structure Analysis Of Xylanase-wt
At Ph4.0 189 aa protein 4XQD_B GI:929984787

<400> 505
Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser Tyr
 1               5                  10                  15
Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly Gly
            20                  25                  30
Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly Lys
        35                  40                  45
Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly Ser
    50                  55                  60
Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser Arg
65                  70                  75                  80

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Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr Asn
                85                  90                  95
Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly Ser
            100                 105                 110
Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile
        115                 120                 125
Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His Arg
    130                 135                 140
Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala Gln
145                 150                 155                 160
Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val Glu
                165                 170                 175
Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185


<210> 506
<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, X-ray Structure Analysis Of Xylanase-n44e
      With Mes At Ph6.0 189 aa protein 4XQW_A
      GI:929984788

<400> 506
Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser Tyr
 1               5                  10                  15
Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly Gly
            20                  25                  30
Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Glu Phe Val Gly Gly Lys
        35                  40                  45
Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly Ser
    50                  55                  60
Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser Arg
65                  70                  75                  80
Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr Asn
                85                  90                  95
Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly Ser
            100                 105                 110
Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile
        115                 120                 125
Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His Arg
    130                 135                 140
Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala Gln
145                 150                 155                 160
Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val Glu
                165                 170                 175
Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185


<210> 507
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<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Neutron And X-ray Structure Analysis Of
Xylanase: N44d At Ph6 189 aa protein 4XPV_A
GI:931139811

<400> 507
Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser Tyr
1 5 10 15
Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly Gly
20 25 30
Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asp Phe Val Gly Gly Lys
35 40 45
Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly Ser
50 55 60
Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser Arg
65 70 75 80
Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr Asn
85 90 95
Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly Ser
100 105 110
Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile
115 120 125
Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His Arg
130 135 140
Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala Gln
145 150 155 160
Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val Glu
165 170 175
Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
180 185

<210> 508
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> truncated xylanase 5 [Trichoderma reesei] 28 aa
protein ANW82584.1 GI:1048222282

<400> 508
Met Val Ser Phe Ser Ser Leu Val Val Ala Leu Val Gly Ile Ala Ser
1 5 10 15
Ser Trp Ala Leu Trp Arg Asn Pro Ser Thr Gln Thr
20 25

<210> 509
<211> 28

<212> PRT
<213> Artificial Sequence

<220>
<223> truncated xylanase 5 [Trichoderma reesei] 28 aa
protein ANW82585.1 GI:1048222284

<400> 509
Met Val Ser Phe Ser Ser Leu Val Val Ala Leu Val Gly Ile Ala Ser
1 5 10 15
Ser Trp Ala Leu Trp Arg Asn Pro Ser Thr Gln Thr
20 25

<210> 510
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> xylanase [Trichoderma reesei] 226 aa protein
ANX99792.1 GI:1049178838

<400> 510
Met Val Ser Phe Ser Ser Leu Val Val Ala Leu Val Gly Ile Ala Ser
1 5 10 15
Ser Trp Ala Ala Pro Leu Glu Glu Ser Pro Asn Ala Asn Ile Thr Glu
20 25 30
Arg Gly Pro Ser Asn Phe Val Leu Gly Gly His Asn Ala Val Arg Arg
35 40 45
Ala Ala Ile Asn Tyr Asn Gln Asp Tyr Thr Thr Gly Gly Asp Val Val
50 55 60
Tyr Thr His Ser Asn Thr Gly Phe Ala Val Asn Trp Ser Tyr Pro Asn
65 70 75 80
Asp Phe Val Val Gly Val Gly Trp Asn Pro Gly Gly Ser Ala Pro Ile
85 90 95
Asn Phe Ser Gly Asn Phe Gly Val Gly Ser Gly Val Gly Leu Leu Ser
100 105 110
Val Tyr Gly Trp Ser Thr Asn Pro Leu Val Glu Tyr Tyr Val Val Glu
115 120 125
Asp Asn Phe Gly Phe Ser Ser Gly Gly Thr Val Lys Gly Ser Val Thr
130 135 140
Ser Asp Gly Ser Ser Tyr Thr Ile Trp Glu Asn Thr Arg Val Asn Glu
145 150 155 160
Pro Ser Ile Val Gly Thr Ala Thr Phe Asn Gln Tyr Ile Ser Ile Arg
165 170 175
Asn Ser Lys Arg Ser Ser Gly Thr Val Thr Val Ala Asn His Phe Asn
180 185 190
Ala Trp Lys Ser Leu Gly Met Asn Leu Gly Thr Met Asn Tyr Gln Val
195 200 205
Ile Ala Val Glu Gly Trp Gly Gly Gln Gly Gly Val Gln Gln Thr Val
210 215 220
Ser Asn
225

<210> 511
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> xylanase [Trichoderma reesei] 226 aa protein
ANX99793.1 GI:1049178840

<400> 511
Met Val Ser Phe Ser Ser Leu Val Val Ala Leu Val Gly Ile Ala Ser
1 5 10 15
Ser Leu Ala Ala Pro Leu Glu Glu Ser Leu Asn Ala Asn Ile Thr Glu
20 25 30
Arg Gly Pro Asn Asn Phe Val Leu Gly Gly His Asn Ala Val Arg Arg
35 40 45
Ala Ala Ile Asn Tyr Asn Gln Asp Tyr Thr Thr Gly Gly Asp Val Val
50 55 60
Tyr Thr His Ser Asn Thr Gly Phe Ala Val Asn Trp Ser Tyr Pro Asn
65 70 75 80
Asp Phe Val Val Gly Val Gly Trp Asn Pro Gly Gly Ser Ala Pro Ile
85 90 95
Asn Phe Ser Gly Asn Phe Gly Val Gly Ser Gly Val Gly Leu Leu Ser
100 105 110
Val Tyr Gly Trp Ser Thr Asn Pro Leu Val Glu Tyr Tyr Val Val Glu
115 120 125
Asp Asn Phe Gly Phe Ser Ser Gly Gly Thr Val Lys Gly Ser Val Thr
130 135 140
Ser Asp Gly Ser Ser Tyr Thr Ile Trp Glu Asn Thr Arg Val Asn Glu
145 150 155 160
Pro Ser Ile Val Gly Thr Ala Thr Phe Asn Gln Tyr Ile Ser Ile Arg
165 170 175
Asn Ser Lys Arg Ser Ser Gly Thr Val Thr Ile Ala Asn His Phe Asn
180 185 190
Ala Trp Lys Ser Leu Gly Met Asn Leu Gly Thr Leu Asn Tyr Gln Val
195 200 205
Ile Ala Val Glu Gly Trp Gly Gly Gln Gly Gly Val Gln Gln Thr Val
210 215 220
Ser Asn
225


<210> 512
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> xylanase [Trichoderma reesei] 226 aa protein
ANX99794.1 GI:1049178842

<400> 512

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Met Val Ser Phe Ser Ser Leu Val Val Ala Leu Val Gly Ile Ala Ser
 1               5                  10                  15
Ser Leu Ala Ala Pro Leu Glu Glu Ser Leu Asn Ala Asn Ile Thr Glu
            20                  25                  30
Arg Gly Pro Asn Asn Phe Val Leu Gly Gly His Asn Ala Val Arg Arg
        35                  40                  45
Ala Ala Ile Asn Tyr Asn Gln Asp Tyr Thr Thr Gly Gly Asp Val Val
    50                  55                  60
Tyr Thr His Ser Asn Thr Gly Phe Ala Val Asn Trp Ser Tyr Pro Asn
65                  70                  75                  80
Asp Phe Val Val Gly Val Gly Trp Asn Pro Gly Gly Ser Ala Pro Ile
                85                  90                  95
Asn Phe Ser Gly Asn Phe Gly Val Gly Ser Gly Val Gly Leu Leu Ser
            100                 105                 110
Val Tyr Gly Trp Ser Thr Asn Pro Leu Val Glu Tyr Tyr Val Val Glu
        115                 120                 125
Asp Asn Phe Gly Phe Ser Ser Gly Gly Thr Val Lys Gly Ser Val Thr
    130                 135                 140
Ser Asp Gly Ser Ser Tyr Thr Ile Trp Glu Asn Thr Arg Val Asn Glu
145                 150                 155                 160
Pro Ser Ile Val Gly Thr Ala Thr Phe Asn Gln Tyr Ile Ser Ile Arg
                165                 170                 175
Asn Ser Lys Arg Ser Ser Gly Thr Val Thr Ile Ala Asn His Phe Asn
            180                 185                 190
Ala Trp Lys Ser Leu Gly Met Asn Leu Gly Thr Leu Asn Tyr Gln Val
        195                 200                 205
Ile Ala Val Glu Gly Trp Gly Gly Gln Gly Gly Val Gln Gln Thr Val
    210                 215                 220
Ser Asn
225
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<210> 513
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> xylanase [Trichoderma reesei] 226 aa protein
ANX99795.1 GI:1049178844

<400> 513

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

```
Asn Phe Ser Gly Asn Phe Gly Val Gly Ser Gly Val Gly Leu Leu Ser
            100                 105                 110
Val Tyr Gly Trp Ser Thr Asn Pro Leu Val Glu Tyr Tyr Val Val Glu
        115                 120                 125
Asp Asn Phe Gly Phe Ser Ser Gly Gly Thr Val Lys Gly Ser Val Thr
    130                 135                 140
Ser Asp Gly Ser Ser Tyr Thr Ile Trp Glu Asn Thr Arg Val Asn Glu
145                 150                 155                 160
Pro Ser Ile Val Gly Thr Ala Thr Phe Asn Gln Tyr Ile Ser Ile Arg
                165                 170                 175
Asn Ser Lys Arg Ser Ser Gly Thr Val Thr Ile Ala Asn His Phe Asn
            180                 185                 190
Ala Trp Lys Ser Leu Gly Met Asn Leu Gly Thr Leu Asn Tyr Gln Val
        195                 200                 205
Ile Ala Val Glu Gly Trp Gly Gly Gln Gly Gly Val Gln Gln Thr Val
    210                 215                 220
Ser Asn
225
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<210> 514
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> xylanase 2, partial [Trichoderma reesei] 190 aa
protein APU51339.1 GI:1130479396

<400> 514

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

<210> 515
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> xylanase 2, partial [Trichoderma reesei] 190 aa
protein APU51340.1 GI:1130479398

<400> 515
Gln Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
 1               5                  10                  15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
            20                  25                  30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
        35                  40                  45
Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
    50                  55                  60
Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65                  70                  75                  80
Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
                85                  90                  95
Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
            100                 105                 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
        115                 120                 125
Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
    130                 135                 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145                 150                 155                 160
Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
                165                 170                 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
            180                 185                 190


<210> 516
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Microed Structure Of Xylanase At 2.3 A
Resolution
190 aa protein 5K7P_A GI:1175128641

<400> 516
Gln Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
 1               5                  10                  15
Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
            20                  25                  30
Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly

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


<210> 517
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 18, chitinase
      [Trichoderma reesei QM6a] 411 aa protein
      EGR44650.1 GI:340514387

<400> 517
Met Phe Phe Thr Lys Ala Val Gly Gly Leu Gly Leu Leu Ala Ser Leu
 1               5                  10                  15
Ala Ser Ser Ala Pro Asn Pro Ile Ala Arg Arg Gln Ala Pro Gly Ala
            20                  25                  30
Gln Asn Val Val Tyr Trp Gly Gln Asn Gly Gly Gly Thr Val Glu Asn
        35                  40                  45
Asn Asp Leu Ser Ala Tyr Cys Thr Pro Thr Ser Gly Ile Asp Ile Ile
    50                  55                  60
Val Leu Ser Phe Leu Tyr Gln Trp Gly Gln Gly Ser Ser Ala Leu Gly
65                  70                  75                  80
Gly Thr Ile Gly Gln Ser Cys Gly Ile Thr Thr Ser Gly Glu Pro Gln
                85                  90                  95
Asn Cys Asp Ala Leu Thr Ala Ala Ile Thr Lys Cys Lys Thr Ala Gly
            100                 105                 110
Val Lys Ile Ile Leu Ser Leu Gly Gly Ala Ser Ala Phe Ser Ser Phe
        115                 120                 125
Gln Thr Ala Asp Gln Ala Ala Gln Ala Gly Gln Tyr Leu Trp Asn Ala
    130                 135                 140
Tyr Gly Gly Gly Ser Gly Val Thr Arg Pro Leu Gly Asn Asn Val Met
145                 150                 155                 160
Asp Gly Phe Asp Leu Asp Ile Glu Ser Asn Pro Gly Thr Asn Glu Asn
                165                 170                 175
```

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

<210> 518
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 5 [Trichoderma reesei QM6a] 473 aa protein EGR44819.1 GI:340514558

<400> 518

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

```
Ile Leu Pro Thr Cys Pro Ala Thr Pro Gln Asp Lys Phe Asp Tyr Val
            100                 105                 110
Trp Asp Gly Ser Asp Asn Cys Gln Phe Asn Leu Thr Lys Thr Ala Leu
        115                 120                 125
Lys Tyr Asn Pro Asn Leu Tyr Val Tyr Ala Asp Ala Trp Ser Ala Pro
    130                 135                 140
Gly Cys Met Lys Thr Val Gly Thr Glu Asn Leu Gly Gly Gln Ile Cys
145                 150                 155                 160
Gly Val Arg Gly Thr Asp Cys Lys His Asp Trp Arg Gln Ala Tyr Ala
                165                 170                 175
Asp Tyr Leu Val Gln Tyr Val Arg Phe Tyr Lys Glu Glu Gly Ile Asp
            180                 185                 190
Ile Ser Leu Leu Gly Ala Trp Asn Glu Pro Asp Phe Asn Pro Phe Thr
        195                 200                 205
Tyr Glu Ser Met Leu Ser Asp Gly Tyr Gln Ala Lys Asp Phe Leu Glu
    210                 215                 220
Val Leu Tyr Pro Thr Leu Lys Lys Ala Phe Pro Lys Val Asp Val Ser
225                 230                 235                 240
Cys Cys Asp Ala Thr Gly Ala Arg Gln Glu Arg Asn Ile Leu Tyr Glu
                245                 250                 255
Leu Gln Gln Ala Gly Gly Glu Arg Tyr Phe Asp Ile Ala Thr Trp His
            260                 265                 270
Asn Tyr Gln Ser Asn Pro Glu Arg Pro Phe Asn Ala Gly Gly Lys Pro
        275                 280                 285
Asn Ile Gln Thr Glu Trp Ala Asp Gly Thr Gly Pro Trp Asn Ser Thr
    290                 295                 300
Trp Asp Tyr Ser Gly Gln Leu Ala Glu Gly Leu Gln Trp Ala Leu Tyr
305                 310                 315                 320
Met His Asn Ala Phe Val Asn Ser Asp Thr Ser Gly Tyr Thr His Trp
                325                 330                 335
Trp Cys Ala Gln Asn Thr Asn Gly Asp Asn Ala Leu Ile Arg Leu Asp
            340                 345                 350
Arg Asp Ser Tyr Glu Val Ser Ala Arg Leu Trp Ala Phe Ala Gln Tyr
        355                 360                 365
Phe Arg Phe Ala Arg Pro Gly Ser Val Arg Ile Gly Ala Thr Ser Asp
    370                 375                 380
Val Glu Asn Val Tyr Val Thr Ala Tyr Val Asn Lys Asn Gly Thr Val
385                 390                 395                 400
Ala Ile Pro Val Ile Asn Ala Ala His Phe Pro Tyr Asp Leu Thr Ile
                405                 410                 415
Asp Leu Glu Gly Ile Lys Lys Arg Lys Leu Ser Glu Tyr Leu Thr Asp
            420                 425                 430
Asn Ser His Asn Val Thr Leu Gln Ser Arg Tyr Lys Val Ser Gly Ser
        435                 440                 445
Ser Leu Lys Val Thr Val Glu Pro Arg Ala Met Lys Thr Phe Trp Leu
    450                 455                 460
Glu Pro Gln Ser Thr Phe Ala Val Ile
465                 470
```

<210> 519
<211> 223
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 11 [Trichoderma reesei QM6a]
223 aa protein EGR45030.1 GI:340514771

<400> 519
Met Val Ser Phe Thr Ser Leu Leu Ala Gly Val Ala Ala Ile Ser Gly
 1               5                  10                  15
Val Leu Ala Ala Pro Ala Ala Glu Val Glu Ser Val Ala Val Glu Lys
            20                  25                  30
Arg Gln Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr
        35                  40                  45
Ser Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro
    50                  55                  60
Gly Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly
65                  70                  75                  80
Gly Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser
                85                  90                  95
Gly Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp
            100                 105                 110
Ser Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr
        115                 120                 125
Tyr Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp
    130                 135                 140
Gly Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser
145                 150                 155                 160
Ile Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn
                165                 170                 175
His Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp
            180                 185                 190
Ala Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala
        195                 200                 205
Val Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
    210                 215                 220


<210> 520
<211> 401
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 18, chitinase [Trichoderma reesei QM6a] 401 aa protein EGR45486.1 GI:340515230

<400> 520
Met Leu Ser Arg Thr Leu Leu Thr Ala Leu Gly Leu Thr Thr Ile Ala
 1               5                  10                  15
Ala Ala Ala Pro Ser Gln Thr Val Lys Thr Arg Gln Ala Pro Gly Gly
            20                  25                  30
Gln Asn Ala Val Tyr Trp Gly Ala Thr Asn Asn Glu Asn Asp Asn Leu
        35                  40                  45

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

<210> 521
<211> 919
<212> PRT
<213> Artificial Sequence

<220>

<223> xylanase regulator 1 [Trichoderma reesei QM6a] 920
aa protein EGR48040.1 GI:340517797

<400> 521
Met Leu Ser Asn Pro Leu Arg Arg Tyr Ser Ala Tyr Pro Asp Ile Ser
 1               5                  10                  15
Ser Ala Ser Phe Asp Pro Asn Tyr His Gly Ser Gln Ser His Leu His
            20                  25                  30
Ser Ile Asn Val Asn Thr Phe Gly Asn Ser His Pro Tyr Pro Met Gln
        35                  40                  45
His Leu Ala Gln His Ala Glu Leu Ser Ser Ser Arg Met Ile Arg Ala
    50                  55                  60
Ser Pro Val Gln Pro Lys Gln Arg Gln Gly Ser Leu Ile Ala Ala Arg
65                  70                  75                  80
Lys Asn Ser Thr Gly Thr Ala Gly Pro Ile Arg Arg Arg Ile Ser Arg
                85                  90                  95
Ala Cys Asp Gln Cys Asn Gln Leu Arg Thr Lys Cys Asp Gly Leu His
            100                 105                 110
Pro Cys Ala His Cys Ile Glu Phe Gly Leu Gly Cys Glu Tyr Val Arg
        115                 120                 125
Glu Arg Lys Lys Arg Gly Lys Ala Ser Arg Lys Asp Ile Ala Ala Gln
    130                 135                 140
Gln Ala Ala Ala Ala Ala Ala Gln His Ser Gly Gln Val Gln Asp Gly
145                 150                 155                 160
Pro Glu Asp Gln His Arg Lys Leu Ser Arg Gln Gln Ser Glu Ser Ser
                165                 170                 175
Arg Gly Ser Ala Glu Leu Ala Gln Pro Ala His Asp Pro Pro His Gly
            180                 185                 190
His Ile Glu Gly Ser Val Ser Ser Phe Ser Asp Asn Gly Leu Ser Gln
        195                 200                 205
His Ala Ala Met Gly Gly Met Asp Gly Leu Glu Asp His His Gly His
    210                 215                 220
Val Gly Val Asp Pro Ala Leu Gly Arg Thr Gln Leu Glu Ala Ser Ser
225                 230                 235                 240
Ala Met Gly Leu Gly Ala Tyr Gly Glu His Pro Gly Tyr Glu Ser Pro
                245                 250                 255
Gly Met Asn Gly His Val Met Val Pro Pro Ser Tyr Gly Ala Gln Thr
            260                 265                 270
Thr Met Ala Gly Tyr Ser Gly Ile Ser Tyr Ala Ala Gln Ala Pro Ser
        275                 280                 285
Pro Ala Thr Tyr Ser Ser Asp Gly Asn Phe Arg Leu Thr Gly His Ile
    290                 295                 300
His Asp Tyr Pro Leu Ala Asn Gly Ser Ser Pro Ser Trp Gly Gln Ser
305                 310                 315                 320
Asp Leu Arg Tyr Pro Val Leu Glu Pro Leu Leu Pro His Leu Gly Asn
                325                 330                 335
Ile Leu Pro Val Ser Leu Ala Cys Asp Leu Ile Asp Leu Tyr Phe Ser
            340                 345                 350
Ser Ser Ser Ser Ala Gln Met His Pro Met Ser Pro Tyr Val Leu Gly
        355                 360                 365
Phe Val Phe Arg Lys Arg Ser Phe Leu His Pro Thr Asn Pro Arg Arg
    370                 375                 380
Cys Gln Pro Ala Leu Leu Ala Ser Met Leu Trp Val Ala Ala Gln Thr
385                 390                 395                 400

```
Ser Glu Ala Ser Phe Leu Thr Ser Leu Pro Ser Ala Arg Ser Lys Val
                405                 410                 415
Cys Gln Lys Leu Leu Glu Leu Thr Val Gly Leu Leu Gln Pro Leu Ile
            420                 425                 430
His Thr Gly Thr Asn Ser Pro Ser Pro Lys Thr Ser Pro Val Val Gly
        435                 440                 445
Ala Ala Ala Leu Gly Val Leu Gly Val Ala Met Pro Gly Ser Leu Asn
    450                 455                 460
Met Asp Ser Leu Ala Gly Glu Thr Gly Ala Phe Gly Ala Ile Gly Ser
465                 470                 475                 480
Leu Asp Asp Val Ile Thr Tyr Val His Leu Ala Thr Val Val Ser Ala
                485                 490                 495
Ser Glu Tyr Lys Gly Ala Ser Leu Arg Trp Trp Gly Ala Ala Trp Ser
            500                 505                 510
Leu Ala Arg Glu Leu Lys Leu Gly Arg Glu Leu Pro Pro Gly Asn Pro
        515                 520                 525
Pro Ala Asn Gln Glu Asp Gly Glu Gly Leu Ser Glu Asp Val Asp Glu
    530                 535                 540
His Asp Leu Asn Arg Asn Asn Thr Arg Phe Val Thr Glu Glu Glu Arg
545                 550                 555                 560
Glu Glu Arg Arg Arg Ala Trp Trp Leu Val Tyr Ile Val Asp Arg His
                565                 570                 575
Leu Ala Leu Cys Tyr Asn Arg Pro Leu Phe Leu Leu Asp Ser Glu Cys
            580                 585                 590
Ser Asp Leu Tyr His Pro Met Asp Asp Ile Lys Trp Gln Ala Gly Lys
        595                 600                 605
Phe Arg Ser His Asp Ala Gly Asn Ser Ser Ile Asn Ile Asp Ser Ser
    610                 615                 620
Met Thr Asp Glu Phe Gly Asp Ser Pro Arg Ala Ala Arg Gly Ala His
625                 630                 635                 640
Tyr Glu Cys Arg Gly Arg Ser Ile Phe Gly Tyr Phe Leu Ser Leu Met
                645                 650                 655
Thr Ile Leu Gly Glu Ile Val Asp Val His His Ala Lys Ser His Pro
            660                 665                 670
Arg Phe Gly Val Gly Phe Arg Ser Ala Arg Asp Trp Asp Glu Gln Val
        675                 680                 685
Ala Glu Ile Thr Arg His Leu Asp Met Tyr Glu Glu Ser Leu Lys Arg
    690                 695                 700
Phe Val Ala Lys His Leu Pro Leu Ser Ser Lys Asp Lys Glu Gln His
705                 710                 715                 720
Glu Met His Asp Ser Gly Ala Val Thr Asp Met Gln Ser Pro Leu Ser
                725                 730                 735
Val Arg Thr Asn Ala Ser Ser Arg Met Thr Glu Ser Glu Ile Gln Ala
            740                 745                 750
Ser Ile Val Val Ala Tyr Ser Thr His Val Met His Val Leu His Ile
        755                 760                 765
Leu Leu Ala Asp Lys Trp Asp Pro Ile Asn Leu Leu Asp Asp Asp Asp
    770                 775                 780
Leu Trp Ile Ser Ser Glu Gly Phe Val Thr Ala Thr Ser His Ala Val
785                 790                 795                 800
Ser Ala Ala Glu Ala Ile Ser Gln Ile Leu Glu Phe Asp Pro Gly Leu
                805                 810                 815
Glu Phe Met Pro Phe Phe Tyr Gly Val Tyr Leu Leu Gln Gly Ser Phe
            820                 825                 830
```

Leu Leu Leu Leu Ile Ala Asp Lys Leu Gln Ala Glu Ala Ser Pro Ser
        835                 840                 845
Val Ile Lys Ala Cys Glu Thr Ile Val Arg Ala His Glu Ala Cys Val
    850                 855                 860
Val Thr Leu Ser Thr Glu Tyr Gln Arg Asn Phe Ser Lys Val Met Arg
865                 870                 875                 880
Ser Ala Leu Ala Leu Ile Arg Gly Arg Val Pro Glu Asp Leu Ala Glu
                885                 890                 895
Gln Gln Gln Arg Arg Arg Glu Leu Leu Ala Leu Tyr Arg Trp Thr Gly
            900                 905                 910
Asn Gly Thr Gly Leu Ala Leu
        915

<210> 522
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> predicted protein, partial [Trichoderma reesei
      QM6a] 241 aa protein EGR49987.1 GI:340519749

<400> 522
Leu Arg Ile Leu Pro Val Gly Asp Ser Ile Thr Tyr Gly Phe Leu Ser
 1               5                  10                  15
Asp Gln Asp Gly Gly Asp Gly Asn Gly Tyr Arg Leu Gln Leu Arg Gln
            20                  25                  30
His Leu Ser Lys Asp Arg Val Val Phe Ala Gly Thr Glu Thr Ser Gly
        35                  40                  45
Asn Met Thr Asp Gly Tyr Tyr Leu Ile Val Ser Ser Ser Leu His Arg
    50                  55                  60
Gln Ala Ala Trp Asn Gly Lys Thr Ile Gln Tyr Ile Ser Asp His Val
65                  70                  75                  80
Thr Pro Ser Leu Glu Gln Arg Pro Asn Ile Ile Leu Leu His Ala Gly
                85                  90                  95
Thr Asn Asp Met Asn Pro Asn Gly Ala Ile Ser Arg Glu Gly His Asp
            100                 105                 110
Pro Val Ala Ala Ser Glu Arg Leu Gly Ser Leu Val Asp Lys Met Thr
        115                 120                 125
Thr Leu Cys Pro Asp Ala Val Ile Leu Val Ala Met Ile Ile Gly Thr
    130                 135                 140
Cys Asn Asp Glu Gln Ala Pro Gln Thr Lys Val Phe Gln Ser Leu Ile
145                 150                 155                 160
Pro Asn Val Val Ala Pro Arg Leu Glu Ser Gly Lys His Val Leu Ala
                165                 170                 175
Val Asp Phe Ser Thr Phe Pro Leu Asp Lys Leu Arg Asp Cys Ile His
            180                 185                 190
Pro Thr Asn Glu Gly Tyr His Leu Leu Gly Tyr Tyr Trp Tyr Asp Phe
        195                 200                 205
Ile Ala Gln Ile Pro Arg Asp Trp Ile Thr Ala Pro Val Gly Glu Asp
    210                 215                 220
Pro Gln Arg Pro Glu Glu Gln Asn Leu Ala Met Arg Leu Glu Thr Asp
225                 230                 235                 240

Leu

<210> 523
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<223> transcription factor [Trichoderma reesei QM6a] 733
aa protein EGR51484.1 GI:340521249

<400> 523
Met Ser Phe Ser Asn Pro Arg Arg Arg Thr Pro Val Thr Arg Pro Gly
 1               5                  10                  15
Thr Asp Cys Glu His Gly Leu Ser Leu Lys Thr Thr Met Thr Leu Arg
            20                  25                  30
Lys Gly Ala Thr Phe His Ser Pro Thr Ser Pro Ser Ala Ser Ser Ala
        35                  40                  45
Ala Gly Asp Phe Val Pro Pro Thr Leu Thr Arg Ser Gln Ser Ala Phe
    50                  55                  60
Asp Asp Val Val Asp Ala Ser Arg Arg Arg Ile Ala Met Thr Leu Asn
65                  70                  75                  80
Asp Ile Asp Glu Ala Leu Ser Lys Ala Ser Leu Ser Asp Lys Ser Pro
                85                  90                  95
Arg Pro Lys Pro Leu Arg Asp Thr Ser Leu Pro Val Pro Arg Gly Phe
            100                 105                 110
Leu Glu Pro Pro Val Val Asp Pro Ala Met Asn Lys Gln Glu Pro Glu
        115                 120                 125
Arg Arg Val Leu Arg Pro Arg Ser Val Arg Arg Thr Arg Asn His Ala
    130                 135                 140
Ser Asp Ser Gly Ile Gly Ser Ser Val Val Ser Thr Asn Asp Lys Ala
145                 150                 155                 160
Gly Ala Ala Asp Ser Thr Lys Lys Pro Gln Ala Ser Ala Leu Thr Arg
                165                 170                 175
Ser Ala Ala Ser Ser Thr Thr Ala Met Leu Pro Ser Leu Ser His Arg
            180                 185                 190
Ala Val Asn Arg Ile Arg Glu His Thr Leu Arg Pro Leu Leu Glu Lys
        195                 200                 205
Pro Thr Leu Lys Glu Phe Glu Pro Ile Val Leu Asp Val Pro Arg Arg
    210                 215                 220
Ile Arg Ser Lys Glu Ile Ile Cys Leu Arg Asp Leu Glu Lys Thr Leu
225                 230                 235                 240
Ile Phe Met Ala Pro Glu Lys Ala Lys Ser Ala Ala Leu Tyr Leu Asp
                245                 250                 255
Phe Cys Leu Thr Ser Val Arg Cys Ile Gln Ala Thr Val Glu Tyr Leu
            260                 265                 270
Thr Asp Arg Glu Gln Val Arg Pro Gly Asp Arg Pro Tyr Thr Asn Gly
        275                 280                 285
Tyr Phe Ile Asp Leu Lys Glu Gln Ile Tyr Gln Tyr Gly Lys Gln Leu
    290                 295                 300
Ala Ala Ile Lys Glu Lys Gly Ser Leu Ala Asp Asp Met Asp Ile Asp
305                 310                 315                 320

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Pro Ser Asp Glu Val Arg Leu Tyr Gly Gly Val Ala Glu Asn Gly Arg
                325                 330                 335
Pro Ala Glu Leu Ile Arg Val Lys Lys Asp Gly Thr Ala Tyr Ser Met
            340                 345                 350
Ala Thr Gly Lys Ile Val Asp Met Thr Glu Ser Pro Thr Pro Leu Lys
        355                 360                 365
Arg Ser Leu Ser Glu Gln Arg Glu Asp Glu Glu Glu Ile Met Arg Ser
    370                 375                 380
Met Ala Arg Arg Lys Lys Asn Ala Thr Pro Glu Glu Leu Ala Pro Lys
385                 390                 395                 400
Lys Cys Arg Glu Pro Gly Cys Thr Lys Glu Phe Lys Arg Pro Cys Asp
                405                 410                 415
Leu Thr Lys His Glu Lys Thr His Ser Arg Pro Trp Lys Cys Pro Ile
            420                 425                 430
Pro Thr Cys Lys Tyr His Glu Tyr Gly Trp Pro Thr Glu Lys Glu Met
        435                 440                 445
Asp Arg His Ile Asn Asp Lys His Ser Asp Ala Pro Ala Met Tyr Glu
    450                 455                 460
Cys Leu Phe Lys Pro Cys Pro Tyr Lys Ser Lys Arg Glu Ser Asn Cys
465                 470                 475                 480
Lys Gln His Met Glu Lys Ala His Gly Trp Thr Tyr Val Arg Thr Lys
                485                 490                 495
Thr Asn Gly Lys Lys Ala Pro Ser Gln Asn Gly Ser Thr Ala Gln Gln
            500                 505                 510
Thr Pro Pro Leu Ala Asn Val Ser Thr Pro Ser Ser Thr Pro Ser Tyr
        515                 520                 525
Ser Val Pro Thr Pro Pro Gln Asp Gln Val Met Ser Thr Asp Phe Pro
    530                 535                 540
Met Tyr Pro Ala Asp Asp Asp Trp Leu Ala Thr Tyr Gly Ala Gln Pro
545                 550                 555                 560
Asn Thr Ile Asp Ala Met Asp Leu Gly Leu Glu Asn Leu Ser Pro Ala
                565                 570                 575
Ser Ala Ala Ser Ser Tyr Glu Gln Tyr Pro Pro Tyr Gln Asn Gly Ser
            580                 585                 590
Thr Phe Ile Ile Asn Asp Glu Asp Ile Tyr Ala Ala His Val Gln Ile
        595                 600                 605
Pro Ala Gln Leu Pro Thr Pro Glu Gln Val Tyr Thr Lys Met Met Pro
    610                 615                 620
Gln Gln Met Pro Val Tyr His Val Gln Gln Glu Pro Cys Thr Thr Val
625                 630                 635                 640
Pro Ile Leu Gly Glu Pro Gln Phe Ser Pro Asn Ala Gln Gln Asn Ala
                645                 650                 655
Val Leu Tyr Thr Pro Thr Ser Leu Arg Glu Val Asp Glu Gly Phe Asp
            660                 665                 670
Glu Ser Tyr Ala Ala Asp Gly Ala Asp Phe Gln Leu Phe Pro Ala Thr
        675                 680                 685
Val Asp Lys Thr Asp Val Phe Gln Ser Leu Phe Thr Asp Met Pro Ser
    690                 695                 700
Ala Asn Leu Gly Phe Ser Gln Thr Thr Gln Pro Asp Ile Phe Asn Gln
705                 710                 715                 720
Ile Asp Trp Ser Asn Leu Asp Tyr Gln Gly Phe Gln Glu
                725                 730
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<210> 524
<211> 347
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 10 [Trichoderma reesei
QM6a]
347 aa protein EGR52056.1 GI:340521822

<400> 524
Met Lys Ala Asn Val Ile Leu Cys Leu Leu Ala Pro Leu Val Ala Ala
 1               5                  10                  15
Leu Pro Thr Glu Thr Ile His Leu Asp Pro Glu Leu Ala Ala Leu Arg
            20                  25                  30
Ala Asn Leu Thr Glu Arg Thr Ala Asp Leu Trp Asp Arg Gln Ala Ser
        35                  40                  45
Gln Ser Ile Asp Gln Leu Ile Lys Arg Lys Gly Lys Leu Tyr Phe Gly
    50                  55                  60
Thr Ala Thr Asp Arg Gly Leu Leu Gln Arg Glu Lys Asn Ala Ala Ile
65                  70                  75                  80
Ile Gln Ala Asp Leu Gly Gln Val Thr Pro Glu Asn Ser Met Lys Trp
                85                  90                  95
Gln Ser Leu Glu Asn Asn Gln Gly Gln Leu Asn Trp Gly Asp Ala Asp
            100                 105                 110
Tyr Leu Val Asn Phe Ala Gln Gln Asn Gly Lys Ser Ile Arg Gly His
        115                 120                 125
Thr Leu Ile Trp His Ser Gln Leu Pro Ala Trp Val Asn Asn Ile Asn
    130                 135                 140
Asn Ala Asp Thr Leu Arg Gln Val Ile Arg Thr His Val Ser Thr Val
145                 150                 155                 160
Val Gly Arg Tyr Lys Gly Lys Ile Arg Ala Trp Asp Val Val Asn Glu
                165                 170                 175
Ile Phe Asn Glu Asp Gly Thr Leu Arg Ser Ser Val Phe Ser Arg Leu
            180                 185                 190
Leu Gly Glu Glu Phe Val Ser Ile Ala Phe Arg Ala Ala Arg Asp Ala
        195                 200                 205
Asp Pro Ser Ala Arg Leu Tyr Ile Asn Asp Tyr Asn Leu Asp Arg Ala
    210                 215                 220
Asn Tyr Gly Lys Val Asn Gly Leu Lys Thr Tyr Val Ser Lys Trp Ile
225                 230                 235                 240
Ser Gln Gly Val Pro Ile Asp Gly Ile Gly Ser Gln Ser His Leu Ser
                245                 250                 255
Gly Gly Gly Gly Ser Gly Thr Leu Gly Ala Leu Gln Gln Leu Ala Thr
            260                 265                 270
Val Pro Val Thr Glu Leu Ala Ile Thr Glu Leu Asp Ile Gln Gly Ala
        275                 280                 285
Pro Thr Thr Asp Tyr Thr Gln Val Val Gln Ala Cys Leu Ser Val Ser
    290                 295                 300
Lys Cys Val Gly Ile Thr Val Trp Gly Ile Ser Asp Lys Asp Ser Trp
305                 310                 315                 320
Arg Ala Ser Thr Asn Pro Leu Leu Phe Asp Ala Asn Phe Asn Pro Lys
                325                 330                 335
Pro Ala Tyr Asn Ser Ile Val Gly Ile Leu Gln

340 345

<210> 525
<211> 401
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 18, chitinase
[Trichoderma reesei QM6a] 401 aa protein
EGR52465.1 GI:340522232

<400> 525
Met Phe Phe Ser Lys Ala Leu Ala Ala Ala Gly Leu Leu Ala Thr Ala
1 5 10 15
Ala Tyr Ala Ala Pro Thr Met Glu Lys Arg Ala Ala Gly Gly Lys Leu
20 25 30
Val Val Tyr Trp Gly Ala Glu Asp Asp Ser Thr Thr Leu Ala Asn Val
35 40 45
Cys Ala Asp Ser Ser Tyr Asp Ile Val Asn Leu Ala Phe Leu Ser Arg
50 55 60
Phe Phe Ala Gly Gly Gly Tyr Pro Glu Leu Ser Leu Ser Thr Leu Gly
65 70 75 80
Gly Pro Ser Ala Ala Gln Arg Ala Ala Gly Ala Thr Asn Leu Gln Asp
85 90 95
Gly Thr Ser Leu Ile Pro Ala Ile Gln Ala Cys Gln Ala Ala Gly Lys
100 105 110
Leu Val Ile Leu Ser Met Gly Gly Ala Val Asp Phe Ser Ala Val Thr
115 120 125
Leu Ser Ser Asp Ala Gln Gly Gln Gln Leu Ala Asp Thr Val Trp Asn
130 135 140
Leu Phe Leu Gly Gly Thr Ala Asn Pro Thr Leu Arg Pro Phe Gly Ser
145 150 155 160
Val Lys Leu Asp Gly Val Asp Leu Asp Asn Glu Thr Gly Asn Pro Thr
165 170 175
Gly Tyr Leu Ala Met Ala Gln Arg Phe Lys Ser Asn Phe Ala Lys Asp
180 185 190
Thr Ser Lys Lys Tyr Tyr Leu Thr Ala Ala Pro Gln Cys Pro Phe Pro
195 200 205
Asp Ala Ser Glu Pro Leu Asn Val Cys Gln Leu Ala Asp Tyr Ile Trp
210 215 220
Val Gln Phe Tyr Asn Asn Gly Asn Cys Asn Ile Ala Gln Ser Gly Phe
225 230 235 240
Asn Asn Ala Val Lys Asn Trp Ser Lys Ser Ile Gly Asn Ala Thr Leu
245 250 255
Phe Ile Gly Ala Leu Ala Ser Gly Ala Asp Gly Asp Gln Gly Tyr Val
260 265 270
Ser Ala Ser Ser Leu Leu Ser Ala Tyr Gln Gly Val Ser Ala Leu Asn
275 280 285
Leu Pro Asn Ile Gly Gly Ile Met Leu Trp Glu Ala Gln Leu Ala Val
290 295 300
Lys Asn Gly Asn Phe Gln Lys Thr Val Lys Ala Gly Ile Ala Ser Gly
305 310 315 320

```
Thr Thr Pro Pro Pro Pro Pro Pro Thr Gly Gly Cys Ser Trp Ala Gly
                325                 330                 335
His Cys Ala Gly Ala Ser Cys Ser Thr Asp Asn Asp Cys Ser Asp Asp
            340                 345                 350
Leu Thr Cys Asn Gly Gly Val Cys Gly Thr Ala Gly Ser Thr Pro Ala
        355                 360                 365
Pro Thr Cys Ser Trp Glu Gly His Cys Leu Gly Ala Ser Cys Gly Asn
    370                 375                 380
Asp Asn Asp Cys Ser Asp Pro Tyr Ser Cys Lys Asn Gly Val Cys Ser
385                 390                 395                 400
Asn
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<210> 526
<211> 324
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 18 [Trichoderma reesei QM6a]
      324 aa protein EGR52759.1 GI:340522526

<400> 526

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

225 230 235 240
Glu Gln Gln Asn Asn Tyr Asn Tyr Gln Thr Trp Glu Asp Trp Ala Lys
245 250 255
Thr Ser Pro Asn Pro Asn Val Lys Leu Leu Val Gly Ile Pro Ala Gly
260 265 270
Pro Asn Ala Gly His Gly Tyr Val Ser Asp Ala Gln Leu Lys Ser Val
275 280 285
Phe Glu Tyr Ser Lys Lys Phe Asp Thr Phe Ala Gly Ala Met Met Trp
290 295 300
Asp Met Ser Gln Leu Tyr Gln Asn Ser Gly Phe Glu Asp Gln Val Val
305 310 315 320
Asp Ala Leu Lys

<210> 527
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 11 [Trichoderma reesei QM6a]
229 aa protein EGR52985.1 GI:340522752

<400> 527
Met Val Ala Phe Ser Ser Leu Ile Cys Ala Leu Thr Ser Ile Ala Ser
1 5 10 15
Thr Leu Ala Met Pro Thr Gly Leu Glu Pro Glu Ser Ser Val Asn Val
20 25 30
Thr Glu Arg Gly Met Tyr Asp Phe Val Leu Gly Ala His Asn Asp His
35 40 45
Arg Arg Arg Ala Ser Ile Asn Tyr Asp Gln Asn Tyr Gln Thr Gly Gly
50 55 60
Gln Val Ser Tyr Ser Pro Ser Asn Thr Gly Phe Ser Val Asn Trp Asn
65 70 75 80
Thr Gln Asp Asp Phe Val Val Gly Val Gly Trp Thr Thr Gly Ser Ser
85 90 95
Ala Pro Ile Asn Phe Gly Gly Ser Phe Ser Val Asn Ser Gly Thr Gly
100 105 110
Leu Leu Ser Val Tyr Gly Trp Ser Thr Asn Pro Leu Val Glu Tyr Tyr
115 120 125
Ile Met Glu Asp Asn His Asn Tyr Pro Ala Gln Gly Thr Val Lys Gly
130 135 140
Thr Val Thr Ser Asp Gly Ala Thr Tyr Thr Ile Trp Glu Asn Thr Arg
145 150 155 160
Val Asn Glu Pro Ser Ile Gln Gly Thr Ala Thr Phe Asn Gln Tyr Ile
165 170 175
Ser Val Arg Asn Ser Pro Arg Thr Ser Gly Thr Val Thr Val Gln Asn
180 185 190
His Phe Asn Ala Trp Ala Ser Leu Gly Leu His Leu Gly Gln Met Asn
195 200 205
Tyr Gln Val Val Ala Val Glu Gly Trp Gly Gly Ser Gly Ser Ala Ser
210 215 220

Gln Ser Val Ser Asn
225

<210> 528
<211> 324
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 18 [Trichoderma reesei QM6a] 324 aa protein P_006961069.1 I:589098093

<400> 528
Met Pro Ser Leu Thr Ala Leu Ala Gly Leu Leu Ala Leu Val Pro Ser
 1               5                  10                  15
Ala Leu Ala Gly Trp Asn Pro Asp Ser Lys Gln Asn Ile Ala Val Tyr
            20                  25                  30
Trp Gly Gln Asn Ser Ala Asn Ser Gln Ser Thr Gln Gln Arg Leu Ser
        35                  40                  45
Phe Tyr Cys Asn Asp Asp Asn Ile Asn Val Ile Glu Ile Ala Phe Leu
    50                  55                  60
Asn Gly Ile Asn Pro Pro Met Thr Asn Phe Ala Asn Ala Gly Asp Arg
65                  70                  75                  80
Cys Thr Pro Phe Ser Asp Asn Pro Trp Leu Leu Ser Cys Pro Glu Ile
                85                  90                  95
Glu Ala Asp Ile Lys Thr Cys Gln Ala Asn Gly Lys Thr Ile Leu Leu
            100                 105                 110
Ser Leu Gly Gly Asp Thr Tyr Ser Gln Gly Gly Trp Ala Ser Pro Glu
        115                 120                 125
Ala Ala Gln Asp Ala Ala Ala Gln Val Trp Ala Met Phe Gly Pro Val
    130                 135                 140
Gln Ser Asp Ser Ser Ala Pro Arg Pro Phe Gly Asp Ala Val Val Asp
145                 150                 155                 160
Gly Phe Asp Phe Asp Phe Glu Ser Thr Thr Asn Asn Leu Val Ala Phe
                165                 170                 175
Gly Ala Gln Leu Arg Thr Leu Ser Asp Ala Ala Ala Thr Asp Ser Asn
            180                 185                 190
Lys Lys Phe Tyr Leu Ala Ala Ala Pro Gln Cys Phe Phe Pro Asp Ala
        195                 200                 205
Ala Val Gly Pro Leu Ile Asn Ala Val Pro Met Asp Trp Ile Gln Ile
    210                 215                 220
Gln Phe Tyr Asn Asn Pro Cys Gly Val Ser Ala Tyr Thr Pro Gly Ser
225                 230                 235                 240
Glu Gln Gln Asn Asn Tyr Asn Tyr Gln Thr Trp Glu Asp Trp Ala Lys
                245                 250                 255
Thr Ser Pro Asn Pro Asn Val Lys Leu Leu Val Gly Ile Pro Ala Gly
            260                 265                 270
Pro Asn Ala Gly His Gly Tyr Val Ser Asp Ala Gln Leu Lys Ser Val
        275                 280                 285
Phe Glu Tyr Ser Lys Lys Phe Asp Thr Phe Ala Gly Ala Met Met Trp
    290                 295                 300
Asp Met Ser Gln Leu Tyr Gln Asn Ser Gly Phe Glu Asp Gln Val Val
305                 310                 315                 320

Asp Ala Leu Lys

<210> 529
<211> 401
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 18, chitinase
[Trichoderma reesei QM6a] 41 aa protein
XP_006961376.1 I:589098707

<400> 529
Met Phe Phe Ser Lys Ala Leu Ala Ala Ala Gly Leu Leu Ala Thr Ala
 1               5                  10                  15
Ala Tyr Ala Ala Pro Thr Met Glu Lys Arg Ala Ala Gly Gly Lys Leu
            20                  25                  30
Val Val Tyr Trp Gly Ala Glu Asp Asp Ser Thr Thr Leu Ala Asn Val
        35                  40                  45
Cys Ala Asp Ser Ser Tyr Asp Ile Val Asn Leu Ala Phe Leu Ser Arg
    50                  55                  60
Phe Phe Ala Gly Gly Gly Tyr Pro Glu Leu Ser Leu Ser Thr Leu Gly
65                  70                  75                  80
Gly Pro Ser Ala Ala Gln Arg Ala Ala Gly Ala Thr Asn Leu Gln Asp
                85                  90                  95
Gly Thr Ser Leu Ile Pro Ala Ile Gln Ala Cys Gln Ala Ala Gly Lys
            100                 105                 110
Leu Val Ile Leu Ser Met Gly Gly Ala Val Asp Phe Ser Ala Val Thr
        115                 120                 125
Leu Ser Ser Asp Ala Gln Gly Gln Gln Leu Ala Asp Thr Val Trp Asn
    130                 135                 140
Leu Phe Leu Gly Gly Thr Ala Asn Pro Thr Leu Arg Pro Phe Gly Ser
145                 150                 155                 160
Val Lys Leu Asp Gly Val Asp Leu Asp Asn Glu Thr Gly Asn Pro Thr
                165                 170                 175
Gly Tyr Leu Ala Met Ala Gln Arg Phe Lys Ser Asn Phe Ala Lys Asp
            180                 185                 190
Thr Ser Lys Lys Tyr Tyr Leu Thr Ala Ala Pro Gln Cys Pro Phe Pro
        195                 200                 205
Asp Ala Ser Glu Pro Leu Asn Val Cys Gln Leu Ala Asp Tyr Ile Trp
    210                 215                 220
Val Gln Phe Tyr Asn Asn Gly Asn Cys Asn Ile Ala Gln Ser Gly Phe
225                 230                 235                 240
Asn Asn Ala Val Lys Asn Trp Ser Lys Ser Ile Gly Asn Ala Thr Leu
                245                 250                 255
Phe Ile Gly Ala Leu Ala Ser Gly Ala Asp Gly Asp Gln Gly Tyr Val
            260                 265                 270
Ser Ala Ser Ser Leu Leu Ser Ala Tyr Gln Gly Val Ser Ala Leu Asn
        275                 280                 285
Leu Pro Asn Ile Gly Gly Ile Met Leu Trp Glu Ala Gln Leu Ala Val
    290                 295                 300
Lys Asn Gly Asn Phe Gln Lys Thr Val Lys Ala Gly Ile Ala Ser Gly

305 310 315 320
Thr Thr Pro Pro Pro Pro Pro Pro Thr Gly Gly Cys Ser Trp Ala Gly
325 330 335
His Cys Ala Gly Ala Ser Cys Ser Thr Asp Asn Asp Cys Ser Asp Asp
340 345 350
Leu Thr Cys Asn Gly Gly Val Cys Gly Thr Ala Gly Ser Thr Pro Ala
355 360 365
Pro Thr Cys Ser Trp Glu Gly His Cys Leu Gly Ala Ser Cys Gly Asn
370 375 380
Asp Asn Asp Cys Ser Asp Pro Tyr Ser Cys Lys Asn Gly Val Cys Ser
385 390 395 400
Asn

<210> 530
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 11 [Trichoderma reesei QM6a]
229 aa protein XP_006961811.1 I:589099577

<400> 530
Met Val Ala Phe Ser Ser Leu Ile Cys Ala Leu Thr Ser Ile Ala Ser
1 5 10 15
Thr Leu Ala Met Pro Thr Gly Leu Glu Pro Glu Ser Ser Val Asn Val
20 25 30
Thr Glu Arg Gly Met Tyr Asp Phe Val Leu Gly Ala His Asn Asp His
35 40 45
Arg Arg Arg Ala Ser Ile Asn Tyr Asp Gln Asn Tyr Gln Thr Gly Gly
50 55 60
Gln Val Ser Tyr Ser Pro Ser Asn Thr Gly Phe Ser Val Asn Trp Asn
65 70 75 80
Thr Gln Asp Asp Phe Val Val Gly Val Gly Trp Thr Thr Gly Ser Ser
85 90 95
Ala Pro Ile Asn Phe Gly Gly Ser Phe Ser Val Asn Ser Gly Thr Gly
100 105 110
Leu Leu Ser Val Tyr Gly Trp Ser Thr Asn Pro Leu Val Glu Tyr Tyr
115 120 125
Ile Met Glu Asp Asn His Asn Tyr Pro Ala Gln Gly Thr Val Lys Gly
130 135 140
Thr Val Thr Ser Asp Gly Ala Thr Tyr Thr Ile Trp Glu Asn Thr Arg
145 150 155 160
Val Asn Glu Pro Ser Ile Gln Gly Thr Ala Thr Phe Asn Gln Tyr Ile
165 170 175
Ser Val Arg Asn Ser Pro Arg Thr Ser Gly Thr Val Thr Val Gln Asn
180 185 190
His Phe Asn Ala Trp Ala Ser Leu Gly Leu His Leu Gly Gln Met Asn
195 200 205
Tyr Gln Val Val Ala Val Glu Gly Trp Gly Gly Ser Gly Ser Ala Ser
210 215 220

Gln Ser Val Ser Asn
225

<210> 531
<211> 347
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 10 [Trichoderma reesei QM6a]
347 aa protein XP_006962419.1 GI:589100793

<400> 531
Met Lys Ala Asn Val Ile Leu Cys Leu Leu Ala Pro Leu Val Ala Ala
 1               5                  10                  15
Leu Pro Thr Glu Thr Ile His Leu Asp Pro Glu Leu Ala Ala Leu Arg
            20                  25                  30
Ala Asn Leu Thr Glu Arg Thr Ala Asp Leu Trp Asp Arg Gln Ala Ser
        35                  40                  45
Gln Ser Ile Asp Gln Leu Ile Lys Arg Lys Gly Lys Leu Tyr Phe Gly
    50                  55                  60
Thr Ala Thr Asp Arg Gly Leu Leu Gln Arg Glu Lys Asn Ala Ala Ile
65                  70                  75                  80
Ile Gln Ala Asp Leu Gly Gln Val Thr Pro Glu Asn Ser Met Lys Trp
                85                  90                  95
Gln Ser Leu Glu Asn Asn Gln Gly Gln Leu Asn Trp Gly Asp Ala Asp
            100                 105                 110
Tyr Leu Val Asn Phe Ala Gln Gln Asn Gly Lys Ser Ile Arg Gly His
        115                 120                 125
Thr Leu Ile Trp His Ser Gln Leu Pro Ala Trp Val Asn Asn Ile Asn
    130                 135                 140
Asn Ala Asp Thr Leu Arg Gln Val Ile Arg Thr His Val Ser Thr Val
145                 150                 155                 160
Val Gly Arg Tyr Lys Gly Lys Ile Arg Ala Trp Asp Val Val Asn Glu
                165                 170                 175
Ile Phe Asn Glu Asp Gly Thr Leu Arg Ser Ser Val Phe Ser Arg Leu
            180                 185                 190
Leu Gly Glu Glu Phe Val Ser Ile Ala Phe Arg Ala Ala Arg Asp Ala
        195                 200                 205
Asp Pro Ser Ala Arg Leu Tyr Ile Asn Asp Tyr Asn Leu Asp Arg Ala
    210                 215                 220
Asn Tyr Gly Lys Val Asn Gly Leu Lys Thr Tyr Val Ser Lys Trp Ile
225                 230                 235                 240
Ser Gln Gly Val Pro Ile Asp Gly Ile Gly Ser Gln Ser His Leu Ser
                245                 250                 255
Gly Gly Gly Gly Ser Gly Thr Leu Gly Ala Leu Gln Gln Leu Ala Thr
            260                 265                 270
Val Pro Val Thr Glu Leu Ala Ile Thr Glu Leu Asp Ile Gln Gly Ala
        275                 280                 285
Pro Thr Thr Asp Tyr Thr Gln Val Val Gln Ala Cys Leu Ser Val Ser
    290                 295                 300
Lys Cys Val Gly Ile Thr Val Trp Gly Ile Ser Asp Lys Asp Ser Trp

```
305                 310                 315                 320
Arg Ala Ser Thr Asn Pro Leu Leu Phe Asp Ala Asn Phe Asn Pro Lys
                325                 330                 335
Pro Ala Tyr Asn Ser Ile Val Gly Ile Leu Gln
            340                 345
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<210> 532
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<223> transcription factor [Trichoderma reesei QM6a] 733
aa protein XP_006962963.1 GI:589101881

<400> 532

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

```
    290                 295                 300
Ala Ala Ile Lys Glu Lys Gly Ser Leu Ala Asp Asp Met Asp Ile Asp
305                 310                 315                 320
Pro Ser Asp Glu Val Arg Leu Tyr Gly Gly Val Ala Glu Asn Gly Arg
                325                 330                 335
Pro Ala Glu Leu Ile Arg Val Lys Lys Asp Gly Thr Ala Tyr Ser Met
            340                 345                 350
Ala Thr Gly Lys Ile Val Asp Met Thr Glu Ser Pro Thr Pro Leu Lys
        355                 360                 365
Arg Ser Leu Ser Glu Gln Arg Glu Asp Glu Glu Glu Ile Met Arg Ser
    370                 375                 380
Met Ala Arg Arg Lys Lys Asn Ala Thr Pro Glu Glu Leu Ala Pro Lys
385                 390                 395                 400
Lys Cys Arg Glu Pro Gly Cys Thr Lys Glu Phe Lys Arg Pro Cys Asp
                405                 410                 415
Leu Thr Lys His Glu Lys Thr His Ser Arg Pro Trp Lys Cys Pro Ile
            420                 425                 430
Pro Thr Cys Lys Tyr His Glu Tyr Gly Trp Pro Thr Glu Lys Glu Met
        435                 440                 445
Asp Arg His Ile Asn Asp Lys His Ser Asp Ala Pro Ala Met Tyr Glu
    450                 455                 460
Cys Leu Phe Lys Pro Cys Pro Tyr Lys Ser Lys Arg Glu Ser Asn Cys
465                 470                 475                 480
Lys Gln His Met Glu Lys Ala His Gly Trp Thr Tyr Val Arg Thr Lys
                485                 490                 495
Thr Asn Gly Lys Lys Ala Pro Ser Gln Asn Gly Ser Thr Ala Gln Gln
            500                 505                 510
Thr Pro Pro Leu Ala Asn Val Ser Thr Pro Ser Ser Thr Pro Ser Tyr
        515                 520                 525
Ser Val Pro Thr Pro Pro Gln Asp Gln Val Met Ser Thr Asp Phe Pro
    530                 535                 540
Met Tyr Pro Ala Asp Asp Asp Trp Leu Ala Thr Tyr Gly Ala Gln Pro
545                 550                 555                 560
Asn Thr Ile Asp Ala Met Asp Leu Gly Leu Glu Asn Leu Ser Pro Ala
                565                 570                 575
Ser Ala Ala Ser Ser Tyr Glu Gln Tyr Pro Pro Tyr Gln Asn Gly Ser
            580                 585                 590
Thr Phe Ile Ile Asn Asp Glu Asp Ile Tyr Ala Ala His Val Gln Ile
        595                 600                 605
Pro Ala Gln Leu Pro Thr Pro Glu Gln Val Tyr Thr Lys Met Met Pro
    610                 615                 620
Gln Gln Met Pro Val Tyr His Val Gln Gln Glu Pro Cys Thr Thr Val
625                 630                 635                 640
Pro Ile Leu Gly Glu Pro Gln Phe Ser Pro Asn Ala Gln Gln Asn Ala
                645                 650                 655
Val Leu Tyr Thr Pro Thr Ser Leu Arg Glu Val Asp Glu Gly Phe Asp
            660                 665                 670
Glu Ser Tyr Ala Ala Asp Gly Ala Asp Phe Gln Leu Phe Pro Ala Thr
        675                 680                 685
Val Asp Lys Thr Asp Val Phe Gln Ser Leu Phe Thr Asp Met Pro Ser
    690                 695                 700
Ala Asn Leu Gly Phe Ser Gln Thr Thr Gln Pro Asp Ile Phe Asn Gln
705                 710                 715                 720
Ile Asp Trp Ser Asn Leu Asp Tyr Gln Gly Phe Gln Glu
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725 730

<210> 533
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> predicted protein, partial [Trichoderma reesei QM6a] 241 aa protein XP_006964048.1 GI:589104051

<400> 533
Leu Arg Ile Leu Pro Val Gly Asp Ser Ile Thr Tyr Gly Phe Leu Ser
1 5 10 15
Asp Gln Asp Gly Gly Asp Gly Asn Gly Tyr Arg Leu Gln Leu Arg Gln
20 25 30
His Leu Ser Lys Asp Arg Val Val Phe Ala Gly Thr Glu Thr Ser Gly
35 40 45
Asn Met Thr Asp Gly Tyr Tyr Leu Ile Val Ser Ser Ser Leu His Arg
50 55 60
Gln Ala Ala Trp Asn Gly Lys Thr Ile Gln Tyr Ile Ser Asp His Val
65 70 75 80
Thr Pro Ser Leu Glu Gln Arg Pro Asn Ile Ile Leu Leu His Ala Gly
85 90 95
Thr Asn Asp Met Asn Pro Asn Gly Ala Ile Ser Arg Glu Gly His Asp
100 105 110
Pro Val Ala Ala Ser Glu Arg Leu Gly Ser Leu Val Asp Lys Met Thr
115 120 125
Thr Leu Cys Pro Asp Ala Val Ile Leu Val Ala Met Ile Ile Gly Thr
130 135 140
Cys Asn Asp Glu Gln Ala Pro Gln Thr Lys Val Phe Gln Ser Leu Ile
145 150 155 160
Pro Asn Val Val Ala Pro Arg Leu Glu Ser Gly Lys His Val Leu Ala
165 170 175
Val Asp Phe Ser Thr Phe Pro Leu Asp Lys Leu Arg Asp Cys Ile His
180 185 190
Pro Thr Asn Glu Gly Tyr His Leu Leu Gly Tyr Tyr Trp Tyr Asp Phe
195 200 205
Ile Ala Gln Ile Pro Arg Asp Trp Ile Thr Ala Pro Val Gly Glu Asp
210 215 220
Pro Gln Arg Pro Glu Glu Gln Asn Leu Ala Met Arg Leu Glu Thr Asp
225 230 235 240
Leu

<210> 534
<211> 920
<212> PRT
<213> Artificial Sequence

<220>
<223> xylanase regulator 1 [Trichoderma reesei QM6a] 920

aa protein XP_006966092.1 GI:589108139

<400> 534
Met Leu Ser Asn Pro Leu Arg Arg Tyr Ser Ala Tyr Pro Asp Ile Ser
 1               5                  10                  15
Ser Ala Ser Phe Asp Pro Asn Tyr His Gly Ser Gln Ser His Leu His
            20                  25                  30
Ser Ile Asn Val Asn Thr Phe Gly Asn Ser His Pro Tyr Pro Met Gln
        35                  40                  45
His Leu Ala Gln His Ala Glu Leu Ser Ser Ser Arg Met Ile Arg Ala
    50                  55                  60
Ser Pro Val Gln Pro Lys Gln Arg Gln Gly Ser Leu Ile Ala Ala Arg
65                  70                  75                  80
Lys Asn Ser Thr Gly Thr Ala Gly Pro Ile Arg Arg Arg Ile Ser Arg
                85                  90                  95
Ala Cys Asp Gln Cys Asn Gln Leu Arg Thr Lys Cys Asp Gly Leu His
            100                 105                 110
Pro Cys Ala His Cys Ile Glu Phe Gly Leu Gly Cys Glu Tyr Val Arg
        115                 120                 125
Glu Arg Lys Lys Arg Gly Lys Ala Ser Arg Lys Asp Ile Ala Ala Gln
    130                 135                 140
Gln Ala Ala Ala Ala Ala Ala Gln His Ser Gly Gln Val Gln Asp Gly
145                 150                 155                 160
Pro Glu Asp Gln His Arg Lys Leu Ser Arg Gln Gln Ser Glu Ser Ser
                165                 170                 175
Arg Gly Ser Ala Glu Leu Ala Gln Pro Ala His Asp Pro Pro His Gly
            180                 185                 190
His Ile Glu Gly Ser Val Ser Ser Phe Ser Asp Asn Gly Leu Ser Gln
        195                 200                 205
His Ala Ala Met Gly Gly Met Asp Gly Leu Glu Asp His His Gly His
    210                 215                 220
Val Gly Val Asp Pro Ala Leu Gly Arg Thr Gln Leu Glu Ala Ser Ser
225                 230                 235                 240
Ala Met Gly Leu Gly Ala Tyr Gly Glu Val His Pro Gly Tyr Glu Ser
                245                 250                 255
Pro Gly Met Asn Gly His Val Met Val Pro Pro Ser Tyr Gly Ala Gln
            260                 265                 270
Thr Thr Met Ala Gly Tyr Ser Gly Ile Ser Tyr Ala Ala Gln Ala Pro
        275                 280                 285
Ser Pro Ala Thr Tyr Ser Ser Asp Gly Asn Phe Arg Leu Thr Gly His
    290                 295                 300
Ile His Asp Tyr Pro Leu Ala Asn Gly Ser Ser Pro Ser Trp Gly Gln
305                 310                 315                 320
Ser Asp Leu Arg Tyr Pro Val Leu Glu Pro Leu Leu Pro His Leu Gly
                325                 330                 335
Asn Ile Leu Pro Val Ser Leu Ala Cys Asp Leu Ile Asp Leu Tyr Phe
            340                 345                 350
Ser Ser Ser Ser Ser Ala Gln Met His Pro Met Ser Pro Tyr Val Leu
        355                 360                 365
Gly Phe Val Phe Arg Lys Arg Ser Phe Leu His Pro Thr Asn Pro Arg
    370                 375                 380
Arg Cys Gln Pro Ala Leu Leu Ala Ser Met Leu Trp Val Ala Ala Gln
385                 390                 395                 400
Thr Ser Glu Ala Ser Phe Leu Thr Ser Leu Pro Ser Ala Arg Ser Lys

```
                405                 410                 415
Val Cys Gln Lys Leu Leu Glu Leu Thr Val Gly Leu Leu Gln Pro Leu
            420                 425                 430
Ile His Thr Gly Thr Asn Ser Pro Ser Pro Lys Thr Ser Pro Val Val
        435                 440                 445
Gly Ala Ala Ala Leu Gly Val Leu Gly Val Ala Met Pro Gly Ser Leu
    450                 455                 460
Asn Met Asp Ser Leu Ala Gly Glu Thr Gly Ala Phe Gly Ala Ile Gly
465                 470                 475                 480
Ser Leu Asp Asp Val Ile Thr Tyr Val His Leu Ala Thr Val Val Ser
                485                 490                 495
Ala Ser Glu Tyr Lys Gly Ala Ser Leu Arg Trp Trp Gly Ala Ala Trp
            500                 505                 510
Ser Leu Ala Arg Glu Leu Lys Leu Gly Arg Glu Leu Pro Pro Gly Asn
        515                 520                 525
Pro Pro Ala Asn Gln Glu Asp Gly Glu Gly Leu Ser Glu Asp Val Asp
    530                 535                 540
Glu His Asp Leu Asn Arg Asn Asn Thr Arg Phe Val Thr Glu Glu Glu
545                 550                 555                 560
Arg Glu Glu Arg Arg Arg Ala Trp Trp Leu Val Tyr Ile Val Asp Arg
                565                 570                 575
His Leu Ala Leu Cys Tyr Asn Arg Pro Leu Phe Leu Leu Asp Ser Glu
            580                 585                 590
Cys Ser Asp Leu Tyr His Pro Met Asp Asp Ile Lys Trp Gln Ala Gly
        595                 600                 605
Lys Phe Arg Ser His Asp Ala Gly Asn Ser Ser Ile Asn Ile Asp Ser
    610                 615                 620
Ser Met Thr Asp Glu Phe Gly Asp Ser Pro Arg Ala Ala Arg Gly Ala
625                 630                 635                 640
His Tyr Glu Cys Arg Gly Arg Ser Ile Phe Gly Tyr Phe Leu Ser Leu
                645                 650                 655
Met Thr Ile Leu Gly Glu Ile Val Asp Val His His Ala Lys Ser His
            660                 665                 670
Pro Arg Phe Gly Val Gly Phe Arg Ser Ala Arg Asp Trp Asp Glu Gln
        675                 680                 685
Val Ala Glu Ile Thr Arg His Leu Asp Met Tyr Glu Glu Ser Leu Lys
    690                 695                 700
Arg Phe Val Ala Lys His Leu Pro Leu Ser Ser Lys Asp Lys Glu Gln
705                 710                 715                 720
His Glu Met His Asp Ser Gly Ala Val Thr Asp Met Gln Ser Pro Leu
                725                 730                 735
Ser Val Arg Thr Asn Ala Ser Ser Arg Met Thr Glu Ser Glu Ile Gln
            740                 745                 750
Ala Ser Ile Val Val Ala Tyr Ser Thr His Val Met His Val Leu His
        755                 760                 765
Ile Leu Leu Ala Asp Lys Trp Asp Pro Ile Asn Leu Leu Asp Asp Asp
    770                 775                 780
Asp Leu Trp Ile Ser Ser Glu Gly Phe Val Thr Ala Thr Ser His Ala
785                 790                 795                 800
Val Ser Ala Ala Glu Ala Ile Ser Gln Ile Leu Glu Phe Asp Pro Gly
                805                 810                 815
Leu Glu Phe Met Pro Phe Phe Tyr Gly Val Tyr Leu Leu Gln Gly Ser
            820                 825                 830
Phe Leu Leu Leu Leu Ile Ala Asp Lys Leu Gln Ala Glu Ala Ser Pro
```

```
        835                 840                 845
Ser Val Ile Lys Ala Cys Glu Thr Ile Val Arg Ala His Glu Ala Cys
    850                 855                 860
Val Val Thr Leu Ser Thr Glu Tyr Gln Arg Asn Phe Ser Lys Val Met
865                 870                 875                 880
Arg Ser Ala Leu Ala Leu Ile Arg Gly Arg Val Pro Glu Asp Leu Ala
                885                 890                 895
Glu Gln Gln Gln Arg Arg Arg Glu Leu Leu Ala Leu Tyr Arg Trp Thr
            900                 905                 910
Gly Asn Gly Thr Gly Leu Ala Leu
        915                 920


<210> 535
<211> 401
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 18, chitinase
      [Trichoderma reesei QM6a] 401 aa protein
      XP_006968673.1 GI:589113301

<400> 535
Met Leu Ser Arg Thr Leu Leu Thr Ala Leu Gly Leu Thr Thr Ile Ala
 1               5                  10                  15
Ala Ala Ala Pro Ser Gln Thr Val Lys Thr Arg Gln Ala Pro Gly Gly
            20                  25                  30
Gln Asn Ala Val Tyr Trp Gly Ala Thr Asn Asn Glu Asn Asp Asn Leu
        35                  40                  45
Ser Thr Tyr Cys Thr Ala Ser Ser Gly Ile Asp Ile Val Ile Leu Ser
    50                  55                  60
Phe Leu Asp Ile Tyr Gly Ala Thr Gly Asn Phe Pro Ser Gly Asn Met
65                  70                  75                  80
Gly Asn Ser Cys Tyr Val Gly Thr Asn Gly Val Pro Gln Leu Cys Asp
                85                  90                  95
Asp Leu Ala Ser Ser Ile Ala Thr Cys Gln Ala Ala Gly Ile Lys Val
            100                 105                 110
Ile Ile Ser Leu Gly Gly Ala Ala Ser Ser Tyr Ser Leu Gln Ser Gln
        115                 120                 125
Ser Gln Ala Val Ala Ile Gly Gln Tyr Leu Trp Asn Ala Tyr Gly Asn
    130                 135                 140
Ser Gly Asn Thr Thr Val Gln Arg Pro Phe Gly Asn Val Phe Val Asn
145                 150                 155                 160
Gly Phe Asp Phe Asp Ile Glu Leu Asn Ala Gly Ser Gln Tyr Tyr Gln
                165                 170                 175
Tyr Leu Ile Ser Thr Leu Arg Ser Asn Phe Ala Asn Asp Pro Lys Asn
            180                 185                 190
Thr Tyr Tyr Ile Thr Gly Ala Pro Gln Cys Pro Ile Pro Glu Pro Asn
        195                 200                 205
Met Gly Glu Ile Ile Ser Thr Ser Gln Phe Asp Tyr Leu Trp Val Gln
    210                 215                 220
Phe Tyr Asn Asn Asn Pro Val Cys Ser Leu Gly Leu Pro Gly Asp Ala
225                 230                 235                 240
```

```
Pro Phe Asn Phe Asn Asp Trp Val Ser Phe Ile Ser Thr Thr Pro Ser
                245                 250                 255
Lys Asn Ala Lys Leu Phe Val Gly Ala Pro Ala Ser Thr Leu Gly Ala
            260                 265                 270
Asn Gly Asn Ala Gly Gly Ala Lys Tyr Tyr Ala Thr Pro Glu Gln Leu
        275                 280                 285
Ala Gly Ile Val Asn Ser Val Lys Ser Ser Pro Phe Phe Gly Gly Ile
    290                 295                 300
Met Leu Trp Asp Ala Gly Tyr Ser Asp Ser Asn Val Asn Asn Gly Cys
305                 310                 315                 320
Asn Tyr Ala Gln Glu Ala Lys Asn Ile Leu Leu Thr Gly Thr Ala Cys
                325                 330                 335
Gly Gly Glu Ser Ser Pro Pro Pro Ser Thr Thr Thr Thr Ala Val Pro
            340                 345                 350
Pro Pro Ala Ser Ser Thr Pro Ser Asn Pro Ser Gly Gly Ser Val Pro
        355                 360                 365
Gln Trp Gly Gln Cys Gly Gly Asp Gly Tyr Thr Gly Pro Thr Gln Cys
    370                 375                 380
Val Ala Pro Tyr Lys Cys Val Ala Thr Ser Glu Trp Trp Ser Ser Cys
385                 390                 395                 400
Gln
```

<210> 536
<211> 223
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 11 [Trichoderma reesei QM6a] 223 aa protein XP_006968947.1 GI:589113849

<400> 536

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

145 150 155 160
Ile Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn
165 170 175
His Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp
180 185 190
Ala Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala
195 200 205
Val Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
210 215 220

<210> 537
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 5 [Trichoderma reesei QM6a]
473 aa protein XP_006969226.1 GI:589114407

<400> 537
Met Lys Ser Ser Ile Ser Val Val Leu Ala Leu Leu Gly His Ser Ala
1 5 10 15
Ala Trp Ser Tyr Ala Thr Lys Ser Gln Tyr Arg Ala Asn Ile Lys Ile
20 25 30
Asn Ala Arg Gln Thr Tyr Gln Thr Met Ile Gly Gly Gly Cys Ser Gly
35 40 45
Ala Phe Gly Ile Ala Cys Gln Gln Phe Gly Ser Ser Gly Leu Ser Pro
50 55 60
Glu Asn Gln Gln Lys Val Thr Gln Ile Leu Phe Asp Glu Asn Ile Gly
65 70 75 80
Gly Leu Ser Ile Val Arg Asn Asp Ile Gly Ser Ser Pro Gly Thr Thr
85 90 95
Ile Leu Pro Thr Cys Pro Ala Thr Pro Gln Asp Lys Phe Asp Tyr Val
100 105 110
Trp Asp Gly Ser Asp Asn Cys Gln Phe Asn Leu Thr Lys Thr Ala Leu
115 120 125
Lys Tyr Asn Pro Asn Leu Tyr Val Tyr Ala Asp Ala Trp Ser Ala Pro
130 135 140
Gly Cys Met Lys Thr Val Gly Thr Glu Asn Leu Gly Gly Gln Ile Cys
145 150 155 160
Gly Val Arg Gly Thr Asp Cys Lys His Asp Trp Arg Gln Ala Tyr Ala
165 170 175
Asp Tyr Leu Val Gln Tyr Val Arg Phe Tyr Lys Glu Glu Gly Ile Asp
180 185 190
Ile Ser Leu Leu Gly Ala Trp Asn Glu Pro Asp Phe Asn Pro Phe Thr
195 200 205
Tyr Glu Ser Met Leu Ser Asp Gly Tyr Gln Ala Lys Asp Phe Leu Glu
210 215 220
Val Leu Tyr Pro Thr Leu Lys Lys Ala Phe Pro Lys Val Asp Val Ser
225 230 235 240
Cys Cys Asp Ala Thr Gly Ala Arg Gln Glu Arg Asn Ile Leu Tyr Glu
245 250 255
Leu Gln Gln Ala Gly Gly Glu Arg Tyr Phe Asp Ile Ala Thr Trp His

```
            260                 265                 270
Asn Tyr Gln Ser Asn Pro Glu Arg Pro Phe Asn Ala Gly Gly Lys Pro
        275                 280                 285
Asn Ile Gln Thr Glu Trp Ala Asp Gly Thr Gly Pro Trp Asn Ser Thr
    290                 295                 300
Trp Asp Tyr Ser Gly Gln Leu Ala Glu Gly Leu Gln Trp Ala Leu Tyr
305                 310                 315                 320
Met His Asn Ala Phe Val Asn Ser Asp Thr Ser Gly Tyr Thr His Trp
                325                 330                 335
Trp Cys Ala Gln Asn Thr Asn Gly Asp Asn Ala Leu Ile Arg Leu Asp
            340                 345                 350
Arg Asp Ser Tyr Glu Val Ser Ala Arg Leu Trp Ala Phe Ala Gln Tyr
        355                 360                 365
Phe Arg Phe Ala Arg Pro Gly Ser Val Arg Ile Gly Ala Thr Ser Asp
    370                 375                 380
Val Glu Asn Val Tyr Val Thr Ala Tyr Val Asn Lys Asn Gly Thr Val
385                 390                 395                 400
Ala Ile Pro Val Ile Asn Ala Ala His Phe Pro Tyr Asp Leu Thr Ile
                405                 410                 415
Asp Leu Glu Gly Ile Lys Lys Arg Lys Leu Ser Glu Tyr Leu Thr Asp
            420                 425                 430
Asn Ser His Asn Val Thr Leu Gln Ser Arg Tyr Lys Val Ser Gly Ser
        435                 440                 445
Ser Leu Lys Val Thr Val Glu Pro Arg Ala Met Lys Thr Phe Trp Leu
    450                 455                 460
Glu Pro Gln Ser Thr Phe Ala Val Ile
465                 470
```

<210> 538
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 18, chitinase
[Trichoderma reesei QM6a] 411 aa protein
XP_0069693971. GI:589114749

<400> 538

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

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

<210> 539
<211> 302
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Crystal Structure Of An
Endo-beta-1,4-xylanase (glycoside Hydrolase Family
10/gh10) Enzyme From Trichoderma Reesei 302 aa
protein 4XV0_A GI:756143139

<220>
<221> VARIANT
<222> 1

<223> Xaa = Any Amino Acid

<400> 539
Xaa Ala Ser Gln Ser Ile Asp Gln Leu Ile Lys Arg Lys Gly Lys Leu
 1               5                  10                  15
Tyr Phe Gly Thr Ala Thr Asp Arg Gly Leu Leu Gln Arg Glu Lys Asn
            20                  25                  30
Ala Ala Ile Ile Gln Ala Asp Leu Gly Gln Val Thr Pro Glu Asn Ser
        35                  40                  45
Met Lys Trp Gln Ser Leu Glu Asn Asn Gln Gly Gln Leu Asn Trp Gly
    50                  55                  60
Asp Ala Asp Tyr Leu Val Asn Phe Ala Gln Gln Asn Gly Lys Ser Ile
65                  70                  75                  80
Arg Gly His Thr Leu Ile Trp His Ser Gln Leu Pro Ala Trp Val Asn
                85                  90                  95
Asn Ile Asn Asn Ala Asp Thr Leu Arg Gln Val Ile Arg Thr His Val
            100                 105                 110
Ser Thr Val Val Gly Arg Tyr Lys Gly Lys Ile Arg Ala Trp Asp Val
        115                 120                 125
Val Asn Glu Ile Phe Asn Glu Asp Gly Thr Leu Arg Ser Ser Val Phe
    130                 135                 140
Ser Arg Leu Leu Gly Glu Glu Phe Val Ser Ile Ala Phe Arg Ala Ala
145                 150                 155                 160
Arg Asp Ala Asp Pro Ser Ala Arg Leu Tyr Ile Asn Asp Tyr Asn Leu
                165                 170                 175
Asp Arg Ala Asn Tyr Gly Lys Val Asn Gly Leu Lys Thr Tyr Val Ser
            180                 185                 190
Lys Trp Ile Ser Gln Gly Val Pro Ile Asp Gly Ile Gly Ser Gln Ser
        195                 200                 205
His Leu Ser Gly Gly Gly Gly Ser Gly Thr Leu Gly Ala Leu Gln Gln
    210                 215                 220
Leu Ala Thr Val Pro Val Thr Glu Leu Ala Ile Thr Glu Leu Asp Ile
225                 230                 235                 240
Gln Gly Ala Pro Thr Thr Asp Tyr Thr Gln Val Val Gln Ala Cys Leu
                245                 250                 255
Ser Val Ser Lys Cys Val Gly Ile Thr Val Trp Gly Ile Ser Asp Lys
            260                 265                 270
Asp Ser Trp Arg Ala Ser Thr Asn Pro Leu Leu Phe Asp Ala Asn Phe
        275                 280                 285
Asn Pro Lys Pro Ala Tyr Asn Ser Ile Val Gly Ile Leu Gln
    290                 295                 300


<210> 540
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Endo-1,4-beta-xylanase G0R947.1 GI:1042851765

<400> 540
Met Val Ala Phe Ser Ser Leu Ile Cys Ala Leu Thr Ser Ile Ala Ser
 1               5                  10                  15

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

<210> 541
<211> 223
<212> PRT
<213> Artificial Sequence

<220>
<223> Endo-beta-1,4-xylanase 223 aa protein GRUP7.1
GI:142851766

<400> 541

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

```
Ser Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr
        115                 120                 125
Tyr Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp
    130                 135                 140
Gly Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser
145                 150                 155                 160
Ile Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn
                165                 170                 175
His Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp
            180                 185                 190
Ala Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala
        195                 200                 205
Val Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
    210                 215                 220


<210> 542
<211> 347
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Endo-1,4-beta-xylanase 3; Short=
      Xylanase 3; AltName: Full=1,4-beta-D-xylan
      xylanohydrolase 3; Flags: Precursor 347 aa protein
      G0RA32.1 GI:1042851767

<400> 542
Met Lys Ala Asn Val Ile Leu Cys Leu Leu Ala Pro Leu Val Ala Ala
 1               5                  10                  15
Leu Pro Thr Glu Thr Ile His Leu Asp Pro Glu Leu Ala Ala Leu Arg
            20                  25                  30
Ala Asn Leu Thr Glu Arg Thr Ala Asp Leu Trp Asp Arg Gln Ala Ser
        35                  40                  45
Gln Ser Ile Asp Gln Leu Ile Lys Arg Lys Gly Lys Leu Tyr Phe Gly
    50                  55                  60
Thr Ala Thr Asp Arg Gly Leu Leu Gln Arg Glu Lys Asn Ala Ala Ile
65                  70                  75                  80
Ile Gln Ala Asp Leu Gly Gln Val Thr Pro Glu Asn Ser Met Lys Trp
                85                  90                  95
Gln Ser Leu Glu Asn Asn Gln Gly Gln Leu Asn Trp Gly Asp Ala Asp
            100                 105                 110
Tyr Leu Val Asn Phe Ala Gln Gln Asn Gly Lys Ser Ile Arg Gly His
        115                 120                 125
Thr Leu Ile Trp His Ser Gln Leu Pro Ala Trp Val Asn Asn Ile Asn
    130                 135                 140
Asn Ala Asp Thr Leu Arg Gln Val Ile Arg Thr His Val Ser Thr Val
145                 150                 155                 160
Val Gly Arg Tyr Lys Gly Lys Ile Arg Ala Trp Asp Val Val Asn Glu
                165                 170                 175
Ile Phe Asn Glu Asp Gly Thr Leu Arg Ser Ser Val Phe Ser Arg Leu
            180                 185                 190
Leu Gly Glu Glu Phe Val Ser Ile Ala Phe Arg Ala Ala Arg Asp Ala
        195                 200                 205
```

```
Asp Pro Ser Ala Arg Leu Tyr Ile Asn Asp Tyr Asn Leu Asp Arg Ala
    210                 215                 220
Asn Tyr Gly Lys Val Asn Gly Leu Lys Thr Tyr Val Ser Lys Trp Ile
225                 230                 235                 240
Ser Gln Gly Val Pro Ile Asp Gly Ile Gly Ser Gln Ser His Leu Ser
                245                 250                 255
Gly Gly Gly Gly Ser Gly Thr Leu Gly Ala Leu Gln Gln Leu Ala Thr
            260                 265                 270
Val Pro Val Thr Glu Leu Ala Ile Thr Glu Leu Asp Ile Gln Gly Ala
        275                 280                 285
Pro Thr Thr Asp Tyr Thr Gln Val Val Gln Ala Cys Leu Ser Val Ser
    290                 295                 300
Lys Cys Val Gly Ile Thr Val Trp Gly Ile Ser Asp Lys Asp Ser Trp
305                 310                 315                 320
Arg Ala Ser Thr Asn Pro Leu Leu Phe Asp Ala Asn Phe Asn Pro Lys
                325                 330                 335
Pro Ala Tyr Asn Ser Ile Val Gly Ile Leu Gln
            340                 345
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<210> 543
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Endo-beta-1,4-xylanase: P36218.1 GI:549460

<400> 543

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

```
        195                 200                 205
Tyr Gln Val Val Ala Val Glu Gly Trp Gly Gly Ser Gly Ser Ala Ser
    210                 215                 220
Gln Ser Val Ser Asn
225
```

<210> 544
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> hypothetical protein M419DRAFT_104468 [Trichoderma reesei RUT C-30] 411 aa protein ETR97430.1 GI:572273844

<400> 544

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

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


<210> 545
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> endo beta-1,4-xylanase isotype 2 [Trichoderma
      reesei RUT C-30] 229 aa protein ETR98398.1
      GI:572274931

<400> 545
Met Val Ala Phe Ser Ser Leu Ile Cys Ala Leu Thr Ser Ile Ala Ser
 1               5                  10                  15
Thr Leu Ala Met Pro Thr Gly Leu Glu Pro Glu Ser Ser Val Asn Val
            20                  25                  30
Thr Glu Arg Gly Met Tyr Asp Phe Val Leu Gly Ala His Asn Asp His
        35                  40                  45
Arg Arg Arg Ala Ser Ile Asn Tyr Asp Gln Asn Tyr Gln Thr Gly Gly
    50                  55                  60
Gln Val Ser Tyr Ser Pro Ser Asn Thr Gly Phe Ser Val Asn Trp Asn
65                  70                  75                  80
Thr Gln Asp Asp Phe Val Val Gly Val Gly Trp Thr Thr Gly Ser Ser
                85                  90                  95
Ala Pro Ile Asn Phe Gly Gly Ser Phe Ser Val Asn Ser Gly Thr Gly
            100                 105                 110
Leu Leu Ser Val Tyr Gly Trp Ser Thr Asn Pro Leu Val Glu Tyr Tyr
        115                 120                 125
Ile Met Glu Asp Asn His Asn Tyr Pro Ala Gln Gly Thr Val Lys Gly
    130                 135                 140
Thr Val Thr Ser Asp Gly Ala Thr Tyr Thr Ile Trp Glu Asn Thr Arg
145                 150                 155                 160
Val Asn Glu Pro Ser Ile Gln Gly Thr Ala Thr Phe Asn Gln Tyr Ile
                165                 170                 175
Ser Val Arg Asn Ser Pro Arg Thr Ser Gly Thr Val Thr Val Gln Asn
            180                 185                 190
His Phe Asn Ala Trp Ala Ser Leu Gly Leu His Leu Gly Gln Met Asn
```

```
        195                 200                 205
Tyr Gln Val Val Ala Val Glu Gly Trp Gly Gly Ser Gly Ser Ala Ser
    210                 215                 220
Gln Ser Val Ser Asn
225
```

<210> 546
<211> 401
<212> PRT
<213> Artificial Sequence

<220>
<223> hypothetical protein M419DRAFT_114979 [Trichoderma reesei RUT C-30] 401 aa protein ETR98463.1 GI:572274996

<400> 546

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

```
Leu Pro Asn Ile Gly Gly Ile Met Leu Trp Glu Ala Gln Leu Ala Val
    290                 295                 300
Lys Asn Gly Asn Phe Gln Lys Thr Val Lys Ala Gly Ile Ala Ser Gly
305                 310                 315                 320
Thr Thr Pro Pro Pro Pro Pro Pro Thr Gly Gly Cys Ser Trp Ala Gly
                325                 330                 335
His Cys Ala Gly Ala Ser Cys Ser Thr Asp Asn Asp Cys Ser Asp Asp
            340                 345                 350
Leu Thr Cys Asn Gly Gly Val Cys Gly Thr Ala Gly Ser Thr Pro Ala
        355                 360                 365
Pro Thr Cys Ser Trp Glu Gly His Cys Leu Gly Ala Ser Cys Gly Asn
    370                 375                 380
Asp Asn Asp Cys Ser Asp Pro Tyr Ser Cys Lys Asn Gly Val Cys Ser
385                 390                 395                 400
Asn
```

<210> 547
<211> 401
<212> PRT
<213> Artificial Sequence

<220>
<223> hypothetical protein M419DRAFT_133349 [Trichoderma reesei RUT C-30] 401 aa protein ETR98658.1 GI:572275208

<400> 547

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

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

<210> 548
<211> 827
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase [Trichoderma reesei RUT C-30]
      827 aa protein ETS00190.1 GI:572276883

<400> 548

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

```
        115                 120                 125
Asn Ala Phe Gly Pro Tyr Asn Ala Ser Tyr Thr Gly Pro Arg Pro Phe
    130                 135                 140
Asp Asp Ile Thr Thr Gly Leu Pro Thr Ser Val Asp Gly Phe Asp Phe
145                 150                 155                 160
Asp Ile Glu Ala Asp Phe Pro Asn Gly Pro Tyr Ile Lys Met Ile Glu
                165                 170                 175
Thr Phe Arg Ser Leu Asp Ser Ser Met Leu Ile Thr Gly Ala Pro Gln
            180                 185                 190
Cys Pro Thr Asn Pro Gln Tyr Phe Val Met Lys Asp Met Ile Gln Gln
        195                 200                 205
Ala Ala Phe Asp Lys Leu Phe Ile Gln Phe Tyr Asn Asn Pro Val Cys
    210                 215                 220
Asp Ala Ile Pro Gly Asn Thr Ala Gly Asp Lys Phe Asn Tyr Asp Asp
225                 230                 235                 240
Trp Glu Ala Val Ile Ala Gly Ser Ala Lys Ser Lys Ser Ala Lys Leu
                245                 250                 255
Tyr Ile Gly Leu Pro Ala Ile Gln Glu Pro Asn Glu Ser Gly Tyr Ile
            260                 265                 270
Asp Pro Ile Ala Met Lys Asn Leu Val Cys Gln Tyr Lys Asp Arg Pro
        275                 280                 285
His Phe Gly Gly Leu Ser Leu Trp Asp Leu Ser Arg Gly Leu Val Asn
    290                 295                 300
Asn Ile Asn Gly Thr Ser Phe Asn Gln Trp Ala Leu Asp Ala Leu Gln
305                 310                 315                 320
Tyr Gly Cys Asn Pro Ile Pro Thr Thr Thr Thr Thr Thr Ser Thr Ala
                325                 330                 335
Ser Ser Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser
            340                 345                 350
Lys Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser Thr
        355                 360                 365
Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala
    370                 375                 380
Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser
385                 390                 395                 400
Lys Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys Val Ser Thr
                405                 410                 415
Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala
            420                 425                 430
Ser Ser Thr Ser Lys Val Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser
        435                 440                 445
Lys Val Ser Ala Lys Ala Thr Thr Ser Thr Lys Ala Ser Thr Thr Val
    450                 455                 460
Lys Pro Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser Thr
465                 470                 475                 480
Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala
                485                 490                 495
Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser Lys Ala Ser Thr Thr Ser
            500                 505                 510
Lys Ala Ala Thr Thr Ser Val Lys Pro Thr Ser Lys Thr Ser Thr Ser
        515                 520                 525
Ser Lys Pro Asn Val Ser Ala Ser Ser Ser Asn Val Gly Arg Asp Ala
    530                 535                 540
Thr Ser Leu Val Glu Ala Ser Thr Ser Thr Ser Ala Ala Val Leu Tyr
```

```
545                 550                 555                 560
Pro Thr Thr Thr Ser Arg Trp Ser Asn Ser Thr Ile Thr Arg Ser Ser
                565                 570                 575
Ser Leu Thr Thr Pro Ile Val Ser Asp Pro Ala Ser Leu Thr Thr Ser
            580                 585                 590
Val Val Tyr Thr Thr Ser Val His Thr Val Thr Lys Cys Pro Ala Tyr
        595                 600                 605
Val Thr Asp Cys Pro Ala Gly Gly Tyr Val Thr Thr Glu Thr Ile Pro
    610                 615                 620
Leu Tyr Thr Thr Val Cys Pro Ile Ser Glu Ala Thr Gln Thr Ala Ala
625                 630                 635                 640
Pro Thr Val Thr Thr Glu Ala Pro Gln Pro Trp Thr Thr Ser Thr Val
                645                 650                 655
Tyr Thr Thr Arg Val Tyr Thr Ile Thr Ser Cys Ala Pro Gly Val Val
            660                 665                 670
Asp Cys Pro Ala Asn Gln Val Thr Thr Glu Thr Ile Pro Trp Tyr Thr
        675                 680                 685
Thr Val Cys Pro Val Thr Ala Thr Ala Thr Pro Val Gly Pro Gly Ser
    690                 695                 700
Val Val Phe Pro Gln Asn Thr Glu Val Gly Gln Pro Ser Leu Val Gly
705                 710                 715                 720
Pro Val Val Glu Ala Ala Tyr Pro Thr Ala Ser Ser Ser Leu Gln Thr
                725                 730                 735
Leu Val Lys Pro Ala Thr Ser Val Gly Val Pro Gln Gly Ser Pro Ala
            740                 745                 750
Gly Ser Ser Val Ala Pro Gly Ser Ser Ser Lys Pro Thr Ala Pro Ala
        755                 760                 765
Gly Pro Pro Ser Tyr Pro Thr Gly Gly Ser Gly Asn Ala Ser Pro Ser
    770                 775                 780
Gly Ser Trp Ser Gly Val Pro Val Gly Pro Ser Ser Val Pro Gly Ile
785                 790                 795                 800
Pro Glu Ala Asn Ala Ala Ser Val Met Ser Ala Ser Leu Phe Gly Leu
                805                 810                 815
Val Ile Val Met Ala Ala Gln Val Phe Val Leu
            820                 825


<210> 549
<211> 920
<212> PRT
<213> Artificial Sequence

<220>
<223> xylanase regulator 1 [Trichoderma reesei RUT C-30]
      920 aa protein ETS02023.1 GI:572278872

<400> 549
Met Leu Ser Asn Pro Leu Arg Arg Tyr Ser Ala Tyr Pro Asp Ile Ser
 1               5                  10                  15
Ser Ala Ser Phe Asp Pro Asn Tyr His Gly Ser Gln Ser His Leu His
            20                  25                  30
Ser Ile Asn Val Asn Thr Phe Gly Asn Ser His Pro Tyr Pro Met Gln
        35                  40                  45
His Leu Ala Gln His Ala Glu Leu Ser Ser Ser Arg Met Ile Arg Ala
```

```
    50                  55                  60
Ser Pro Val Gln Pro Lys Gln Arg Gln Gly Ser Leu Ile Ala Ala Arg
65                  70                  75                  80
Lys Asn Ser Thr Gly Thr Ala Gly Pro Ile Arg Arg Arg Ile Ser Arg
                85                  90                  95
Ala Cys Asp Gln Cys Asn Gln Leu Arg Thr Lys Cys Asp Gly Leu His
            100                 105                 110
Pro Cys Ala His Cys Ile Glu Phe Gly Leu Gly Cys Glu Tyr Val Arg
        115                 120                 125
Glu Arg Lys Lys Arg Gly Lys Ala Ser Arg Lys Asp Ile Ala Ala Gln
    130                 135                 140
Gln Ala Ala Ala Ala Ala Ala Gln His Ser Gly Gln Val Gln Asp Gly
145                 150                 155                 160
Pro Glu Asp Gln His Arg Lys Leu Ser Arg Gln Gln Ser Glu Ser Ser
                165                 170                 175
Arg Gly Ser Ala Glu Leu Ala Gln Pro Ala His Asp Pro Pro His Gly
            180                 185                 190
His Ile Glu Gly Ser Val Ser Ser Phe Ser Asp Asn Gly Leu Ser Gln
        195                 200                 205
His Ala Ala Met Gly Gly Met Asp Gly Leu Glu Asp His His Gly His
    210                 215                 220
Val Gly Val Asp Pro Ala Leu Gly Arg Thr Gln Leu Glu Ala Ser Ser
225                 230                 235                 240
Ala Met Gly Leu Gly Ala Tyr Gly Glu Val His Pro Gly Tyr Glu Ser
                245                 250                 255
Pro Gly Met Asn Gly His Val Met Val Pro Pro Ser Tyr Gly Ala Gln
            260                 265                 270
Thr Thr Met Ala Gly Tyr Ser Gly Ile Ser Tyr Ala Ala Gln Ala Pro
        275                 280                 285
Ser Pro Ala Thr Tyr Ser Ser Asp Gly Asn Phe Arg Leu Thr Gly His
    290                 295                 300
Ile His Asp Tyr Pro Leu Ala Asn Gly Ser Ser Pro Ser Trp Gly Gln
305                 310                 315                 320
Ser Asp Leu Arg Tyr Pro Val Leu Glu Pro Leu Leu Pro His Leu Gly
                325                 330                 335
Asn Ile Leu Pro Val Ser Leu Ala Cys Asp Leu Ile Asp Leu Tyr Phe
            340                 345                 350
Ser Ser Ser Ser Ser Ala Gln Met His Pro Met Ser Pro Tyr Val Leu
        355                 360                 365
Gly Phe Val Phe Arg Lys Arg Ser Phe Leu His Pro Thr Asn Pro Arg
    370                 375                 380
Arg Cys Gln Pro Ala Leu Leu Ala Ser Met Leu Trp Val Ala Ala Gln
385                 390                 395                 400
Thr Ser Glu Ala Ser Phe Leu Thr Ser Leu Pro Ser Ala Arg Ser Lys
                405                 410                 415
Val Cys Gln Lys Leu Leu Glu Leu Thr Val Gly Leu Leu Gln Pro Leu
            420                 425                 430
Ile His Thr Gly Thr Asn Ser Pro Ser Pro Lys Thr Ser Pro Val Val
        435                 440                 445
Gly Ala Ala Ala Leu Gly Val Leu Gly Val Ala Met Pro Gly Ser Leu
    450                 455                 460
Asn Met Asp Ser Leu Ala Gly Glu Thr Gly Ala Phe Gly Ala Ile Gly
465                 470                 475                 480
Ser Leu Asp Asp Val Ile Thr Tyr Val His Leu Ala Thr Val Val Ser
```

```
                485                 490                 495
Ala Ser Glu Tyr Lys Gly Ala Ser Leu Arg Trp Trp Gly Ala Ala Trp
            500                 505                 510
Ser Leu Ala Arg Glu Leu Lys Leu Gly Arg Glu Leu Pro Pro Gly Asn
        515                 520                 525
Pro Pro Ala Asn Gln Glu Asp Gly Glu Gly Leu Ser Glu Asp Val Asp
    530                 535                 540
Glu His Asp Leu Asn Arg Asn Asn Thr Arg Phe Val Thr Glu Glu Glu
545                 550                 555                 560
Arg Glu Glu Arg Arg Arg Ala Trp Trp Leu Val Tyr Ile Val Asp Arg
                565                 570                 575
His Leu Ala Leu Cys Tyr Asn Arg Pro Leu Phe Leu Leu Asp Ser Glu
            580                 585                 590
Cys Ser Asp Leu Tyr His Pro Met Asp Asp Ile Lys Trp Gln Ala Gly
        595                 600                 605
Lys Phe Arg Ser His Asp Ala Gly Asn Ser Ser Ile Asn Ile Asp Ser
    610                 615                 620
Ser Met Thr Asp Glu Phe Gly Asp Ser Pro Arg Ala Ala Arg Gly Ala
625                 630                 635                 640
His Tyr Glu Cys Arg Gly Arg Ser Ile Phe Gly Tyr Phe Leu Ser Leu
                645                 650                 655
Met Thr Ile Leu Gly Glu Ile Val Asp Val His His Ala Lys Ser His
            660                 665                 670
Pro Arg Phe Gly Val Gly Phe Arg Ser Ala Arg Asp Trp Asp Glu Gln
        675                 680                 685
Val Ala Glu Ile Thr Arg His Leu Asp Met Tyr Glu Glu Ser Leu Lys
    690                 695                 700
Arg Phe Val Ala Lys His Leu Pro Leu Ser Ser Lys Asp Lys Glu Gln
705                 710                 715                 720
His Glu Met His Asp Ser Gly Ala Val Thr Asp Met Gln Ser Pro Leu
                725                 730                 735
Ser Val Arg Thr Asn Ala Ser Ser Arg Met Thr Glu Ser Glu Ile Gln
            740                 745                 750
Ala Ser Ile Val Val Ala Tyr Ser Thr His Val Met His Val Leu His
        755                 760                 765
Ile Leu Leu Ala Asp Lys Trp Asp Pro Ile Asn Leu Leu Asp Asp Asp
    770                 775                 780
Asp Leu Trp Ile Ser Ser Glu Gly Phe Val Thr Ala Thr Ser His Ala
785                 790                 795                 800
Val Ser Ala Ala Glu Ala Ile Ser Gln Ile Leu Glu Phe Asp Pro Gly
                805                 810                 815
Leu Glu Phe Met Pro Phe Phe Tyr Gly Val Tyr Leu Leu Gln Gly Ser
            820                 825                 830
Phe Leu Leu Leu Leu Ile Ala Asp Lys Leu Gln Ala Glu Ala Ser Pro
        835                 840                 845
Ser Val Ile Lys Ala Cys Glu Thr Ile Val Arg Ala His Glu Ala Cys
    850                 855                 860
Val Val Thr Leu Ser Thr Glu Tyr Gln Arg Asn Phe Ser Lys Val Met
865                 870                 875                 880
Arg Ser Ala Leu Ala Leu Ile Arg Gly Arg Val Pro Glu Asp Leu Ala
                885                 890                 895
Glu Gln Gln Gln Arg Arg Arg Glu Leu Leu Ala Leu Tyr Arg Trp Thr
            900                 905                 910
Gly Asn Gly Thr Gly Leu Ala Leu
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915 920

<210> 550
<211> 267
<212> PRT
<213> Artificial Sequence

<220>
<223> SGNH hydrolase [Trichoderma reesei RUT C-30] 267
aa protein ETS03411.1 GI:572280314

<400> 550
Met Leu Leu Val Gln Val Arg Pro Ser Ser Ser Pro Ala Ile Asp Leu
1 5 10 15
Ile Arg Gly Thr Glu Leu Arg Ile Leu Pro Val Gly Asp Ser Ile Thr
20 25 30
Tyr Gly Phe Leu Ser Asp Gln Asp Gly Gly Asp Gly Asn Gly Tyr Arg
35 40 45
Leu Gln Leu Arg Gln His Leu Ser Lys Asp Arg Val Val Phe Ala Gly
50 55 60
Thr Glu Thr Ser Gly Asn Met Thr Asp Gly Tyr Tyr Ala Ala Trp Asn
65 70 75 80
Gly Lys Thr Ile Gln Tyr Ile Ser Asp His Val Thr Pro Ser Leu Glu
85 90 95
Gln Arg Pro Asn Ile Ile Leu Leu His Ala Gly Thr Asn Asp Met Asn
100 105 110
Pro Asn Gly Ala Ile Ser Arg Glu Gly His Asp Pro Val Ala Ala Ser
115 120 125
Glu Arg Leu Gly Ser Leu Val Asp Lys Met Thr Thr Leu Cys Pro Asp
130 135 140
Ala Val Ile Leu Val Ala Met Ile Ile Gly Thr Cys Asn Asp Glu Gln
145 150 155 160
Ala Pro Gln Thr Lys Val Phe Gln Ser Leu Ile Pro Asn Val Val Ala
165 170 175
Pro Arg Leu Glu Ser Gly Lys His Val Leu Ala Val Asp Phe Ser Thr
180 185 190
Phe Pro Leu Asp Lys Leu Arg Asp Cys Ile His Pro Thr Asn Glu Gly
195 200 205
Tyr His Leu Leu Gly Tyr Tyr Trp Tyr Asp Phe Ile Ala Gln Ile Pro
210 215 220
Arg Asp Trp Ile Thr Ala Pro Val Gly Glu Asp Pro Gln Arg Pro Glu
225 230 235 240
Glu Gln Asn Leu Ala Met Arg Leu Glu Thr Asp Leu Leu Leu Leu Gly
245 250 255
Leu Leu Gly Leu Leu Val Val Leu Met Tyr Ala
260 265

<210> 551
<211> 347
<212> PRT
<213> Artificial Sequence

<220>
<223> xylanase III [Trichoderma reesei RUT C-30] 347 aa
protein ETS05245.1 GI:572282231

<400> 551
Met Lys Ala Asn Val Ile Leu Cys Leu Leu Ala Pro Leu Val Ala Ala
 1               5                  10                  15
Leu Pro Thr Glu Thr Ile His Leu Asp Pro Glu Leu Ala Ala Leu Arg
            20                  25                  30
Ala Asn Leu Thr Glu Arg Thr Ala Asp Leu Trp Asp Arg Gln Ala Ser
        35                  40                  45
Gln Ser Ile Asp Gln Leu Ile Lys Arg Lys Gly Lys Leu Tyr Phe Gly
    50                  55                  60
Thr Ala Thr Asp Arg Gly Leu Leu Gln Arg Glu Lys Asn Ala Ala Ile
65                  70                  75                  80
Ile Gln Ala Asp Leu Gly Gln Val Thr Pro Glu Asn Ser Met Lys Trp
                85                  90                  95
Gln Ser Leu Glu Asn Asn Gln Gly Gln Leu Asn Trp Gly Asp Ala Asp
            100                 105                 110
Tyr Leu Val Asn Phe Ala Gln Gln Asn Gly Lys Ser Ile Arg Gly His
        115                 120                 125
Thr Leu Ile Trp His Ser Gln Leu Pro Ala Trp Val Asn Asn Ile Asn
    130                 135                 140
Asn Ala Asp Thr Leu Arg Gln Val Ile Arg Thr His Val Ser Thr Val
145                 150                 155                 160
Val Gly Arg Tyr Lys Gly Lys Ile Arg Ala Trp Asp Val Val Asn Glu
                165                 170                 175
Ile Phe Asn Glu Asp Gly Thr Leu Arg Ser Ser Val Phe Ser Arg Leu
            180                 185                 190
Leu Gly Glu Glu Phe Val Ser Ile Ala Phe Arg Ala Ala Arg Asp Ala
        195                 200                 205
Asp Pro Ser Ala Arg Leu Tyr Ile Asn Asp Tyr Asn Leu Asp Arg Ala
    210                 215                 220
Asn Tyr Gly Lys Val Asn Gly Leu Lys Thr Tyr Val Ser Lys Trp Ile
225                 230                 235                 240
Ser Gln Gly Val Pro Ile Asp Gly Ile Gly Ser Gln Ser His Leu Ser
                245                 250                 255
Gly Gly Gly Gly Ser Gly Thr Leu Gly Ala Leu Gln Gln Leu Ala Thr
            260                 265                 270
Val Pro Val Thr Glu Leu Ala Ile Thr Glu Leu Asp Ile Gln Gly Ala
        275                 280                 285
Pro Thr Thr Asp Tyr Thr Gln Val Val Gln Ala Cys Leu Ser Val Ser
    290                 295                 300
Lys Cys Val Gly Ile Thr Val Trp Gly Ile Ser Asp Lys Asp Ser Trp
305                 310                 315                 320
Arg Ala Ser Thr Asn Pro Leu Leu Phe Asp Ala Asn Phe Asn Pro Lys
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Pro Ala Tyr Asn Ser Ile Val Gly Ile Leu Gln
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GI:572283462

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

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P36217.2 GI:1042782319

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


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Short=Xylanase 3; AltName: Full=1,4-beta-D-xylan
xylanohydrolase 3; Flags: Precursor 347 aa protein
A0A024SIB3.1 GI:1042851768

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Met Lys Ala Asn Val Ile Leu Cys Leu Leu Ala Pro Leu Val Ala Ala
 1               5                  10                  15
Leu Pro Thr Glu Thr Ile His Leu Asp Pro Glu Leu Ala Ala Leu Arg
            20                  25                  30

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Ala Asn Leu Thr Glu Arg Thr Ala Asp Leu Trp Asp Arg Gln Ala Ser
        35                  40                  45
Gln Ser Ile Asp Gln Leu Ile Lys Arg Lys Gly Lys Leu Tyr Phe Gly
    50                  55                  60
Thr Ala Thr Asp Arg Gly Leu Leu Gln Arg Glu Lys Asn Ala Ala Ile
65                  70                  75                  80
Ile Gln Ala Asp Leu Gly Gln Val Thr Pro Glu Asn Ser Met Lys Trp
                85                  90                  95
Gln Ser Leu Glu Asn Asn Gln Gly Gln Leu Asn Trp Gly Asp Ala Asp
            100                 105                 110
Tyr Leu Val Asn Phe Ala Gln Gln Asn Gly Lys Ser Ile Arg Gly His
        115                 120                 125
Thr Leu Ile Trp His Ser Gln Leu Pro Ala Trp Val Asn Asn Ile Asn
    130                 135                 140
Asn Ala Asp Thr Leu Arg Gln Val Ile Arg Thr His Val Ser Thr Val
145                 150                 155                 160
Val Gly Arg Tyr Lys Gly Lys Ile Arg Ala Trp Asp Val Val Asn Glu
                165                 170                 175
Ile Phe Asn Glu Asp Gly Thr Leu Arg Ser Ser Val Phe Ser Arg Leu
            180                 185                 190
Leu Gly Glu Glu Phe Val Ser Ile Ala Phe Arg Ala Ala Arg Asp Ala
        195                 200                 205
Asp Pro Ser Ala Arg Leu Tyr Ile Asn Asp Tyr Asn Leu Asp Arg Ala
    210                 215                 220
Asn Tyr Gly Lys Val Asn Gly Leu Lys Thr Tyr Val Ser Lys Trp Ile
225                 230                 235                 240
Ser Gln Gly Val Pro Ile Asp Gly Ile Gly Ser Gln Ser His Leu Ser
                245                 250                 255
Gly Gly Gly Gly Ser Gly Thr Leu Gly Ala Leu Gln Gln Leu Ala Thr
            260                 265                 270
Val Pro Val Thr Glu Leu Ala Ile Thr Glu Leu Asp Ile Gln Gly Ala
        275                 280                 285
Pro Thr Thr Asp Tyr Thr Gln Val Val Gln Ala Cys Leu Ser Val Ser
    290                 295                 300
Lys Cys Val Gly Ile Thr Val Trp Gly Ile Ser Asp Lys Asp Ser Trp
305                 310                 315                 320
Arg Ala Ser Thr Asn Pro Leu Leu Phe Asp Ala Asn Phe Asn Pro Lys
                325                 330                 335
Pro Ala Tyr Asn Ser Ile Val Gly Ile Leu Gln
            340                 345
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      aa protein DAA5861.1 GI:1232265

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

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                245                 250                 255
Phe Ile Gly Ala Leu Ala Ser Gly Ala Asp Gly Asp Gln Gly Tyr Val
            260                 265                 270
Ser Ala Ser Ser Leu Leu Ser Ala Tyr Gln Gly Val Ser Ala Leu Asn
        275                 280                 285
Leu Pro Asn Ile Gly Gly Ile Met Leu Trp Glu Ala Gln Leu Ala Val
    290                 295                 300
Lys Asn Gly Asn Phe Gln Lys Thr Val Lys Ala Gly Ile Ala Ser Gly
305                 310                 315                 320
Thr Thr Pro Pro Pro Pro Pro Pro Thr Gly Gly Cys Ser Trp Ala Gly
                325                 330                 335
His Cys Ala Gly Ala Ser Cys Ser Thr Asp Asn Asp Cys Ser Asp Asp
            340                 345                 350
Leu Thr Cys Asn Gly Gly Val Cys Gly Thr Ala Gly Ser Thr Pro Ala
        355                 360                 365
Pro Thr Cys Ser Trp Glu Gly His Cys Leu Gly Ala Ser Cys Gly Asn
    370                 375                 380
Asp Asn Asp Cys Ser Asp Pro Tyr Ser Cys Lys Asn Gly Val Cys Ser
385                 390                 395                 400
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Short=Xylanase 3; AltName: Full=1,4-beta-D-xylan
xylanohydrolase 3; Flags: Precursor 347 aa protein

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


<210> 678
<211> 994
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-galactosidase [Aspergillus niger] 994 aa
      protein AOV94178.1 GI:1078570522

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Met Lys Leu Gln Ser Ile Leu Ser Cys Trp Ala Ile Leu Val Ala Gln
 1               5                  10                  15
Ile Trp Ala Thr Thr Asp Gly Leu Thr Asp Leu Val Ala Trp Asp Pro
            20                  25                  30
Tyr Ser Leu Thr Val Asn Gly Asn Arg Leu Phe Val Tyr Ser Gly Glu
        35                  40                  45
Phe His Tyr Pro Arg Leu Pro Val Pro Glu Met Trp Leu Asp Val Phe
    50                  55                  60
Gln Lys Met Arg Ala His Gly Phe Asn Ala Val Ser Leu Tyr Phe Phe
65                  70                  75                  80
Trp Asp Tyr His Ser Pro Ile Asn Gly Thr Tyr Asp Phe Glu Thr Gly
                85                  90                  95
Ala His Asn Ile Gln Arg Leu Phe Asp Tyr Ala Gln Glu Ala Gly Ile
            100                 105                 110
Tyr Ile Ile Ala Arg Ala Gly Pro Tyr Cys Asn Ala Glu Phe Asn Gly
        115                 120                 125
Gly Gly Leu Ala Leu Tyr Leu Ser Asp Gly Ser Gly Gly Glu Leu Arg
    130                 135                 140
Thr Ser Asp Ala Thr Tyr His Gln Ala Trp Thr Pro Trp Ile Glu Arg
145                 150                 155                 160
Ile Gly Lys Ile Ile Ala Glu Asn Ser Ile Thr Asn Gly Gly Pro Val
                165                 170                 175
Ile Leu Asn Gln Ile Glu Asn Glu Leu Gln Glu Thr Thr His Ser Ala
            180                 185                 190
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Ser Asn Thr Leu Val Glu Tyr Met Glu Gln Ile Glu Glu Ala Phe Arg
        195                 200                 205
Ala Ala Gly Val Asp Val Pro Phe Thr Ser Asn Glu Lys Gly Gln Arg
    210                 215                 220
Ser Arg Ser Trp Ser Thr Asp Tyr Glu Asp Val Gly Gly Ala Val Asn
225                 230                 235                 240
Val Tyr Gly Leu Asp Ser Tyr Pro Gly Gly Leu Ser Cys Thr Asn Pro
                245                 250                 255
Ser Thr Gly Phe Ser Val Leu Arg Asn Tyr Tyr Gln Trp Phe Gln Asn
            260                 265                 270
Thr Ser Tyr Thr Gln Pro Glu Tyr Leu Pro Glu Phe Glu Gly Gly Trp
        275                 280                 285
Phe Ser Ala Trp Gly Ala Asp Ser Phe Tyr Asp Gln Cys Thr Ser Glu
    290                 295                 300
Leu Ser Pro Gln Phe Ala Asp Val Tyr Tyr Lys Asn Ile Ile Gly Gln
305                 310                 315                 320
Arg Val Thr Leu Gln Asn Leu Tyr Met Leu Tyr Gly Gly Thr Asn Trp
                325                 330                 335
Gly His Leu Ala Ala Pro Val Val Tyr Thr Ser Tyr Asp Tyr Ser Ala
            340                 345                 350
Pro Leu Arg Glu Thr Arg Gln Ile Arg Asp Lys Leu Ser Gln Thr Lys
        355                 360                 365
Leu Val Gly Leu Phe Thr Arg Val Ser Ser Gly Leu Leu Gly Val Glu
    370                 375                 380
Met Glu Gly Asn Gly Thr Ser Tyr Thr Ser Thr Thr Ser Ala Tyr Thr
385                 390                 395                 400
Trp Val Leu Arg Asn Pro Asn Thr Thr Ala Gly Phe Tyr Val Val Gln
                405                 410                 415
Gln Asp Thr Thr Ser Ser Gln Thr Asp Ile Thr Phe Ser Leu Asn Val
            420                 425                 430
Asn Thr Ser Ala Gly Ala Phe Thr Leu Pro Asn Ile Asn Leu Gln Gly
        435                 440                 445
Arg Gln Ser Lys Val Ile Ser Thr Asp Tyr Pro Leu Gly His Ser Thr
    450                 455                 460
Leu Leu Tyr Val Ser Thr Asp Ile Ala Thr Tyr Gly Thr Phe Gly Asp
465                 470                 475                 480
Thr Asp Val Val Val Leu Tyr Ala Arg Ser Gly Gln Glu Val Ser Phe
                485                 490                 495
Ser Phe Lys Asn Thr Thr Lys Leu Thr Phe Glu Glu Tyr Gly Asp Ser
            500                 505                 510
Val Asn Leu Thr Ser Ser Ser Gly Asn Arg Thr Ile Thr Ser Tyr Thr
        515                 520                 525
Tyr Thr Gln Gly Ser Gly Thr Ser Val Val Lys Phe Ser Asn Gly Ala
    530                 535                 540
Ile Phe Tyr Leu Val Glu Thr Glu Thr Ala Phe Arg Phe Trp Ala Pro
545                 550                 555                 560
Pro Thr Thr Thr Asp Pro Tyr Val Thr Ala Glu Gln Gln Ile Phe Val
                565                 570                 575
Leu Gly Pro Tyr Leu Val Arg Asn Val Ser Ile Ser Gly Ser Val Val
            580                 585                 590
Asp Leu Val Gly Asp Asn Asp Asn Ala Thr Thr Val Glu Val Phe Ala
        595                 600                 605
Gly Ser Ser Ala Lys Ala Val Lys Trp Asn Gly Lys Glu Ile Thr Val
    610                 615                 620
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Thr Lys Thr Asp Tyr Gly Ser Leu Val Gly Ser Ile Gly Gly Ala Asp
625                 630                 635                 640
Ser Ser Ser Ile Thr Ile Pro Ser Leu Thr Gly Trp Lys Val Arg Asp
                645                 650                 655
Ser Leu Pro Glu Ile Gln Ser Ser Tyr Asp Asp Ser Lys Trp Thr Val
            660                 665                 670
Cys Asn Lys Thr Thr Thr Leu Ser Pro Val Asp Pro Leu Ser Leu Pro
        675                 680                 685
Val Leu Phe Ala Ser Asp Tyr Gly Tyr Tyr Thr Gly Ile Lys Ile Tyr
    690                 695                 700
Arg Gly Arg Phe Asp Gly Thr Asn Val Thr Gly Ala Asn Leu Thr Ala
705                 710                 715                 720
Gln Gly Gly Leu Ala Phe Gly Trp Asn Val Trp Leu Asn Gly Asp Leu
                725                 730                 735
Val Ala Ser Leu Pro Gly Asp Ala Asp Glu Thr Ser Ser Asn Ala Ala
            740                 745                 750
Ile Asp Phe Ser Asn His Thr Leu Lys Gln Thr Asp Asn Leu Leu Thr
        755                 760                 765
Val Val Ile Asp Tyr Thr Gly His Asp Glu Thr Ser Thr Gly Asp Gly
    770                 775                 780
Val Glu Asn Pro Arg Gly Leu Leu Gly Ala Thr Leu Asn Gly Gly Ser
785                 790                 795                 800
Phe Thr Ser Trp Lys Ile Gln Gly Asn Ala Gly Gly Ala Ala Gly Ala
                805                 810                 815
Tyr Glu Leu Asp Pro Val Arg Ala Pro Met Asn Glu Gly Gly Leu Leu
            820                 825                 830
Ala Glu Arg Gln Gly Trp His Leu Pro Gly Tyr Lys Ala Lys Ser Ser
        835                 840                 845
Asp Gly Trp Thr Asp Gly Ser Pro Leu Asp Gly Leu Asn Lys Ser Gly
    850                 855                 860
Val Ala Phe Tyr Leu Thr Thr Phe Thr Leu Asp Leu Pro Lys Asn Tyr
865                 870                 875                 880
Asp Val Pro Leu Gly Ile Gln Phe Thr Ser Pro Ser Thr Val Asp Pro
                885                 890                 895
Val Arg Ile Gln Leu Phe Ile Asn Gly Tyr Gln Tyr Gly Lys Tyr Val
            900                 905                 910
Pro Tyr Leu Gly Pro Gln Thr Thr Phe Pro Ile Pro Pro Gly Ile Ile
        915                 920                 925
Asn Asn Arg Asp Lys Asn Thr Ile Gly Leu Ser Leu Trp Ala Gln Thr
    930                 935                 940
Asp Ala Gly Ala Lys Leu Glu Asn Ile Glu Leu Ile Ser Tyr Gly Ala
945                 950                 955                 960
Tyr Glu Ser Gly Phe Asp Ala Gly Asn Gly Thr Gly Phe Asp Leu Asn
                965                 970                 975
Gly Ala Lys Leu Gly Tyr Gln Pro Glu Trp Thr Glu Ala Arg Ala Lys
            980                 985                 990
Tyr Thr
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<212> PRT
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protein AOV94179.1 GI:1078570524

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

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Ser Lys Tyr Tyr Glu Thr Lys Leu Leu Ser Leu Phe Thr Arg Ser Ala
385                 390                 395                 400
Arg Asp Leu Thr Met Thr Asp Leu Ile Gly Asn Gly Thr Gln Tyr Thr
                405                 410                 415
Asn Asn Thr Ala Val Lys Ala Tyr Glu Leu Arg Asn Pro Thr Thr Asn
            420                 425                 430
Ala Gly Phe Tyr Val Thr Leu His Glu Asp Ser Thr Val Gly Thr Asn
        435                 440                 445
Glu Ala Phe Asn Leu Arg Val Asn Thr Ser Ala Gly Asn Leu Ile Val
    450                 455                 460
Pro Arg Arg Gly Gly Ser Ile Arg Leu Asn Gly His Gln Ser Lys Ile
465                 470                 475                 480
Ile Val Thr Asp Phe Thr Phe Gly Ser Glu Thr Leu Leu Tyr Ser Thr
                485                 490                 495
Ala Glu Val Leu Thr Tyr Ala Val Ile Asp Lys Lys Pro Thr Leu Val
            500                 505                 510
Leu Trp Val Pro Thr Gly Glu Ser Gly Glu Phe Ala Val Lys Gly Ala
        515                 520                 525
Lys Ser Gly Ser Val Val Ser Lys Cys Gln Ser Cys Pro Ala Ile Asn
    530                 535                 540
Phe His Gln Gln Gly Gly Asn Leu Ile Val Gly Phe Thr Gln Phe Gln
545                 550                 555                 560
Gly Met Ser Val Val Gln Ile Asp Asn Asp Ile Arg Val Val Leu Leu
                565                 570                 575
Asp Arg Thr Ala Ala Tyr Lys Phe Trp Ala Pro Ala Leu Thr Glu Asp
            580                 585                 590
Pro Leu Val Pro Glu Asp Glu Ala Val Leu Ile Gln Gly Pro Tyr Leu
        595                 600                 605
Val Arg Ser Ala Ser Leu Glu Lys Ser Thr Leu Ala Ile Lys Gly Asp
    610                 615                 620
Ser Ile Asn Glu Thr Ala Val Glu Ile Phe Ala Pro Glu Asn Val Lys
625                 630                 635                 640
Thr Ile Thr Trp Asn Gly Lys Gln Leu Lys Thr Ser Lys Ser Ser Tyr
                645                 650                 655
Gly Ser Leu Lys Ala Thr Ile Ala Ala Pro Ala Ser Ile Gln Leu Pro
            660                 665                 670
Ala Phe Thr Ser Trp Lys Val Asn Asp Ser Leu Pro Glu Arg Leu Pro
        675                 680                 685
Thr Tyr Asp Ala Ser Gly Pro Ala Trp Val Asp Ala Asn His Met Thr
    690                 695                 700
Thr Ala Asn Pro Ser Lys Pro Ala Thr Leu Pro Val Leu Tyr Ala Asp
705                 710                 715                 720
Glu Tyr Gly Phe His Asn Gly Val Arg Leu Trp Arg Gly Tyr Phe Asn
                725                 730                 735
Gly Thr Ala Ser Gly Val Phe Leu Asn Val Gln Gly Gly Ser Ala Phe
            740                 745                 750
Gly Phe Ser Ala Tyr Leu Asn Gly His Phe Leu Gly Ser Tyr Leu Gly
        755                 760                 765
Asn Ala Ser Ile Glu Gln Ala Asn Gln Thr Phe Leu Phe Pro Asn Asn
    770                 775                 780
Ile Thr His Pro Thr Thr Gln Asn Thr Leu Leu Val Ile His Asp Asp
785                 790                 795                 800
Thr Gly His Asp Glu Thr Thr Gly Ala Leu Asn Pro Arg Gly Ile Leu
                805                 810                 815
```

Glu Ala Arg Leu Leu Pro Ser Asp Thr Thr Asn Asn Ser Thr Ser Pro
820 825 830
Glu Phe Thr His Trp Arg Ile Ala Gly Thr Ala Gly Gly Glu Ser Asn
835 840 845
Leu Asp Pro Val Arg Gly Ala Trp Asn Glu Asp Gly Leu Tyr Ala Glu
850 855 860
Arg Val Gly Trp His Leu Pro Gly Phe Asp Asp Ser Thr Trp Ser Ser
865 870 875 880
Ala Ser Ser Ser Leu Ser Phe Thr Gly Ala Thr Val Lys Phe Phe Arg
885 890 895
Thr Thr Ile Pro Leu Asp Ile Pro Arg Gly Leu Asp Val Ser Ile Ser
900 905 910
Phe Val Leu Gly Thr Pro Asp Asn Ala Pro Asn Ala Tyr Arg Ala Gln
915 920 925
Leu Phe Val Asn Gly Tyr Gln Tyr Gly Arg Phe Asn Pro Tyr Ile Gly
930 935 940
Asn Gln Val Val Phe Pro Val Pro Val Gly Val Leu Asp Tyr Thr Gly
945 950 955 960
Glu Asn Thr Ile Gly Val Ala Val Trp Ala Gln Thr Glu Asp Gly Ala
965 970 975
Gly Ile Thr Val Asp Trp Lys Val Asn Tyr Val Ala Asp Ser Ser Leu
980 985 990
Asp Val Ser Gly Leu Glu Thr Gly Glu Leu Arg Pro Gly Trp Ser Ala
995 1000 1005
Glu Arg Leu Lys Phe Ala
1010

<210> 680
<211> 1030
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-galactosidase [Aspergillus niger] 1030 aa
protein AOV94180.1 GI:1078570526

<400> 680
Met Lys Thr Ser Phe Leu Leu Ala Ile Gly Leu Ala Val Glu Ala Cys
1 5 10 15
Leu Gly Leu Val Ser Ala Pro Asn Tyr Val Arg Gln Ile Asn Ala Thr
20 25 30
Asp Ser Ser Leu Gln Asp Ile Val Thr Trp Asp Glu Tyr Ser Ile Arg
35 40 45
Val Arg Gly Glu Arg Ile Leu Leu Leu Leu Gly Glu Phe His Pro Phe
50 55 60
Arg Leu Pro Cys Pro Gly Leu Trp Leu Asp Val Phe Gln Lys Val Arg
65 70 75 80
Ala Leu Gly Phe Ser Ala Val Ser Phe Tyr Val Asp Trp Ala Leu Leu
85 90 95
Glu Gly Glu Arg Gly Ser Ile Arg Ala Asp Gly Val Phe Ala Leu Glu
100 105 110
Glu Phe Phe Gln Ala Ala Thr Glu Ala Gly Leu Tyr Leu Thr Ala Arg
115 120 125

```
Pro Gly Pro Tyr Ile Asn Ala Glu Val Ser Gly Gly Gly Phe Pro Gly
    130                 135                 140
Trp Leu Lys Arg Val Gln Gly Arg Leu Lys Thr Thr Asp Gln Gly Tyr
145                 150                 155                 160
Leu Asp Ala Ile Thr Pro Tyr Met Gln Ala Ile Gly Arg Ile Ile Ala
                165                 170                 175
Lys Ala Gln Ile Thr Asn Gly Gly Pro Val Ile Leu Phe Gln Pro Glu
            180                 185                 190
Asn Glu Tyr Thr Ala Cys Val Gln Asp Glu Gly Tyr Thr Gln Val Ser
        195                 200                 205
Asn Tyr Ser Met Pro Asp Ile Asn Ser Ser Cys Leu Gln Lys Glu Tyr
    210                 215                 220
Met Ala Tyr Val Glu Glu Gln Tyr Arg Lys Ala Gly Ile Val Val Pro
225                 230                 235                 240
Phe Ile Val Asn Asp Ala Asp Pro Met Gly Asn Phe Ala Pro Gly Thr
                245                 250                 255
Gly Val Gly Ala Val Asp Ile Tyr Ser Phe Asp Asp Tyr Pro Leu Gln
            260                 265                 270
Trp Ser Thr Ala Pro Ser Asn Pro Ser Asn Trp Ser Ser Leu Ile Ser
        275                 280                 285
Pro Leu Leu Ser Tyr Asn Glu Thr Val His Glu Glu Gln Ser Pro Thr
    290                 295                 300
Thr Pro Phe Ser Ile Ser Glu Phe Gln Gly Gly Val Pro Asp Ala Trp
305                 310                 315                 320
Gly Gly Val Gly Ile Glu Thr Ser Ala Ala Tyr Ile Gly Pro Glu Phe
                325                 330                 335
Glu Arg Ile Phe Tyr Lys Ile Asn Tyr Gly Phe Arg Ala Ala Ile Gln
            340                 345                 350
Asn Leu Tyr Met Ile Phe Gly Gly Thr Asn Trp Gly Asn Leu Gly His
        355                 360                 365
Ser Gly Gly Tyr Thr Ser Tyr Asp Val Gly Ala Ala Ile Ala Glu Asp
    370                 375                 380
Arg Gln Val Ile Arg Glu Lys Tyr Ser Glu Leu Lys Leu Gln Ser Asn
385                 390                 395                 400
Phe Leu Gln Ala Ser Ser Ala Tyr Leu Glu Thr His Ser Asp Asn Gly
                405                 410                 415
Ser Tyr Gly Ile Tyr Thr Asp Ala Thr Ser Leu Ala Val Thr Arg Leu
            420                 425                 430
Ala Gly Asn Pro Thr Asn Phe Tyr Val Val Arg His Gly Glu Leu Thr
        435                 440                 445
Ser Arg Glu Ser Thr Ser Tyr Lys Leu Arg Val Asn Thr Ser Ala Gly
    450                 455                 460
Asn Leu Ala Ile Pro Gln Leu Ser Gly Ser Leu Ser Leu His Gly Arg
465                 470                 475                 480
Asp Ser Lys Ile His Leu Val Asp Tyr Asn Val Gly Asn Val Ser Leu
                485                 490                 495
Ile Tyr Ser Thr Ala Glu Leu Phe Thr Trp Lys Gln Ala Gly Ser Lys
            500                 505                 510
Ser Val Val Val Leu Tyr Gly Gly Glu Asp Glu Leu His Glu Phe Ala
        515                 520                 525
Val Pro Ala Asn Lys Gly Lys Pro Thr Ser Ile Glu Gly Asp Gly Leu
    530                 535                 540
Gln Val Gln Gln Ile Asn Ser Thr Thr Val Ile Gln Trp Ala Val Gln
545                 550                 555                 560
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```
Pro Ser Arg Arg Val Val His Phe Ser Asp Thr Leu Glu Val His Leu
                565                 570                 575
Leu Trp Arg Asn Glu Ala Tyr Asn Tyr Trp Val Leu Asp Leu Pro Val
            580                 585                 590
Pro Gly Ala Ile Gly Arg His Val Ser Arg Ser His Thr Asn Arg Ser
        595                 600                 605
Val Ile Val Lys Ala Gly Tyr Leu Leu Arg Thr Ala Glu Ile Ile Gly
    610                 615                 620
Thr Ser Leu Tyr Leu Thr Gly Asp Ile Asn Thr Thr Thr Thr Ile Glu
625                 630                 635                 640
Leu Ile Ser Ala Pro Gln Pro Val Thr Ser Ile Leu Phe Asn Lys Asn
                645                 650                 655
Arg Ile Pro Thr Thr Ile Thr Ser Pro Gly Arg Leu Thr Gly Thr Leu
            660                 665                 670
Thr Tyr His Lys Pro Asn Ile Ser Leu Pro Asp Leu Thr Thr Leu Asp
        675                 680                 685
Trp Tyr Tyr Leu Asn Thr Leu Pro Glu Val His Asp Pro Thr Tyr Asp
    690                 695                 700
Asp His Leu Trp Thr Pro Cys Thr His Thr Thr Thr Ala Asn Pro Arg
705                 710                 715                 720
Asn Leu Thr Thr Pro Thr Ser Leu Tyr Ala Ser Asp Tyr Gly Tyr Asn
                725                 730                 735
Gly Gly Thr Leu Leu Tyr Arg Gly Thr Phe Thr Ala Thr Gly Asn Glu
            740                 745                 750
Thr Ser Leu Tyr Leu Leu Thr Glu Gly Gly Tyr Ala Tyr Gly His Ser
        755                 760                 765
Ile Trp Leu Asn Asn Thr Phe Leu Ala Ser Trp Pro Gly Asn Pro Ala
    770                 775                 780
Phe Leu Leu Ser Asn Gln Thr Ile Thr Phe Pro Ser Pro Leu Thr Pro
785                 790                 795                 800
Gly Thr Thr Tyr Lys Leu Thr Ile Leu Ile Asp His Leu Gly Asn Asp
                805                 810                 815
Glu Asn Phe Pro Ala Asn Gly Glu Phe Met Lys Asp Pro Arg Gly Ile
            820                 825                 830
Leu Asp Tyr Thr Leu His Gly Arg Asp Asp Lys Ser Ala Ile Ser Trp
        835                 840                 845
Lys Met Thr Gly Asn Phe Gly Gly Glu Ser Tyr Ala Asp Leu Ser Arg
    850                 855                 860
Gly Pro Leu Asn Glu Gly Ala Leu Phe Ala Glu Arg Lys Gly Tyr His
865                 870                 875                 880
Leu Pro Gly Ala Pro Thr Glu Gln Trp Thr Lys Arg Ser Pro Phe Asp
                885                 890                 895
Gly Leu Pro Glu Asp Glu Arg Pro Gly Val Gly Phe Phe Ala Thr Lys
            900                 905                 910
Phe Asp Leu Gln Ile Pro Asp Gly Tyr Asp Val Pro Ile Ser Val Val
        915                 920                 925
Phe Glu Asn Ser Thr Met Ala Gly Asp Gly Ser Gly Pro Ala Arg Phe
    930                 935                 940
Arg Ser Glu Leu Phe Val Asn Gly Trp Gln Phe Gly Lys Tyr Val Asn
945                 950                 955                 960
His Ile Gly Pro Gln Leu Ser Tyr Pro Val Pro Glu Gly Ile Leu Asn
                965                 970                 975
Tyr Asn Gly Ser Asn Tyr Leu Ala Leu Thr Ile Trp Ala Met Asp Glu
            980                 985                 990
```

Lys Ser Phe Lys Leu Asp Gly Leu Arg Leu Gln Ala Asn Ala Val Val
995 1000 1005
Gln Ser Gly Tyr Arg Lys Pro Ser Leu Val Lys Gly Glu Val Tyr Lys
1010 1015 1020
Glu Arg Val Asp Ser Tyr
1025 1030

<210> 681
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> lactase B [Aspergillus luchuensis] 81 aa protein
GAT22890.1 GI:1002328951

<400> 681
Met Thr Leu Gln Cys Lys Leu Glu Ser Ala Cys Ser Ser Thr Pro His
1 5 10 15
Asn Ala Met Val Ser Val Leu Gln Gln Asp Gln Trp Ala Gly Glu Pro
20 25 30
Ala Glu Gln Gln Pro His Leu Ser Ala Val Ala Ala Met Gly Arg Asp
35 40 45
Asn Glu Cys Thr Met Phe Glu Pro Gly Leu Ser Gly His Leu Leu Arg
50 55 60
Gly Gly His Glu Ala Thr Gln Val Arg Asn Met Val Ile Glu Ile Leu
65 70 75 80
Phe

<210> 682
<211> 1015
<212> PRT
<213> Artificial Sequence

<220>
<223> lactase B [Aspergillus luchuensis] 1015 aa protein
GAT26827.1 GI:1002325961

<400> 682
Met Thr Arg Ile Thr Lys Leu Cys Ala Leu Leu Leu Ser Ser Thr Gly
1 5 10 15
Leu Leu Ala Ala Ala Gln Asn Gln Thr Glu Thr Gly Trp Pro Leu Tyr
20 25 30
Asp Asp Gly Leu Thr Thr Asp Ile Gln Trp Asp His Tyr Ser Phe Lys
35 40 45
Val His Gly Glu Arg Ile Phe Val Phe Ser Gly Glu Phe His Tyr Trp
50 55 60
Arg Ile Pro Val Pro Gly Leu Trp Arg Asp Ile Leu Glu Lys Ile Lys
65 70 75 80
Ala Ala Gly Phe Thr Thr Phe Ser Ile Tyr Ser Ser Trp Ala Trp His
85 90 95

```
Ala Pro Asn Asn His Thr Val Asp Phe Ser Thr Gly Ala Arg Asp Ile
            100                 105                 110
Thr Pro Ile Phe Glu Leu Ala Lys Glu Leu Gly Met Tyr Ile Ile Val
        115                 120                 125
Arg Pro Gly Pro Tyr Ile Asn Ala Glu Ala Ser Ala Gly Gly Phe Pro
    130                 135                 140
Leu Trp Leu Thr Thr Gly Asp Tyr Gly Thr Leu Arg Asn Asn Asp Ser
145                 150                 155                 160
Arg Tyr Thr Ala Ala Trp Lys Pro Tyr Phe Glu Lys Met Thr Glu Ile
                165                 170                 175
Thr Ser Arg Tyr Gln Val Thr Asn Gly His Asn Thr Phe Cys Tyr Gln
            180                 185                 190
Ile Glu Asn Glu Tyr Gly Asp Gln Trp Leu Ser Asp Pro Ser Glu Arg
        195                 200                 205
Val Pro Asn Glu Thr Ala Ile Ala Tyr Met Glu Leu Leu Glu Ser Ser
    210                 215                 220
Ala Arg Glu Asn Gly Ile Leu Val Pro Phe Thr Ala Asn Asp Pro Asn
225                 230                 235                 240
Met Asn Ala Met Ala Trp Ser Arg Asp Trp Ser Asn Ala Gly Gly Asn
                245                 250                 255
Val Asp Val Val Gly Leu Asp Ser Tyr Pro Ser Cys Trp Thr Cys Asp
            260                 265                 270
Val Ser Gln Cys Thr Ser Thr Asn Gly Glu Tyr Val Ala Tyr Gln Val
        275                 280                 285
Val Glu Tyr Tyr Asp Tyr Phe Leu Glu Phe Ser Pro Thr Met Pro Ser
    290                 295                 300
Phe Met Pro Glu Phe Gln Gly Gly Ser Tyr Asn Pro Trp Ala Gly Pro
305                 310                 315                 320
Glu Gly Gly Cys Gly Asp Asp Thr Gly Val Asp Phe Val Asn Leu Phe
                325                 330                 335
Tyr Arg Trp Asn Ile Ala Gln Arg Val Thr Ala Met Ser Leu Tyr Met
            340                 345                 350
Leu Tyr Gly Gly Thr Asn Trp Gly Ala Ile Ala Ala Pro Val Thr Ala
        355                 360                 365
Thr Ser Tyr Asp Tyr Ser Ser Pro Ile Ser Glu Asp Arg Ser Ile Ser
    370                 375                 380
Ser Lys Tyr Tyr Glu Thr Lys Leu Leu Ser Leu Phe Thr Arg Ser Ala
385                 390                 395                 400
Arg Asp Leu Thr Met Thr Asp Leu Ile Gly Asn Gly Thr Gln Tyr Thr
                405                 410                 415
Asn Asn Thr Ala Val Lys Ala Tyr Glu Leu Arg Asn Pro Thr Thr Asn
            420                 425                 430
Ala Gly Phe Tyr Val Thr Leu His Glu Asp Ser Thr Val Gly Thr Asn
        435                 440                 445
Glu Ala Phe Ser Leu Arg Val Asn Thr Ser Ala Gly Asn Leu Ile Val
    450                 455                 460
Pro Arg Leu Gly Gly Ser Ile Arg Leu Asn Gly His Gln Ser Lys Ile
465                 470                 475                 480
Ile Val Thr Asp Phe Thr Phe Gly Ser Glu Thr Leu Leu Tyr Ser Thr
                485                 490                 495
Ala Glu Val Leu Thr Tyr Ala Val Leu Asp Lys Lys Pro Thr Leu Val
            500                 505                 510
Leu Trp Val Pro Thr Gly Glu Ser Gly Glu Phe Ala Val Lys Gly Ala
        515                 520                 525
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Lys Ser Gly Ser Val Val Ser Lys Cys Gln Asp Cys Ser Ala Ile Asn
    530                 535                 540
Phe His Gln Gln Gly Gly Asn Leu Val Val Gly Phe Thr Gln Ala Gln
545                 550                 555                 560
Gly Met Ser Ile Val Gln Ile Asp Asn Asp Ile Arg Val Ile Leu Leu
                565                 570                 575
Asp Arg Thr Ala Ala Tyr Glu Phe Trp Ala Pro Ala Leu Thr Glu Asp
            580                 585                 590
Pro Leu Val Pro Glu Asp Glu Ala Val Leu Ile Gln Gly Pro Tyr Leu
        595                 600                 605
Val Arg Ser Ala Ser Leu Glu Lys Ser Thr Leu Ala Ile Lys Gly Asp
    610                 615                 620
Ser Ile Asn Glu Thr Ala Val Glu Ile Phe Ala Pro Asn Asp Val Lys
625                 630                 635                 640
Thr Val Thr Trp Asn Gly Lys Gln Leu Lys Thr Ser Lys Ser Ser Tyr
                645                 650                 655
Gly Ser Leu Lys Ala Thr Ile Ala Ala Pro Val Ser Ile Gln Leu Pro
            660                 665                 670
Ala Phe Thr Ser Trp Lys Val Asn Asp Ser Leu Pro Glu Arg Leu Pro
        675                 680                 685
Thr Tyr Asp Ala Ser Gly Leu Ala Trp Val Asp Ala Asn His Met Thr
    690                 695                 700
Thr Ala Asn Pro Ser Lys Pro Ala Thr Leu Pro Val Leu Cys Ala Asp
705                 710                 715                 720
Glu Tyr Gly Phe His Asn Gly Val Arg Leu Trp Arg Gly Tyr Phe Asn
                725                 730                 735
Gly Thr Ala Ser Gly Val Phe Leu Asn Val Gln Gly Gly Ser Ala Phe
            740                 745                 750
Gly Phe Ser Ala Tyr Leu Asn Gly Gln Phe Leu Gly Ser Tyr Leu Gly
        755                 760                 765
Asn Ala Ser Ile Glu Gln Ala Asn Gln Thr Phe Val Phe Pro Thr Asn
    770                 775                 780
Ile Thr His Pro Thr Thr Gln Asn Thr Leu Leu Ile Ile His Asp Asp
785                 790                 795                 800
Thr Gly His Asp Glu Thr Thr Gly Ala Leu Asn Pro Arg Gly Ile Leu
                805                 810                 815
Glu Ala Arg Leu Leu Pro Ser Thr Thr Thr Asp Asn Thr Ala Ser Pro
            820                 825                 830
Glu Phe Thr His Trp Arg Leu Ala Gly Thr Ala Gly Gly Glu Ser Asn
        835                 840                 845
Leu Asp Pro Val Arg Gly Ala Trp Asn Glu Asp Gly Leu Tyr Ala Glu
    850                 855                 860
Arg Val Gly Trp His Leu Pro Gly Phe Asp Asp Ser Thr Trp Pro Ser
865                 870                 875                 880
Val Ser Ser Ser Ser Leu Ser Phe Thr Gly Ala Thr Val Lys Phe Phe
                885                 890                 895
Arg Thr Thr Ile Pro Leu Asn Ile Pro Arg Gly Leu Asp Val Ser Ile
            900                 905                 910
Ser Phe Val Leu Gly Thr Pro Asp Asn Ala Pro Asn Thr Tyr Arg Ala
        915                 920                 925
Gln Leu Phe Val Asn Gly Tyr Gln Tyr Gly Arg Phe Asn Pro Tyr Ile
    930                 935                 940
Gly Asn Gln Val Val Phe Pro Val Pro Val Gly Val Leu Asp Tyr Ser
945                 950                 955                 960
```

```
Gly Glu Asn Thr Ile Gly Val Ala Val Trp Ala Gln Thr Glu Asp Gly
                965                 970                 975
Ala Ala Ile Thr Val Asp Trp Lys Val Asn Tyr Val Ala Asp Ser Ser
            980                 985                 990
Leu Asp Val Ala Gly Leu Glu Thr Ala Gly Leu Arg Pro Gly Trp Ser
        995                 1000                1005
Val Glu Arg Leu Lys Phe Ala
    1010                1015


<210> 683
<211> 726
<212> PRT
<213> Artificial Sequence

<220>
<223> Putative Lactase B [Aspergillus calidoustus] 726
      aa protein CEN62581.1 GI:972234022

<400> 683
Met Pro Phe Phe Met Pro Glu Phe Gln Gly Gly Ser Tyr Asn Pro Trp
 1               5                  10                  15
Asp Gly Pro Glu Gly Gly Cys Thr Glu Asp Thr Gly Ala Glu Phe Ala
            20                  25                  30
Asn Leu Phe Tyr Arg Trp Asn Ile Ala Gln Arg Val Thr Ala Met Ser
        35                  40                  45
Leu Tyr Met Met Tyr Gly Gly Thr Asn Trp Gly Gly Leu Ala Ala Pro
    50                  55                  60
Val Thr Ala Thr Ser Tyr Asp Tyr Ser Ala Pro Ile Ser Glu Asp Arg
65                  70                  75                  80
Ser Ile Gly Ser Lys Tyr Tyr Glu Thr Lys Leu Leu Ala Leu Phe Thr
                85                  90                  95
Arg Cys Ala Lys Asp Leu Thr Met Thr Asp Arg Ile Asp Asn Gly Thr
            100                 105                 110
Gln Tyr Thr Thr Asn Ala Ala Ile Ser Ala Thr Glu Leu Arg Asn Pro
        115                 120                 125
Glu Thr Asn Ala Ala Phe Tyr Val Thr Asn His Leu Asp Thr Thr Leu
    130                 135                 140
Gly Thr Asp Glu Ser Phe Lys Leu His Val Asp Thr Ser Glu Gly Ala
145                 150                 155                 160
Leu Thr Ile Pro Lys His Gly Gly Ala Ile Arg Leu Asn Gly His Gln
                165                 170                 175
Ser Lys Ile Ile Val Thr Asp Phe Arg Leu Gly Arg Glu Thr Leu Leu
            180                 185                 190
Tyr Ser Thr Ala Glu Val Leu Thr Tyr Ala Val Phe Asp Lys Lys Pro
        195                 200                 205
Thr Leu Val Leu Trp Val Pro Ala Gly Glu Ser Gly Glu Phe Ala Ile
    210                 215                 220
Lys Gly Ala Lys Arg Gly Ser Ala Thr Thr Cys Ser Asp Cys Ser Pro
225                 230                 235                 240
Val Glu Phe His Arg Ser Lys Glu Ser Leu Thr Val Ser Phe Thr Gln
                245                 250                 255
Ala Asp Gly Ile Ser Ile Val Gln Leu Asp Asn Gly Val Arg Val Leu
            260                 265                 270
```

```
Leu Leu Asp Arg Pro Ser Ala Tyr Thr Phe Trp Ala Pro Ala Leu Thr
        275                 280                 285
Asp Asp Pro Leu Val Pro Glu Thr Glu Ser Val Phe Val Ser Gly Pro
    290                 295                 300
Tyr Leu Val Arg Ser Ala Lys Leu Ser Gly Ser Thr Leu Ala Leu Arg
305                 310                 315                 320
Gly Asp Ser Asn Gly Lys Thr Ala Ile Glu Val Phe Ala Pro Lys Lys
                325                 330                 335
Val Asn Lys Ile Thr Trp Asn Gly Arg Arg Ile Lys Val Thr Lys Thr
            340                 345                 350
Arg Tyr Gly Ser Leu Lys Ala Ser Leu Ala Ser Ala Pro Ser Ile Glu
        355                 360                 365
Leu Pro Ala Leu Asp Gly Trp Lys Val Ser Asp Ser Leu Pro Glu Arg
    370                 375                 380
Leu Pro Ala Tyr Asp Asp Ser Gly Ala Ala Trp Val Asp Ala Asp His
385                 390                 395                 400
Met Thr Thr Pro Asn Pro His Lys Pro Ala Thr Leu Pro Val Leu Tyr
                405                 410                 415
Ala Asp Glu Tyr Gly Phe His Asn Gly Val Arg Leu Trp Arg Gly Tyr
            420                 425                 430
Phe Asn Ser Ser Ala Ser Gly Val Phe Leu Asn Ile Gln Gly Gly Ala
        435                 440                 445
Ala Phe Gly Trp Ser Ala Tyr Leu Asn Gly His Phe Leu Asp Ser Tyr
    450                 455                 460
Leu Gly Asp Ala Ser Thr Asn Gln Ala Asn Gly Thr Leu Ser Phe Pro
465                 470                 475                 480
Asp Asp Thr Leu Asn Thr Asp Gly Thr Pro Asn Val Leu Leu Val Ile
                485                 490                 495
His Asp Asp Thr Gly His Asp Gln Thr Thr Gly Val Leu Asn Pro Arg
            500                 505                 510
Gly Ile Leu Glu Ala Arg Leu Leu Pro Leu Asp Thr Glu Ser Asp Thr
        515                 520                 525
Glu Ala Pro Glu Phe Thr His Trp Arg Val Ala Gly Thr Ala Gly Gly
    530                 535                 540
Glu Ser Asp Leu Asp Pro Val Arg Gly Val Tyr Asn Glu Asp Gly Leu
545                 550                 555                 560
Phe Ala Glu Arg Val Gly Trp His Leu Pro Gly Phe Asp Asp Asp Asp
                565                 570                 575
Trp Pro Ala Ala Asn Asn Ser Leu Ser Phe Thr Gly Ala Thr Val Lys
            580                 585                 590
Phe Phe Arg Thr Val Ile Pro Pro Leu Asp Ile Pro Gln Gly Val Asp
        595                 600                 605
Val Ser Ile Ser Phe Val Phe Ser Ala Ser Ser Gly Gly Asn Ser Ser
    610                 615                 620
Ser Ser Ser Ser Ser Thr Gly Gly Asn Thr Arg Ala Phe Arg Ala Gln
625                 630                 635                 640
Leu Phe Val Asn Gly Tyr Gln Tyr Gly Arg Phe Asn Pro Tyr Val Gly
                645                 650                 655
Asn Gln Ile Val Tyr Pro Val Pro Pro Gly Ile Leu Asp Tyr Asn Gly
            660                 665                 670
Glu Asn Thr Ile Gly Val Ala Val Trp Ala Gln Thr Glu Ala Gly Ala
        675                 680                 685
Ser Leu Glu Leu Asp Trp Arg Val Asn Tyr Val Val Asp Ser Ser Leu
    690                 695                 700
```

```
Asp Val Ala Asn Leu Asp Val Gly Gly Leu Arg Pro Glu Trp Glu Glu
705                 710                 715                 720
Glu Arg Leu Ser Phe Ala
                725
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<210> 684
<211> 506
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-glucosidase, lactase phlorizinhydrolase
[Aspergillus oryzae 100-8] 506 aa protein
KDE76127.1 GI:635504017

<400> 684

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

```
    290                 295                 300
Arg Ala Gln Leu Gly Ser Arg Leu Pro Glu Phe Thr Ser Glu Glu Leu
305                 310                 315                 320
Asp Leu Leu Arg Arg Ser Ala Pro Ile Asn Ser Phe Tyr Gly Met Asn
                325                 330                 335
His Tyr Thr Thr Lys Tyr Ala Arg Ala Leu Pro Asp Pro Pro Ala Glu
            340                 345                 350
Asp Asp Cys Thr Gly Asn Val Glu Glu Gly Pro Thr Asn Ser Glu Gly
        355                 360                 365
Lys Thr Met Gly Pro Leu Ser Gly Met Ser Trp Leu Arg Val Thr Pro
    370                 375                 380
Ala Gly Phe Arg Lys Leu Leu Asn Trp Val Trp Asp Arg Tyr Arg Arg
385                 390                 395                 400
Pro Ile Val Val Thr Glu Asn Gly Cys Pro Cys Pro Gly Glu Ser Gln
                405                 410                 415
Met Thr Lys Glu Gln Ala Leu Asp Asp Gln Phe Arg Ile Arg Tyr Phe
            420                 425                 430
Gly Leu Tyr Leu Asp Ala Ile Ser Arg Ala Ile Tyr Asp Asp Gly Val
        435                 440                 445
Lys Val Glu Gly Tyr Tyr Val Trp Ser Leu Met Asp Asn Phe Glu Trp
    450                 455                 460
Ser Ala Gly Tyr Gly Pro Arg Tyr Gly Ile Thr His Val Asp Phe Thr
465                 470                 475                 480
Thr Leu Val Arg Thr Pro Lys Gln Ser Ala Lys Tyr Leu His His Ser
                485                 490                 495
Phe Asn Lys Arg Arg Ala Thr Ser Leu Arg
            500                 505
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<210> 685
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-glucosidase, lactase phlorizinhydrolase
[Aspergillus oryzae 3.042] 483 aa protein
EIT76661.1 GI:391867415

<400> 685

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

```
Leu His Ala Ala Gly Ile Thr Pro Leu Val Thr Leu Phe His Trp Asp
        115                 120                 125
Leu Pro Asp Glu Leu Asp Lys Arg Tyr Gly Gly Leu Leu Asn Lys Glu
    130                 135                 140
Glu Phe Val Ala Asp Phe Ala His Tyr Ala Arg Ile Val Phe Lys Ala
145                 150                 155                 160
Phe Gly Ser Lys Val Lys His Trp Ile Thr Phe Asn Glu Pro Trp Cys
                165                 170                 175
Ser Ser Val Leu Gly Tyr Asn Val Gly Gln Phe Ala Pro Gly Arg Thr
            180                 185                 190
Ser Asp Arg Ser Lys Ser Pro Val Gly Asp Ser Ser Arg Glu Cys Trp
        195                 200                 205
Ile Val Gly His Ser Leu Leu Val Ala His Gly Ala Ala Val Lys Ile
    210                 215                 220
Tyr Arg Asp Glu Phe Lys Ala Ser Asp Gly Gly Glu Ile Gly Ile Thr
225                 230                 235                 240
Leu Asn Gly Asp Trp Ala Glu Pro Trp Asp Pro Glu Asn Pro Ala Asp
                245                 250                 255
Val Glu Ala Cys Asp Arg Lys Ile Glu Phe Ala Ile Ser Trp Phe Ala
            260                 265                 270
Asp Pro Ile Tyr His Gly Lys Tyr Pro Asp Ser Met Val Lys Gln Leu
        275                 280                 285
Gly Asp Arg Leu Pro Lys Trp Thr Pro Glu Asp Ile Ala Leu Val His
    290                 295                 300
Gly Ser Asn Asp Phe Tyr Gly Met Asn His Tyr Cys Ala Asn Phe Ile
305                 310                 315                 320
Lys Ala Lys Thr Gly Glu Ala Asp Pro Asn Asp Thr Ala Gly Asn Leu
                325                 330                 335
Glu Ile Leu Leu Gln Asn Arg Lys Gly Glu Trp Val Gly Pro Glu Thr
            340                 345                 350
Gln Ser Pro Trp Leu Arg Pro Ser Ala Ile Gly Phe Arg Lys Leu Leu
        355                 360                 365
Lys Trp Leu Ser Glu Arg Tyr Asn Tyr Pro Lys Ile Tyr Val Thr Glu
    370                 375                 380
Asn Gly Thr Ser Leu Lys Gly Glu Asn Asp Leu Pro Leu Glu Gln Leu
385                 390                 395                 400
Leu Gln Asp Asp Phe Arg Thr Gln Tyr Phe Arg Asp Tyr Ile Gly Ala
                405                 410                 415
Met Ala Asp Ala Tyr Thr Leu Asp Gly Val Asn Val Arg Ala Tyr Met
            420                 425                 430
Ala Trp Ser Leu Met Asp Asn Phe Glu Trp Ala Glu Gly Tyr Glu Thr
        435                 440                 445
Arg Phe Gly Val Thr Tyr Val Asp Tyr Glu Asn Asn Gln Lys Arg Ile
    450                 455                 460
Pro Lys Gln Ser Ala Lys Ala Ile Gly Glu Ile Phe Asp Gln Tyr Ile
465                 470                 475                 480
Glu Lys Ala
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<210> 686
<211> 506
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-glucosidase, lactase phlorizinhydrolase
[Aspergillus oryzae 3.42] 56 aa protein EIT82651.1
GI:391873626

<400> 686
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 1               5                  10                  15
Asp Gln Ser Cys Lys Asp Arg Leu Pro Ala Val Glu Glu Leu Pro Leu
            20                  25                  30
Pro Pro Thr Phe Thr Trp Gly Thr Ala Thr Ala Ala Tyr Gln Val Glu
        35                  40                  45
Gly Gly Ala Phe Gln Asp Gly Lys Gly Lys Ser Ile Trp Asp Thr Phe
    50                  55                  60
Thr His Leu Asp Pro Ser Arg Thr Asn Gly Glu Asn Gly Asp Ile Ala
65                  70                  75                  80
Cys Asp His Tyr Asn Arg Met Ala Glu Asp Val Val Leu Met Ala Ser
                85                  90                  95
Tyr Gly Val Asp Val Tyr Arg Phe Ser Ile Ala Trp Ala Arg Ile Leu
            100                 105                 110
Pro Leu Gly Gly Arg Gly Asp Pro Ile Asn Glu Lys Gly Ile Ala Phe
        115                 120                 125
Tyr Asn Asn Leu Ile Asp Cys Leu Leu Glu His Asn Ile Glu Pro Val
    130                 135                 140
Val Thr Leu Tyr His Trp Asp Val Pro Gln Gly Leu Tyr Asp Arg Tyr
145                 150                 155                 160
Gly Ala Phe Leu Asp Thr Thr Glu Phe Arg Ala Asp Phe Glu His Phe
                165                 170                 175
Ala Arg Leu Cys Phe Ser Arg Phe Gly Asp Arg Val Lys Arg Trp Ile
            180                 185                 190
Thr Phe Asn Glu Pro Tyr Ile Ile Ala Ile Phe Gly His His Ser Gly
        195                 200                 205
Val Leu Ala Pro Gly Arg Ser Ser Ala Thr Gly Gly Asp Ser Arg Thr
    210                 215                 220
Glu Pro Trp Arg Val Gly His Thr Ile Ile Leu Ala His Thr Ala Ala
225                 230                 235                 240
Val Gln Ala Tyr Ala Thr Asp Phe Gln Pro Thr Gln Lys Gly Asp Ile
                245                 250                 255
Ser Ile Val Leu Asn Gly His Tyr Tyr Glu Pro Trp Asp Ala Gly Ser
            260                 265                 270
Glu Glu His Trp Leu Ala Ala Gln Arg Arg Leu Glu Phe Tyr Ile Gly
        275                 280                 285
Trp Phe Gly Asp Pro Ile Phe Leu Gly Lys Asp Tyr Pro Ala Pro Met
    290                 295                 300
Arg Ala Gln Leu Gly Ser Arg Leu Pro Glu Phe Thr Ser Glu Glu Leu
305                 310                 315                 320
Asp Leu Leu Arg Arg Ser Ala Pro Ile Asn Ser Phe Tyr Gly Met Asn
                325                 330                 335
His Tyr Thr Thr Lys Tyr Ala Arg Ala Leu Pro Asp Pro Pro Ala Glu
            340                 345                 350
Asp Asp Cys Thr Gly Asn Val Glu Glu Gly Pro Thr Asn Ser Glu Gly
        355                 360                 365
Lys Thr Met Gly Pro Leu Ser Gly Met Ser Trp Leu Arg Val Thr Pro
```

```
    370                 375                 380
Ala Gly Phe Arg Lys Leu Leu Asn Trp Val Trp Asp Arg Tyr Arg Arg
385                 390                 395                 400
Pro Ile Val Val Thr Glu Asn Gly Cys Pro Cys Pro Gly Glu Ser Gln
                405                 410                 415
Met Thr Lys Glu Gln Ala Leu Asp Asp Gln Phe Arg Ile Arg Tyr Phe
            420                 425                 430
Gly Leu Tyr Leu Asp Ala Ile Ser Arg Ala Ile Tyr Asp Asp Gly Val
        435                 440                 445
Lys Val Glu Gly Tyr Tyr Val Trp Ser Leu Met Asp Asn Phe Glu Trp
    450                 455                 460
Ser Ala Gly Tyr Gly Pro Arg Tyr Gly Ile Thr His Val Asp Phe Thr
465                 470                 475                 480
Thr Leu Val Arg Thr Pro Lys Gln Ser Ala Lys Tyr Leu His His Ser
                485                 490                 495
Phe Asn Lys Arg Arg Ala Thr Ser Leu Arg
            500                 505


<210> 687
<211> 506
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-glucosidase, lactase phlorizinhydrolase
      [Aspergillus oryzae 3.042] 506 aa protein
      EIT82651.1 GI:391873626

<400> 687
Met Asn Val Asn Met Phe Lys Ala Gly Asp Asp Ile Leu Gln Asp Val
 1               5                  10                  15
Asp Gln Ser Cys Lys Asp Arg Leu Pro Ala Val Glu Glu Leu Pro Leu
            20                  25                  30
Pro Pro Thr Phe Thr Trp Gly Thr Ala Thr Ala Ala Tyr Gln Val Glu
        35                  40                  45
Gly Gly Ala Phe Gln Asp Gly Lys Gly Lys Ser Ile Trp Asp Thr Phe
    50                  55                  60
Thr His Leu Asp Pro Ser Arg Thr Asn Gly Glu Asn Gly Asp Ile Ala
65                  70                  75                  80
Cys Asp His Tyr Asn Arg Met Ala Glu Asp Val Val Leu Met Ala Ser
                85                  90                  95
Tyr Gly Val Asp Val Tyr Arg Phe Ser Ile Ala Trp Ala Arg Ile Leu
            100                 105                 110
Pro Leu Gly Gly Arg Gly Asp Pro Ile Asn Glu Lys Gly Ile Ala Phe
        115                 120                 125
Tyr Asn Asn Leu Ile Asp Cys Leu Leu Glu His Asn Ile Glu Pro Val
    130                 135                 140
Val Thr Leu Tyr His Trp Asp Val Pro Gln Gly Leu Tyr Asp Arg Tyr
145                 150                 155                 160
Gly Ala Phe Leu Asp Thr Thr Glu Phe Arg Ala Asp Phe Glu His Phe
                165                 170                 175
Ala Arg Leu Cys Phe Ser Arg Phe Gly Asp Arg Val Lys Arg Trp Ile
            180                 185                 190
```

```
Thr Phe Asn Glu Pro Tyr Ile Ile Ala Ile Phe Gly His His Ser Gly
        195                 200                 205
Val Leu Ala Pro Gly Arg Ser Ser Ala Thr Gly Gly Asp Ser Arg Thr
    210                 215                 220
Glu Pro Trp Arg Val Gly His Thr Ile Ile Leu Ala His Thr Ala Ala
225                 230                 235                 240
Val Gln Ala Tyr Ala Thr Asp Phe Gln Pro Thr Gln Lys Gly Asp Ile
                245                 250                 255
Ser Ile Val Leu Asn Gly His Tyr Tyr Glu Pro Trp Asp Ala Gly Ser
            260                 265                 270
Glu Glu His Trp Leu Ala Ala Gln Arg Arg Leu Glu Phe Tyr Ile Gly
        275                 280                 285
Trp Phe Gly Asp Pro Ile Phe Leu Gly Lys Asp Tyr Pro Ala Pro Met
    290                 295                 300
Arg Ala Gln Leu Gly Ser Arg Leu Pro Glu Phe Thr Ser Glu Glu Leu
305                 310                 315                 320
Asp Leu Leu Arg Arg Ser Ala Pro Ile Asn Ser Phe Tyr Gly Met Asn
                325                 330                 335
His Tyr Thr Thr Lys Tyr Ala Arg Ala Leu Pro Asp Pro Pro Ala Glu
            340                 345                 350
Asp Asp Cys Thr Gly Asn Val Glu Glu Gly Pro Thr Asn Ser Glu Gly
        355                 360                 365
Lys Thr Met Gly Pro Leu Ser Gly Met Ser Trp Leu Arg Val Thr Pro
    370                 375                 380
Ala Gly Phe Arg Lys Leu Leu Asn Trp Val Trp Asp Arg Tyr Arg Arg
385                 390                 395                 400
Pro Ile Val Val Thr Glu Asn Gly Cys Pro Cys Pro Gly Glu Ser Gln
                405                 410                 415
Met Thr Lys Glu Gln Ala Leu Asp Asp Gln Phe Arg Ile Arg Tyr Phe
            420                 425                 430
Gly Leu Tyr Leu Asp Ala Ile Ser Arg Ala Ile Tyr Asp Asp Gly Val
        435                 440                 445
Lys Val Glu Gly Tyr Tyr Val Trp Ser Leu Met Asp Asn Phe Glu Trp
    450                 455                 460
Ser Ala Gly Tyr Gly Pro Arg Tyr Gly Ile Thr His Val Asp Phe Thr
465                 470                 475                 480
Thr Leu Val Arg Thr Pro Lys Gln Ser Ala Lys Tyr Leu His His Ser
                485                 490                 495
Phe Asn Lys Arg Arg Ala Thr Ser Leu Arg
            500                 505
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<210> 688
<211> 998
<212> PRT
<213> Artificial Sequence

<220>
<223> lactase B [Aspergillus kawachii IFO 4308] 998 aa
protein GAA82087.1 GI:358365465

<400> 688

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

```
Arg Leu Gly Gly Ser Ile Arg Leu Asn Gly His Gln Ser Lys Ile Ile
    450                 455                 460
Val Thr Asp Phe Thr Phe Gly Ser Glu Thr Leu Leu Tyr Ser Thr Ala
465                 470                 475                 480
Glu Val Leu Thr Tyr Ala Val Leu Asp Lys Lys Pro Thr Leu Val Leu
                485                 490                 495
Trp Val Pro Thr Gly Glu Ser Gly Glu Phe Ala Val Lys Gly Ala Lys
            500                 505                 510
Ser Gly Ser Val Val Ser Lys Cys Gln Asp Cys Ser Ala Ile Asn Phe
        515                 520                 525
His Gln Gln Gly Gly Asn Leu Val Val Gly Phe Thr Gln Ala Gln Gly
    530                 535                 540
Met Ser Ile Val Gln Ile Asp Asn Asp Ile Arg Val Ile Leu Leu Asp
545                 550                 555                 560
Arg Thr Ala Ala Tyr Glu Phe Trp Ala Pro Ala Leu Thr Glu Asp Pro
                565                 570                 575
Leu Val Pro Glu Asp Glu Ala Val Leu Ile Gln Gly Pro Tyr Leu Val
            580                 585                 590
Arg Ser Ala Ser Leu Glu Lys Ser Thr Leu Ala Ile Lys Gly Asp Ser
        595                 600                 605
Ile Asn Glu Thr Ala Val Glu Ile Phe Ala Pro Asn Asp Val Lys Thr
    610                 615                 620
Val Thr Trp Asn Gly Lys Gln Leu Lys Thr Ser Lys Ser Ser Tyr Gly
625                 630                 635                 640
Ser Leu Lys Ala Thr Ile Ala Ala Pro Val Ser Ile Gln Leu Pro Ala
                645                 650                 655
Phe Thr Ser Trp Lys Val Asn Asp Ser Leu Pro Glu Arg Leu Pro Thr
            660                 665                 670
Tyr Asp Ala Ser Gly Leu Ala Trp Val Asp Ala Asn His Met Thr Thr
        675                 680                 685
Ala Asn Pro Ser Lys Pro Ala Thr Leu Pro Val Leu Tyr Ala Asp Glu
    690                 695                 700
Tyr Gly Phe His Asn Gly Val Arg Leu Trp Arg Gly Tyr Phe Asn Gly
705                 710                 715                 720
Thr Ala Ser Gly Val Phe Leu Asn Val Gln Gly Gly Ser Ala Phe Gly
                725                 730                 735
Phe Ser Ala Tyr Leu Asn Gly Gln Phe Leu Gly Ser Tyr Leu Gly Asn
            740                 745                 750
Ala Ser Ile Glu Gln Ala Asn Gln Thr Phe Val Phe Pro Thr Asn Ile
        755                 760                 765
Thr His Pro Thr Thr Gln Asn Thr Leu Leu Ile Ile His Asp Asp Thr
    770                 775                 780
Gly His Asp Glu Thr Thr Gly Ala Leu Asn Pro Arg Gly Ile Leu Glu
785                 790                 795                 800
Ala Arg Leu Leu Pro Ser Thr Thr Thr Asp Asn Thr Ala Ser Pro Glu
                805                 810                 815
Phe Thr His Trp Arg Leu Ala Gly Thr Ala Gly Gly Glu Ser Asn Leu
            820                 825                 830
Asp Pro Val Arg Gly Ala Trp Asn Glu Asp Gly Leu Tyr Ala Glu Arg
        835                 840                 845
Val Gly Trp His Leu Pro Gly Phe Asp Asp Ser Thr Trp Pro Ser Val
    850                 855                 860
Ser Ser Ser Ser Leu Ser Phe Thr Gly Ala Thr Val Lys Phe Phe Arg
865                 870                 875                 880
```

```
Thr Thr Ile Pro Leu Asn Ile Pro Arg Gly Leu Asp Val Ser Ile Ser
                885                 890                 895
Phe Val Leu Gly Thr Pro Asp Asn Ala Pro Asn Thr Tyr Arg Ala Gln
            900                 905                 910
Leu Phe Val Asn Gly Tyr Gln Tyr Gly Arg Phe Asn Pro Tyr Ile Gly
        915                 920                 925
Asn Gln Val Val Phe Pro Val Pro Val Gly Val Leu Asp Tyr Ser Gly
    930                 935                 940
Glu Asn Thr Ile Gly Val Ala Val Trp Ala Gln Thr Glu Asp Gly Ala
945                 950                 955                 960
Ala Ile Thr Val Asp Trp Lys Val Asn Tyr Val Ala Asp Ser Ser Leu
                965                 970                 975
Asp Val Ala Gly Leu Glu Thr Ala Gly Leu Arg Pro Gly Trp Ser Val
            980                 985                 990
Glu Arg Leu Lys Phe Ala
        995


<210> 689
<211> 985
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase C;
      AltName: Full=Lactase C; Flags: Precursor 985 aa
      protein A1CE56.1 GI:00680864

<400> 689
Met Arg Ile Leu Ser Leu Leu Phe Leu Leu Leu Leu Gly Phe Leu Ala
 1               5                  10                  15
Gly Asn Arg Val Val Ser Ala Thr Asp His Gly Lys Thr Thr Asp Val
            20                  25                  30
Thr Trp Asp Arg Tyr Ser Leu Ser Val Lys Gly Glu Arg Leu Phe Val
        35                  40                  45
Phe Ser Gly Glu Phe His Tyr Gln Arg Leu Pro Val Pro Glu Met Trp
    50                  55                  60
Leu Asp Val Phe Gln Lys Leu Arg Ala Asn Gly Phe Asn Ala Ile Ser
65                  70                  75                  80
Val Tyr Phe Phe Trp Gly Tyr His Ser Ala Ser Glu Gly Glu Phe Asp
                85                  90                  95
Phe Glu Thr Gly Ala His Asn Ile Gln Arg Leu Phe Asp Tyr Ala Lys
            100                 105                 110
Glu Ala Gly Ile Tyr Val Ile Ala Arg Ala Gly Pro Tyr Cys Asn Ala
        115                 120                 125
Glu Thr Thr Ala Gly Gly Tyr Ala Leu Trp Ala Ala Asn Gly Gln Met
    130                 135                 140
Gly Asn Glu Arg Thr Ser Asp Asp Ala Tyr Tyr Ala Lys Trp Arg Pro
145                 150                 155                 160
Trp Ile Leu Glu Val Gly Lys Ile Ile Ala Ala Asn Gln Ile Thr Asn
                165                 170                 175
Gly Gly Pro Val Ile Leu Asn Gln His Glu Asn Glu Leu Gln Glu Thr
            180                 185                 190
Ser Tyr Glu Ala Asp Asn Thr Leu Val Val Tyr Met Lys Gln Ile Ala
```

```
        195                 200                 205
Arg Val Phe Gln Glu Ala Gly Ile Val Val Pro Ser Ser His Asn Glu
    210                 215                 220
Lys Gly Met Arg Ala Val Ser Trp Ser Thr Asp His His Asp Val Gly
225                 230                 235                 240
Gly Ala Val Asn Ile Tyr Gly Leu Asp Ser Tyr Pro Gly Gly Leu Ser
                245                 250                 255
Cys Thr Asn Pro Ser Ser Gly Phe Asn Leu Val Arg Thr Tyr Tyr Gln
            260                 265                 270
Trp Phe Gln Asn Ser Ser Tyr Thr Gln Pro Glu Tyr Leu Pro Glu Phe
        275                 280                 285
Glu Gly Gly Trp Phe Gln Pro Trp Gly Gly His Asp Tyr Asp Thr Cys
    290                 295                 300
Ala Thr Glu Leu Ser Pro Glu Phe Ala Asp Val Tyr Tyr Lys Asn Asn
305                 310                 315                 320
Ile Gly Ser Arg Val Thr Leu Gln Asn Ile Tyr Met Val Phe Gly Gly
                325                 330                 335
Thr Asn Trp Gly His Ser Ala Ala Pro Val Val Tyr Thr Ser Tyr Asp
            340                 345                 350
Tyr Ser Ala Pro Leu Arg Glu Thr Arg Glu Ile Arg Asp Lys Leu Lys
        355                 360                 365
Gln Thr Lys Leu Ile Gly Leu Phe Thr Arg Val Ser Ser Asp Leu Leu
    370                 375                 380
Lys Thr His Met Glu Gly Asn Gly Thr Gly Tyr Thr Ser Asp Ser Ser
385                 390                 395                 400
Ile Tyr Thr Trp Ala Leu His Asn Pro Asp Thr Asn Ala Gly Phe Tyr
                405                 410                 415
Val Leu Ala His Lys Thr Ser Ser Ser Arg Ser Val Thr Glu Phe Ser
            420                 425                 430
Leu Asn Val Thr Thr Ser Ala Gly Ala Ile Ser Ile Pro Asp Ile Gln
        435                 440                 445
Leu Asp Gly Arg Gln Ser Lys Ile Ile Val Thr Asp Tyr Gln Phe Gly
    450                 455                 460
Lys Ser Ser Ala Leu Leu Tyr Ser Ser Ala Glu Val Leu Thr Tyr Ala
465                 470                 475                 480
Asn Leu Asp Val Asp Val Leu Val Leu Tyr Leu Asn Val Gly Gln Lys
                485                 490                 495
Gly Leu Phe Val Phe Lys Asp Glu Arg Ser Lys Leu Ser Phe Gln Thr
            500                 505                 510
Tyr Gly Asn Thr Asn Val Thr Ala Ser Val Ser Ser His Gly Thr Gln
        515                 520                 525
Tyr Ile Tyr Thr Gln Ala Glu Gly Val Thr Ala Val Lys Phe Ser Asn
    530                 535                 540
Gly Val Leu Ala Tyr Leu Leu Asp Lys Glu Ser Ala Trp Asn Phe Phe
545                 550                 555                 560
Ala Pro Pro Thr Thr Ser Asn Pro Gln Val Ala Pro Asp Glu His Ile
                565                 570                 575
Leu Val Gln Gly Pro Tyr Leu Val Arg Gly Val Thr Ile Asn His Asp
            580                 585                 590
Thr Val Glu Ile Ile Gly Asp Asn Ala Asn Thr Thr Ser Leu Glu Val
        595                 600                 605
Tyr Ala Gly Asn Leu Arg Val Lys Val Val Lys Trp Asn Gly Lys Ala
    610                 615                 620
Ile Lys Ser Arg Arg Thr Ala Tyr Gly Ser Leu Val Gly Arg Ala Pro
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625 630 635 640
Gly Ala Glu Asp Ala Arg Ile Ser Pro Pro Ser Leu Asp Ser Trp Ser
645 650 655
Ala Gln Asp Thr Leu Pro Asp Ile Gln Pro Asp Tyr Asp Asp Ser Arg
660 665 670
Trp Thr Val Cys Asn Lys Thr Ala Ser Val Asn Ala Val Pro Leu Leu
675 680 685
Ser Leu Pro Val Leu Tyr Ser Gly Asp Tyr Gly Tyr His Ala Gly Thr
690 695 700
Lys Val Tyr Arg Gly Arg Phe Asp Gly Arg Asn Val Thr Gly Ala Asn
705 710 715 720
Val Thr Val Gln Asn Gly Val Ala Ser Gly Trp Ala Ala Trp Leu Asn
725 730 735
Gly Gln Phe Val Gly Gly Val Ala Gly Ala Ile Asp Leu Ala Val Thr
740 745 750
Ser Ala Val Leu Ser Phe Asn Ser Ser Leu Leu His Asp Arg Asp Asn
755 760 765
Val Leu Thr Val Val Thr Asp Tyr Thr Gly His Asp Gln Asn Ser Val
770 775 780
Arg Pro Lys Gly Thr Gln Asn Pro Arg Gly Ile Leu Gly Ala Thr Leu
785 790 795 800
Ile Gly Gly Gly Lys Phe Thr Ser Trp Arg Ile Gln Gly Asn Ala Gly
805 810 815
Gly Glu Lys Asn Ile Asp Pro Val Arg Gly Pro Ile Asn Glu Gly Gly
820 825 830
Leu Tyr Gly Glu Arg Met Gly Trp His Leu Pro Gly Tyr Lys Ala Pro
835 840 845
Arg Ser Ala Ala Lys Ser Ser Pro Leu Asp Gly Ile Ser Gly Ala Glu
850 855 860
Gly Arg Phe Tyr Thr Thr Thr Phe Thr Leu Lys Leu Asp Arg Asp Leu
865 870 875 880
Asp Val Pro Ile Gly Leu Gln Leu Gly Ala Pro Ala Gly Thr Gln Ala
885 890 895
Val Val Gln Val Phe Met Asn Gly Tyr Gln Phe Gly His Tyr Leu Pro
900 905 910
His Ile Gly Pro Gln Ser Leu Phe Pro Phe Pro Pro Gly Val Ile Asn
915 920 925
Asn Arg Gly Glu Asn Thr Leu Ala Ile Ser Met Trp Ala Leu Thr Asp
930 935 940
Ala Gly Ala Lys Leu Asp Gln Val Glu Leu Val Ala Tyr Gly Lys Tyr
945 950 955 960
Arg Ser Gly Phe Asp Phe Asn Gln Asp Trp Gly Tyr Leu Gln Pro Gln
965 970 975
Trp Lys Asp Asn Arg Arg Gln Tyr Ala
980 985

<210> 690
<211> 1015
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase B;

AltName: Full=Lactase B; Flags: Precursor 1015 aa protein A1D199.1 GI:00680896

<400> 690

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

```
Lys Asp Leu Thr Met Thr Glu Ala Ile Gly Asn Gly Thr Gln Tyr Thr
                405                 410                 415
Thr Asn Thr Ala Val Arg Ala Phe Glu Leu Arg Asn Pro Gln Thr Asn
            420                 425                 430
Ala Gly Phe Tyr Val Thr Phe His Asn Asp Thr Thr Val Gly Gly Asn
        435                 440                 445
Gln Ala Phe Lys Leu His Val Asn Thr Ser Val Gly Ala Leu Thr Val
    450                 455                 460
Pro Lys Asn Glu Gly Val Ile Gln Leu Asn Gly His Gln Ser Lys Ile
465                 470                 475                 480
Ile Val Thr Asp Phe Thr Leu Gly Lys Arg Thr Leu Leu Tyr Ser Thr
                485                 490                 495
Ala Glu Val Leu Thr Tyr Ala Val Phe Glu Asn Arg Pro Thr Leu Val
            500                 505                 510
Leu Trp Val Pro Thr Gly Glu Ser Gly Glu Phe Ala Ile Lys Gly Thr
        515                 520                 525
Lys Ser Gly Lys Val Glu Asn Gly Asp Gly Cys Ser Gly Ile Asn Phe
    530                 535                 540
Lys Arg Glu Lys Asp Tyr Leu Val Val Asn Phe Ser Gln Ala Lys Gly
545                 550                 555                 560
Leu Ser Val Leu Arg Leu Asp Asn Gly Val Arg Val Val Leu Leu Asp
                565                 570                 575
Lys Ala Ala Ala Tyr Arg Phe Trp Ala Pro Ala Leu Thr Asp Asp Pro
            580                 585                 590
Ile Val Gln Glu Thr Glu Thr Val Leu Val His Gly Pro Tyr Leu Val
        595                 600                 605
Arg Ser Ala Ser Val Ser Lys Ser Thr Leu Ala Leu Arg Gly Asp Ser
    610                 615                 620
Val Glu Lys Thr Thr Leu Glu Ile Phe Ala Pro His Ser Val Arg Lys
625                 630                 635                 640
Ile Thr Trp Asn Gly Lys Glu Val Lys Thr Ser Gln Thr Pro Tyr Gly
                645                 650                 655
Ser Leu Lys Ala Thr Leu Ala Ala Pro Pro Thr Ile Lys Leu Pro Ala
            660                 665                 670
Leu Thr Ser Trp Arg Ser Asn Asp Ser Leu Pro Glu Arg Leu Pro Ser
        675                 680                 685
Tyr Asp Asp Ser Gly Pro Ala Trp Ile Glu Ala Asn His Met Thr Thr
    690                 695                 700
Ser Asn Pro Ser Pro Pro Ala Thr Leu Pro Val Leu Tyr Ala Asp Glu
705                 710                 715                 720
Tyr Gly Phe His Asn Gly Val Arg Leu Trp Arg Gly Tyr Phe Asn Gly
                725                 730                 735
Ser Ala Ser Gly Val Phe Leu Asn Ile Gln Gly Gly Ser Ala Phe Gly
            740                 745                 750
Trp Ser Ala Trp Leu Asn Gly His Phe Leu Asp Ser His Leu Gly Thr
        755                 760                 765
Ala Thr Thr Ser Gln Ala Asn Lys Thr Leu Thr Phe Ser Ser Ser Ile
    770                 775                 780
Leu Asn Pro Thr Glu Asn Val Leu Leu Ile Val His Asp Asp Thr Gly
785                 790                 795                 800
His Asp Gln Thr Thr Gly Ala Leu Asn Pro Arg Gly Ile Ile Glu Ala
                805                 810                 815
Arg Leu Leu Ser Asn Asp Thr Ser Ser Pro Ala Pro Gly Phe Thr Gln
            820                 825                 830
```

```
Trp Arg Ile Ala Gly Thr Ala Gly Gly Glu Ser Asn Leu Asp Pro Ile
        835                 840                 845
Arg Gly Val Phe Asn Glu Asp Gly Leu Phe Ala Glu Arg Met Gly Trp
    850                 855                 860
His Leu Pro Gly Phe Asp Asp Ser Ala Trp Thr Pro Glu Asn Ser Thr
865                 870                 875                 880
Thr Ser Ala Ser Ser Ala Leu Ser Phe Thr Gly Ala Thr Val Arg Phe
                885                 890                 895
Phe Arg Thr Val Val Pro Leu Asp Ile Pro Ala Gly Leu Asp Val Ser
            900                 905                 910
Ile Ser Phe Val Leu Ser Thr Pro Ser Ala Ala Pro Lys Gly Tyr Arg
        915                 920                 925
Ala Gln Leu Phe Val Asn Gly Tyr Gln Tyr Gly Arg Tyr Asn Pro His
    930                 935                 940
Ile Gly Asn Gln Val Val Phe Pro Val Pro Pro Gly Ile Leu Asp Tyr
945                 950                 955                 960
Gln Gly Asp Asn Thr Ile Gly Leu Ala Val Trp Ala Gln Thr Glu Glu
                965                 970                 975
Gly Ala Gly Ile Gln Val Asp Trp Lys Val Asn Tyr Val Ala Asp Ser
            980                 985                 990
Ser Leu Ser Val Ala Gly Phe Gly Lys Gly Leu Arg Pro Gly Trp Thr
        995                 1000                1005
Glu Glu Arg Leu Lys Phe Ala
    1010                1015
```

<210> 691
<211> 1006
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase A;
AltName: Full=Lactase A; Flags: Precursor 1006 aa
protein A1D1Z9.1 GI:300680858

<400> 691

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

```
    130                 135                 140
Gly Gly Gly Phe Pro Gly Trp Leu Gln Arg Val Asn Gly Thr Leu Arg
145                 150                 155                 160
Thr Ser Asp Pro Ala Tyr Leu Lys Ala Thr Asp Asn Tyr Ile Ala His
                165                 170                 175
Val Ala Ala Thr Val Ala Lys Gly Gln Ile Thr Asn Gly Gly Pro Val
            180                 185                 190
Ile Leu Tyr Gln Pro Glu Asn Glu Tyr Ser Gly Ala Cys Cys Asn Ala
        195                 200                 205
Thr Phe Pro Asp Gly Asp Tyr Met Gln Tyr Val Ile Asp Gln Ala Arg
    210                 215                 220
Asn Ala Gly Ile Val Val Pro Leu Ile Asn Asn Asp Ala Trp Thr Gly
225                 230                 235                 240
Gly His Asn Ala Pro Gly Thr Gly Lys Gly Glu Val Asp Ile Tyr Gly
                245                 250                 255
His Asp Ser Tyr Pro Leu Gly Phe Asp Cys Gly His Pro Ser Val Trp
            260                 265                 270
Pro Lys Gly Asn Leu Pro Thr Thr Phe Arg Thr Asp His Leu Arg Glu
        275                 280                 285
Ser Pro Thr Thr Pro Tyr Ser Leu Ile Glu Phe Gln Ala Gly Ser Phe
    290                 295                 300
Asp Pro Trp Gly Gly Pro Gly Phe Ala Ala Cys Ala Ala Leu Val Asn
305                 310                 315                 320
His Glu Phe Glu Arg Val Phe Tyr Lys Asn Asp Leu Ser Phe Gly Ala
                325                 330                 335
Ala Ile Leu Asn Leu Tyr Met Thr Phe Gly Gly Thr Asn Trp Gly Asn
            340                 345                 350
Leu Gly His Pro Gly Gly Tyr Thr Ser Tyr Asp Tyr Gly Ser Pro Leu
        355                 360                 365
Thr Glu Ser Arg Asn Val Thr Arg Glu Lys Tyr Ser Glu Leu Lys Leu
    370                 375                 380
Ile Gly Asn Phe Val Lys Ala Ser Pro Ser Tyr Leu Leu Ala Thr Pro
385                 390                 395                 400
Gly Asn Leu Thr Thr Ser Gly Tyr Ala Asp Thr Ala Asp Leu Thr Val
                405                 410                 415
Thr Pro Leu Leu Gly Asn Gly Thr Gly Ser Tyr Phe Val Val Arg His
            420                 425                 430
Thr Asp Tyr Thr Ser Gln Ala Ser Thr Pro Tyr Lys Leu Ser Leu Pro
        435                 440                 445
Thr Ser Ala Gly Arg Leu Thr Val Pro Gln Leu Gly Gly Thr Leu Thr
    450                 455                 460
Leu Asn Gly Arg Asp Ser Lys Val His Val Val Asp Tyr Asn Val Ala
465                 470                 475                 480
Gly Thr Asn Ile Leu Tyr Ser Thr Ala Glu Val Phe Thr Trp Lys Lys
                485                 490                 495
Phe Gly Asp Ser Lys Val Leu Val Leu Tyr Gly Gly Pro Gly Glu His
            500                 505                 510
His Glu Leu Ala Val Ser Leu Lys Ser Asp Val Gln Val Val Glu Gly
        515                 520                 525
Ser Asn Ser Glu Phe Thr Ser Lys Lys Val Glu Asp Val Val Val Val
    530                 535                 540
Ala Trp Asp Val Ser Ala Ser Arg Arg Ile Val Gln Ile Gly Asp Leu
545                 550                 555                 560
Lys Ile Phe Leu Leu Asp Arg Asn Ser Ala Tyr Asn Tyr Trp Val Pro
```

```
                565                 570                 575
Gln Leu Asp Lys Asp Asp Ser Ser Thr Gly Tyr Ser Ser Glu Lys Thr
            580                 585                 590
Thr Ala Ser Ser Ile Ile Val Lys Ala Gly Tyr Leu Val Arg Thr Ala
        595                 600                 605
Tyr Thr Lys Gly Ser Gly Leu Tyr Leu Thr Ala Asp Phe Asn Ala Thr
    610                 615                 620
Thr Pro Val Glu Val Ile Gly Ala Pro Ser Asn Val Arg Asn Leu Tyr
625                 630                 635                 640
Ile Asn Gly Glu Lys Thr Gln Phe Lys Thr Asp Lys Asn Gly Ile Trp
                645                 650                 655
Ser Thr Gly Val Lys Tyr Ser Ala Pro Lys Ile Lys Leu Pro Ser Met
            660                 665                 670
Lys Asp Leu Asp Trp Lys Tyr Leu Asp Thr Leu Pro Glu Val Gln Ser
        675                 680                 685
Thr Tyr Asp Asp Ser Ala Trp Pro Ala Ala Asp Leu Asp Thr Thr Pro
    690                 695                 700
Asn Thr Leu Arg Pro Leu Thr Met Pro Lys Ser Leu His Ser Ser Asp
705                 710                 715                 720
Tyr Gly Phe His Thr Gly Tyr Leu Ile Tyr Arg Gly His Phe Val Ala
                725                 730                 735
Asp Gly Ser Glu Thr Thr Phe Asp Val Arg Thr Gln Gly Gly Ser Ala
            740                 745                 750
Phe Gly Ser Ser Val Trp Leu Asn Glu Ala Phe Leu Gly Ser Trp Thr
        755                 760                 765
Gly Leu Asn Ala Asn Ala Asp Tyr Asn Ser Thr Tyr Arg Leu Pro Gln
    770                 775                 780
Val Glu Lys Gly Lys Asn Tyr Val Leu Thr Val Val Ile Asp Thr Met
785                 790                 795                 800
Gly Leu Asn Glu Asn Trp Val Val Gly Thr Asp Glu Met Lys Asn Pro
                805                 810                 815
Arg Gly Ile Leu Ser Tyr Lys Leu Ser Gly Arg Asp Ala Ser Ala Ile
            820                 825                 830
Thr Trp Lys Leu Thr Gly Asn Leu Gly Gly Glu Asp Tyr Gln Asp Lys
        835                 840                 845
Ile Arg Gly Pro Leu Asn Glu Gly Gly Leu Tyr Ala Glu Arg Gln Gly
    850                 855                 860
Phe His Gln Pro Glu Pro Pro Ser Lys Lys Trp Lys Ser Ala Ser Pro
865                 870                 875                 880
Leu Asp Gly Leu Ser Lys Pro Gly Ile Gly Phe Tyr Thr Ala Gln Phe
                885                 890                 895
Asp Leu Asp Ile Pro Ser Gly Trp Asp Val Pro Leu Tyr Phe Asn Phe
            900                 905                 910
Gly Asn Ser Thr Lys Ser Ala Tyr Arg Val Gln Leu Tyr Val Asn Gly
        915                 920                 925
Tyr Gln Tyr Gly Lys Phe Val Ser Asn Ile Gly Pro Gln Thr Ser Phe
    930                 935                 940
Pro Val Pro Gln Gly Ile Leu Asn Tyr Gln Gly Thr Asn Trp Val Ala
945                 950                 955                 960
Leu Thr Leu Trp Ala Leu Glu Ser Asp Gly Ala Lys Leu Asp Asp Phe
                965                 970                 975
Glu Leu Val Asn Thr Thr Pro Val Met Thr Ala Leu Ser Lys Ile Arg
            980                 985                 990
Pro Ser Lys Gln Pro Asn Tyr Arg Gln Arg Lys Gly Ala Tyr
```

995 1000 1005

<210> 692
<211> 1011
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase E;
AltName: Full=Lactase E; Flags: Precursor 1011 aa
protein A1DJ58.1 GI: 300680873

<400> 692
Met Lys Phe Leu Leu Arg Arg Phe Ile Ala Leu Ala Ala Ala Ser Ser
1 5 10 15
Val Val Ala Ala Pro Ser Val Ser His Leu Ser Leu Gln Asp Ala Ala
20 25 30
Asn Arg Arg Glu Leu Leu Gln Asp Leu Val Thr Trp Asp Gln His Ser
35 40 45
Leu Phe Val Arg Gly Glu Arg Leu Met Ile Phe Ser Gly Glu Phe His
50 55 60
Pro Phe Arg Leu Pro Val Pro Gly Leu Trp Phe Asp Val Phe Gln Lys
65 70 75 80
Ile Thr Ser Leu Gly Phe Asn Ala Val Ser Phe Tyr Thr Asp Trp Gly
85 90 95
Leu Met Glu Gly Asn Pro Gly His Val Val Thr Asp Gly Ile Trp Ser
100 105 110
Leu Asp Glu Phe Phe Thr Ala Ala Ser Glu Ala Gly Ile Tyr Leu Ile
115 120 125
Ala Arg Pro Gly Pro Tyr Ile Asn Ala Glu Thr Ser Ala Gly Gly Ile
130 135 140
Pro Gly Trp Val Leu Arg Leu Lys Gly Ile Ile Arg Ser Asn Ser Glu
145 150 155 160
Asp Tyr Leu Arg Ala Thr Asp Thr Tyr Met Ala Thr Leu Gly Lys Ile
165 170 175
Ile Ala Lys Ala Gln Ile Thr Asn Gly Gly Pro Val Ile Leu Val Gln
180 185 190
Pro Glu Asn Glu Tyr Thr Thr Trp Pro Asn Val Ser Glu Ser Glu Phe
195 200 205
Pro Thr Thr Met Asn Lys Glu Val Met Ala Tyr Ala Glu Lys Gln Leu
210 215 220
Arg Asp Ala Gly Val Val Val Pro Thr Val Val Asn Asp Asn Lys Asn
225 230 235 240
Leu Gly Tyr Phe Ala Pro Gly Thr Gly Leu Gly Glu Thr Asp Leu Tyr
245 250 255
Gly Ile Asp Ala Tyr Pro Met Arg Tyr Asp Cys Gly Asn Pro Tyr Val
260 265 270
Trp Pro Thr Tyr Arg Phe Pro Arg Asp Trp Gln His Thr His Arg Asn
275 280 285
His Ser Pro Thr Thr Pro Phe Ala Ile Met Glu Phe Gln Gly Gly Ser
290 295 300
Gly Asp Gly Trp Gly Gly Val Thr Glu Asp Gly Cys Ala Ile Leu Val
305 310 315 320

```
Asn Asn Glu Ala Val Arg Val Val Tyr Lys Asn Asn Tyr Gly Phe Gly
                325                 330                 335
Val Gly Val Phe Asn Ile Tyr Met Thr Tyr Gly Gly Thr Asn Trp Gly
            340                 345                 350
Asn Leu Gly Tyr His Gly Gly Tyr Thr Ser Tyr Asp Tyr Gly Ala Ala
        355                 360                 365
Ile Thr Glu Asp Arg Gln Ile Trp Arg Glu Lys Tyr Ser Glu Glu Lys
    370                 375                 380
Leu Gln Ala Asn Phe Leu Lys Val Ser Pro Ala Tyr Leu Thr Ala Thr
385                 390                 395                 400
Pro Gly Asn Gly Val Asn Gly Ser Tyr Thr Gly Asn Lys Asp Ile Ala
                405                 410                 415
Val Thr Pro Leu Phe Gly Asn Gly Thr Thr Thr Asn Phe Tyr Leu Val
            420                 425                 430
Arg His Ala Asp Phe Thr Ser Thr Gly Ser Val Gln Tyr Gln Leu Ser
        435                 440                 445
Val Ser Thr Ser Val Gly Asn Val Thr Ile Pro Gln Leu Gly Gly Ser
    450                 455                 460
Leu Ser Leu Asn Gly Arg Asp Ser Lys Phe His Val Thr Asp Tyr Asp
465                 470                 475                 480
Val Gly Glu Phe Asn Leu Ile Tyr Ser Ser Ala Glu Ile Phe Thr Trp
                485                 490                 495
Ala Lys Gly Asp Asn Lys Lys Arg Val Leu Val Leu Tyr Gly Gly Ala
            500                 505                 510
Gly Glu Leu His Glu Phe Ala Leu Pro Lys His Leu Pro Arg Pro Thr
        515                 520                 525
Val Val Asp Gly Ser Asp Val Lys Met Ala Lys Lys Gly Ser Ala Trp
    530                 535                 540
Val Val Gln Trp Glu Val Thr Ala Gln Arg Arg Val Leu Arg Ala Gly
545                 550                 555                 560
Lys Leu Glu Ile His Leu Leu Trp Arg Asn Asp Ala Tyr Gln His Trp
                565                 570                 575
Val Leu Glu Leu Pro Ala Lys Gln Pro Ile Ala Asn Tyr Ser Ser Pro
            580                 585                 590
Ser Lys Glu Thr Val Leu Val Lys Gly Gly Tyr Leu Leu Arg Ser Ala
        595                 600                 605
Cys Ile Thr Asn Asn Lys Leu His Leu Thr Gly Asp Val Asn Ala Thr
    610                 615                 620
Thr Pro Leu Glu Val Ile Ser Ala Pro Lys Arg Phe Asp Gly Ile Val
625                 630                 635                 640
Phe Asn Gly Gln Ser Leu Lys Ser Thr Arg Ser Lys Ile Gly Asn Leu
                645                 650                 655
Ala Ala Thr Val Arg Tyr Gln Pro Pro Ala Ile Ser Leu Pro Asp Leu
            660                 665                 670
Lys Arg Leu Asp Trp Lys Tyr Leu Asp Ser Leu Pro Glu Ile Ser Pro
        675                 680                 685
Asp Tyr Ser Asp Glu Gly Trp Met Ser Leu Thr Asn Thr Tyr Thr Asn
    690                 695                 700
Asn Thr Arg Lys Phe Thr Gly Pro Thr Cys Leu Tyr Ala Asp Asp Tyr
705                 710                 715                 720
Gly Tyr His Gly Gly Ser Leu Ile Tyr Arg Gly His Phe Lys Ala Asn
                725                 730                 735
Gly Asp Glu Ser Trp Val Phe Leu Asn Thr Ser Gly Gly Val Gly Phe
            740                 745                 750
```

```
Ala Asn Ser Val Trp Leu Asn Gln Thr Phe Leu Gly Ser Trp Thr Gly
        755                 760                 765
Ser Gly Asn Asn Met Thr Tyr Pro Arg Asn Ile Ser Leu Pro His Glu
    770                 775                 780
Leu Ser Pro Gly Lys Pro Tyr Val Phe Thr Val Val Ile Asp His Met
785                 790                 795                 800
Gly Gln Asp Glu Glu Ala Pro Gly Thr Asp Ala Ile Lys Phe Pro Arg
                805                 810                 815
Gly Ile Leu Asp Tyr Ala Leu Ser Gly His Glu Val Ser Asp Leu Lys
            820                 825                 830
Trp Lys Met Thr Gly Asn Leu Gly Gly Glu Gln Tyr Gln Asp Ser Thr
        835                 840                 845
Arg Gly Pro Leu Asn Glu Gly Ala Met Tyr Ala Glu Arg Arg Gly Tyr
    850                 855                 860
His Leu Pro Asn Pro Pro Thr Ser Ser Trp Lys Ser Ser Ser Pro Ile
865                 870                 875                 880
Asn Asp Gly Leu Thr Gly Ala Gly Ile Gly Phe Tyr Ala Thr Ser Phe
                885                 890                 895
Ser Leu Asp Leu Pro Glu Gly Tyr Asp Ile Pro Leu Ser Phe Leu Phe
            900                 905                 910
Asn Asn Ser Ala Ser Asp Ala Arg Ser Gly Thr Ser Tyr Arg Cys Gln
        915                 920                 925
Leu Phe Val Asn Gly Tyr Gln Phe Gly Lys Tyr Val Asn Asp Leu Gly
    930                 935                 940
Pro Gln Thr Asn Phe Pro Val Pro Glu Gly Ile Leu Asn Tyr Asn Gly
945                 950                 955                 960
Val Asn Tyr Val Ala Val Ser Leu Trp Ala Leu Glu Pro Gln Gly Ala
                965                 970                 975
Leu Val Gly Gly Leu Glu Leu Val Ala Ser Thr Pro Ile Leu Ser Ala
            980                 985                 990
Tyr Arg Lys Pro Val Pro Ala Pro Gln Pro Gly Trp Lys Pro Arg Arg
        995                 1000                1005
Gly Ala Tyr
    1010
```

<210> 693
<211> 983
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase C;
AltName: Full=Lactase C; Flags: Precursor 983 aa
protein A1DM65.1 GI: 300680868

<400> 693

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Met Arg Ile Phe Ser Phe Leu Phe Leu Leu Leu Leu Gly Ile Leu Thr
 1               5                  10                  15
Gly Gln Gly Leu Val Ser Gly Thr Asp Asn Gly Lys Thr Thr Asp Val
            20                  25                  30
Thr Trp Asp Lys Tyr Ser Leu Ser Val Lys Gly Gln Arg Leu Phe Val
        35                  40                  45
Phe Ser Gly Glu Phe His Tyr Gln Arg Leu Pro Val Pro Glu Leu Trp
```

```
    50                  55                  60
Leu Asp Val Phe Gln Lys Leu Arg Ala Asn Gly Phe Asn Ala Ile Ser
65                  70                  75                  80
Val Tyr Phe Phe Trp Ser Phe His Ser Ala Ser Glu Gly Glu Phe Asp
                85                  90                  95
Phe Glu Asn Gly Ala His Asp Ile Gln Arg Leu Phe Asp Tyr Ala Lys
            100                 105                 110
Glu Ala Gly Leu Tyr Val Ile Ala Arg Ala Gly Pro Tyr Cys Asn Ala
        115                 120                 125
Glu Thr Ser Ala Gly Gly Phe Ala Leu Trp Ala Ala Asn Gly Gln Met
    130                 135                 140
Gly Asn Glu Arg Thr Ser Asp Glu Ala Tyr Tyr Glu Lys Trp Arg Pro
145                 150                 155                 160
Trp Ile Leu Glu Val Gly Lys Ile Ile Ala Lys Asn Gln Ile Thr Asn
                165                 170                 175
Gly Gly Pro Val Ile Leu Asn Gln His Glu Asn Glu Leu Thr Glu Thr
            180                 185                 190
Thr Tyr Asp Pro Asn His Thr Leu Val Val Tyr Met Lys Gln Ile Ala
        195                 200                 205
Gln Val Phe Glu Glu Ala Gly Ile Val Val Pro Ser Ser His Asn Glu
    210                 215                 220
Lys Gly Met Arg Gly Val Ser Trp Ser Thr Asp Tyr His Asn Val Gly
225                 230                 235                 240
Gly Ala Val Asn Ile Tyr Gly Leu Asp Ser Tyr Pro Gly Gly Leu Ser
                245                 250                 255
Cys Thr Asn Pro Asn Ser Gly Phe Arg Leu Val Arg Thr Tyr Tyr Gln
            260                 265                 270
Trp Phe Gln Asn Tyr Ser Ser Thr Gln Pro Ser Tyr Met Pro Glu Phe
        275                 280                 285
Glu Gly Gly Trp Phe Gln Pro Trp Gly Gly Ser Phe Tyr Asp Thr Cys
    290                 295                 300
Ala Thr Glu Leu Ser Pro Glu Phe Pro Asp Val Tyr Tyr Lys Asn Asn
305                 310                 315                 320
Ile Gly Ser Arg Val Thr Leu His Ser Ile Tyr Met Thr Tyr Gly Gly
                325                 330                 335
Thr Asn Trp Gly His Ser Ala Ala Pro Val Val Tyr Thr Ser Tyr Asp
            340                 345                 350
Tyr Ala Ala Pro Leu Arg Glu Thr Arg Glu Ile Arg Asp Lys Leu Lys
        355                 360                 365
Gln Thr Lys Leu Ile Gly Leu Phe Thr Arg Val Ser Thr Asp Leu Leu
    370                 375                 380
Lys Thr Tyr Met Glu Gly Asn Gly Thr Gly Tyr Thr Ser Asp Ser Ser
385                 390                 395                 400
Ile Tyr Thr Trp Ser Leu Arg Asn Pro Asp Thr Asn Ala Gly Phe Tyr
                405                 410                 415
Val Leu Ala His Ser Thr Ser Ser Ala Arg Asp Val Thr Thr Phe Ser
            420                 425                 430
Leu Asn Ala Thr Thr Ser Ala Gly Ala Ile Ser Ile Pro Asp Ile Glu
        435                 440                 445
Leu Asn Gly Arg Gln Ser Lys Ile Ile Val Thr Asp Tyr Asn Phe Gly
    450                 455                 460
Thr Asn Ser Thr Leu Leu Phe Ser Ser Ala Glu Val Leu Thr Tyr Ala
465                 470                 475                 480
Asn Leu Asp Val Asn Val Leu Val Phe Tyr Leu Asn Val Gly Gln Lys
```

```
                485                 490                 495
Gly Thr Phe Ala Leu Lys Asp Glu Pro Lys Leu Ala Phe Gln Thr Tyr
            500                 505                 510
Gly Asn Ser Asn Val Thr Thr Ser Glu Ser Ser Tyr Gly Thr Gln Tyr
        515                 520                 525
Ser Tyr Thr Gln Gly Glu Gly Val Thr Ala Val Lys Phe Ser Asn Gly
    530                 535                 540
Val Leu Ala Tyr Leu Leu Asp Lys Glu Ser Ala Trp Asn Phe Phe Ala
545                 550                 555                 560
Pro Pro Thr Thr Ser Ser Pro Gln Val Ala Pro Asn Glu His Ile Leu
                565                 570                 575
Val Gln Gly Pro Tyr Leu Val Arg Gly Ala Ser Ile Asn His Gly Thr
            580                 585                 590
Val Glu Ile Thr Gly Asp Asn Ala Asn Thr Thr Ser Ile Glu Val Tyr
        595                 600                 605
Thr Gly Asn Ser Gln Val Lys Lys Val Lys Trp Asn Gly Lys Thr Ile
    610                 615                 620
Glu Thr Arg Lys Thr Ala Tyr Gly Ser Leu Ile Gly Thr Val Pro Gly
625                 630                 635                 640
Ala Glu Asp Val Lys Ile Arg Leu Pro Ser Leu Asp Ser Trp Lys Ala
                645                 650                 655
Gln Asp Thr Leu Pro Glu Ile Gln Pro Asp Tyr Asp Asp Ser Thr Trp
            660                 665                 670
Thr Val Cys Asn Lys Thr Thr Ser Val Asn Ala Ile Ala Pro Leu Ser
        675                 680                 685
Leu Pro Val Leu Tyr Ser Gly Asp Tyr Gly Tyr His Ala Gly Thr Lys
    690                 695                 700
Val Tyr Arg Gly Arg Phe Asp Gly Arg Asn Val Thr Gly Ala Asn Val
705                 710                 715                 720
Thr Val Gln Asn Gly Ala Ala Ala Gly Trp Ala Ala Trp Val Asn Gly
                725                 730                 735
Gln Tyr Ala Gly Gly Ser Ala Gly Ser Pro Ser Leu Ala Ala Thr Ser
            740                 745                 750
Ala Val Leu Thr Phe Asn Gly Leu Ser Leu Lys Asp Arg Asp Asn Val
        755                 760                 765
Leu Thr Val Val Thr Asp Tyr Thr Gly His Asp Gln Asn Ser Val Arg
    770                 775                 780
Pro Lys Gly Thr Gln Asn Pro Arg Gly Ile Leu Gly Ala Thr Leu Thr
785                 790                 795                 800
Gly Gly Gly Asn Phe Thr Ser Trp Arg Ile Gln Gly Asn Ala Gly Gly
                805                 810                 815
Glu Lys Asn Ile Asp Pro Val Arg Gly Pro Met Asn Glu Gly Gly Leu
            820                 825                 830
Tyr Gly Glu Arg Met Gly Trp His Leu Pro Gly Tyr Lys Val Pro Lys
        835                 840                 845
Ser Ala Ser Lys Ser Ser Pro Leu Asp Gly Val Ser Gly Ala Glu Gly
    850                 855                 860
Arg Phe Tyr Thr Thr Thr Phe Lys Leu Lys Leu Asp Lys Asp Leu Asp
865                 870                 875                 880
Val Pro Ile Gly Leu Gln Leu Gly Ala Pro Glu Gly Thr Lys Ala Val
                885                 890                 895
Val Gln Val Phe Met Asn Gly Tyr Gln Phe Gly His Tyr Leu Pro His
            900                 905                 910
Thr Gly Pro Gln Ser Leu Phe Pro Phe Pro Pro Gly Val Ile Asn Asn
```

```
        915                 920                 925
Arg Gly Glu Asn Thr Leu Ala Ile Ser Met Trp Ala Leu Thr Asp Ala
    930                 935                 940
Gly Ala Lys Leu Asp Lys Val Glu Leu Val Ala Tyr Gly Lys Tyr Arg
945                 950                 955                 960
Ser Gly Phe Asp Phe Asn Gln Asp Trp Gly Tyr Leu Gln Pro Gly Trp
                965                 970                 975
Lys Asp Arg Ser Gln Tyr Ala
            980
```

<210> 694
<211> 1017
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase B;
AltName: Full=Lactase B; Flags: Precursor 1017 aa
protein A2QA64.2 GI: 300681011

<400> 694

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

```
Val Asp Val Val Gly Leu Asp Ser Tyr Pro Ser Cys Trp Thr Cys Asp
            260                 265                 270
Val Ser Gln Cys Thr Ser Thr Asn Gly Glu Tyr Val Ala Tyr Gln Val
        275                 280                 285
Val Glu Tyr Tyr Asp Tyr Phe Leu Asp Phe Ser Pro Thr Met Pro Ser
    290                 295                 300
Phe Met Pro Glu Phe Gln Gly Gly Ser Tyr Asn Pro Trp Ala Gly Pro
305                 310                 315                 320
Glu Gly Gly Cys Gly Asp Asp Thr Gly Val Asp Phe Val Asn Leu Phe
                325                 330                 335
Tyr Arg Trp Asn Ile Ala Gln Arg Val Thr Ala Met Ser Leu Tyr Met
            340                 345                 350
Leu Tyr Gly Gly Thr Asn Trp Gly Ala Ile Ala Ala Pro Val Thr Ala
        355                 360                 365
Thr Ser Tyr Asp Tyr Ser Ser Pro Ile Ser Glu Asp Arg Ser Ile Ser
    370                 375                 380
Ser Lys Tyr Tyr Glu Thr Lys Leu Leu Ser Leu Phe Thr Arg Ser Ala
385                 390                 395                 400
Arg Asp Leu Thr Met Thr Asp Leu Ile Gly Asn Gly Thr Gln Tyr Thr
                405                 410                 415
Asn Asn Thr Ala Val Lys Ala Tyr Glu Leu Arg Asn Pro Thr Thr Asn
            420                 425                 430
Ala Gly Phe Tyr Val Thr Leu His Glu Asp Ser Thr Val Gly Thr Asn
        435                 440                 445
Glu Ala Phe Ser Leu Arg Val Asn Thr Ser Ala Gly Asn Leu Ile Val
    450                 455                 460
Pro Arg Leu Gly Gly Ser Ile Arg Leu Asn Gly His Gln Ser Lys Ile
465                 470                 475                 480
Ile Val Thr Asp Phe Thr Phe Gly Ser Glu Thr Leu Leu Tyr Ser Thr
                485                 490                 495
Ala Glu Val Leu Thr Tyr Ala Val Ile Asp Lys Lys Pro Thr Leu Val
            500                 505                 510
Leu Trp Val Pro Thr Asp Glu Ser Gly Glu Phe Ala Val Lys Gly Ala
        515                 520                 525
Lys Ser Gly Ser Val Val Ser Lys Cys Gln Ser Cys Pro Ala Ile Asn
    530                 535                 540
Phe His Gln Gln Gly Gly Asn Leu Ile Val Gly Phe Thr Gln Ser Gln
545                 550                 555                 560
Gly Met Ser Val Val Gln Ile Asp Asn Asp Ile Arg Val Val Leu Leu
                565                 570                 575
Asp Arg Thr Ala Ala Tyr Lys Phe Trp Ala Pro Ala Leu Thr Glu Asp
            580                 585                 590
Pro Leu Val Pro Glu Asp Glu Ala Val Val Leu Ile Gln Gly Pro Tyr
        595                 600                 605
Leu Val Arg Ser Ala Ser Leu Glu Lys Ser Thr Leu Ala Ile Lys Gly
    610                 615                 620
Asp Ser Ile Asn Glu Thr Ala Val Glu Ile Phe Ala Pro Glu Asn Val
625                 630                 635                 640
Lys Thr Ile Thr Trp Asn Gly Lys Gln Leu Lys Thr Ser Lys Ser Ser
                645                 650                 655
Tyr Gly Ser Leu Lys Ala Thr Ile Ala Ala Pro Ala Ser Ile Gln Leu
            660                 665                 670
Pro Ala Phe Thr Ser Trp Lys Val Asn Asp Ser Leu Pro Glu Arg Leu
        675                 680                 685
```

```
Pro Thr Tyr Asp Ala Ser Gly Pro Ala Trp Val Asp Ala Asn His Met
    690                 695                 700
Thr Thr Ala Asn Pro Ser Lys Pro Ala Thr Leu Pro Val Leu Tyr Ala
705                 710                 715                 720
Asp Glu Tyr Gly Phe His Asn Gly Val Arg Leu Trp Arg Gly Tyr Phe
                725                 730                 735
Asn Gly Thr Ala Ser Gly Val Phe Leu Asn Val Gln Gly Gly Ser Ala
            740                 745                 750
Phe Gly Phe Ser Ala Tyr Leu Asn Gly His Phe Leu Gly Ser Tyr Leu
        755                 760                 765
Gly Asn Ala Ser Ile Glu Gln Ala Asn Gln Thr Phe Leu Phe Pro Asn
    770                 775                 780
Asn Ile Thr His Pro Thr Thr Gln Asn Thr Leu Leu Val Ile His Asp
785                 790                 795                 800
Asp Thr Gly His Asp Glu Thr Thr Gly Ala Leu Asn Pro Arg Gly Ile
                805                 810                 815
Leu Glu Ala Arg Leu Leu Pro Ser Asp Thr Thr Asn Asn Ser Thr Ser
            820                 825                 830
Pro Glu Phe Thr His Trp Arg Ile Ala Gly Thr Ala Gly Gly Glu Ser
        835                 840                 845
Asn Leu Asp Pro Val Arg Gly Ala Trp Asn Glu Asp Gly Leu Tyr Ala
    850                 855                 860
Glu Arg Val Gly Trp His Leu Pro Gly Phe Asp Asp Ser Thr Trp Ser
865                 870                 875                 880
Ser Val Ser Ser Ser Ser Ser Leu Ser Phe Thr Gly Ala Thr Val Lys
                885                 890                 895
Phe Phe Arg Thr Thr Ile Pro Leu Asp Ile Pro Arg Gly Leu Asp Val
            900                 905                 910
Ser Ile Ser Phe Val Leu Gly Thr Pro Asp Asn Ala Pro Asn Ala Tyr
        915                 920                 925
Arg Ala Gln Leu Phe Val Asn Gly Tyr Gln Tyr Gly Arg Phe Asn Pro
    930                 935                 940
Tyr Ile Gly Asn Gln Val Val Phe Pro Val Pro Val Gly Val Leu Asp
945                 950                 955                 960
Tyr Thr Gly Glu Asn Thr Ile Gly Val Ala Val Trp Ala Gln Thr Glu
                965                 970                 975
Asp Gly Ala Gly Ile Thr Val Asp Trp Lys Val Asn Tyr Val Ala Asp
            980                 985                 990
Ser Ser Leu Asp Val Ser Gly Leu Glu Thr Gly Glu Leu Arg Pro Gly
        995                 1000                1005
Trp Ser Ala Glu Arg Leu Lys Phe Ala
    1010                1015


<210> 695
<211> 1007
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase A;
      AltName: Full=Lactase A; Flags: Precursor 1007 aa
      protein A2QAN3.1 GI: 300680857
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<400> 695
Met Lys Leu Ser Ser Ala Cys Ala Ile Ala Leu Leu Ala Ala Gln Ala
 1               5                  10                  15
Ala Gly Ala Ser Ile Lys His Arg Ile Asn Gly Phe Thr Leu Thr Glu
            20                  25                  30
His Ser Asp Pro Ala Lys Arg Glu Leu Leu Gln Lys Tyr Val Thr Trp
        35                  40                  45
Asp Asp Lys Ser Leu Phe Ile Asn Gly Glu Arg Ile Met Ile Phe Ser
    50                  55                  60
Gly Glu Phe His Pro Phe Arg Leu Pro Val Lys Glu Leu Gln Leu Asp
65                  70                  75                  80
Ile Phe Gln Lys Val Lys Ala Leu Gly Phe Asn Cys Val Ser Phe Tyr
                85                  90                  95
Val Asp Trp Ala Leu Val Glu Gly Lys Pro Gly Glu Tyr Arg Ala Asp
            100                 105                 110
Gly Ile Phe Asp Leu Glu Pro Phe Phe Asp Ala Ala Ser Glu Ala Gly
        115                 120                 125
Ile Tyr Leu Leu Ala Arg Pro Gly Pro Tyr Ile Asn Ala Glu Ser Ser
    130                 135                 140
Gly Gly Gly Phe Pro Gly Trp Leu Gln Arg Val Asn Gly Thr Leu Arg
145                 150                 155                 160
Ser Ser Asp Lys Ala Tyr Leu Asp Ala Thr Asp Asn Tyr Val Ser His
                165                 170                 175
Val Ala Ala Thr Ile Ala Lys Tyr Gln Ile Thr Asn Gly Gly Pro Ile
            180                 185                 190
Ile Leu Tyr Gln Pro Glu Asn Glu Tyr Thr Ser Gly Cys Cys Gly Val
        195                 200                 205
Glu Phe Pro Asp Pro Val Tyr Met Gln Tyr Val Glu Asp Gln Ala Arg
    210                 215                 220
Asn Ala Gly Val Val Ile Pro Leu Ile Asn Asn Asp Ala Ser Ala Ser
225                 230                 235                 240
Gly Asn Asn Ala Pro Gly Thr Gly Lys Gly Ala Val Asp Ile Tyr Gly
                245                 250                 255
His Asp Ser Tyr Pro Leu Gly Phe Asp Cys Ala Asn Pro Thr Val Trp
            260                 265                 270
Pro Ser Gly Asp Leu Pro Thr Asn Phe Arg Thr Leu His Leu Glu Gln
        275                 280                 285
Ser Pro Thr Thr Pro Tyr Ala Ile Val Glu Phe Gln Gly Gly Ser Tyr
    290                 295                 300
Asp Pro Trp Gly Gly Pro Gly Phe Ala Ala Cys Ser Glu Leu Leu Asn
305                 310                 315                 320
Asn Glu Phe Glu Arg Val Phe Tyr Lys Asn Asp Phe Ser Phe Gln Ile
                325                 330                 335
Ala Ile Met Asn Leu Tyr Met Ile Phe Gly Gly Thr Asn Trp Gly Asn
            340                 345                 350
Leu Gly Tyr Pro Asn Gly Tyr Thr Ser Tyr Asp Tyr Gly Ser Ala Val
        355                 360                 365
Thr Glu Ser Arg Asn Ile Thr Arg Glu Lys Tyr Ser Glu Leu Lys Leu
    370                 375                 380
Leu Gly Asn Phe Ala Lys Val Ser Pro Gly Tyr Leu Thr Ala Ser Pro
385                 390                 395                 400
Gly Asn Leu Thr Thr Ser Gly Tyr Ala Asp Thr Thr Asp Leu Thr Val
                405                 410                 415
Thr Pro Leu Leu Gly Asn Ser Thr Gly Ser Phe Phe Val Val Arg His

```
            420                 425                 430
Ser Asp Tyr Ser Ser Glu Glu Ser Thr Ser Tyr Lys Leu Arg Leu Pro
        435                 440                 445
Thr Ser Ala Gly Ser Val Thr Ile Pro Gln Leu Gly Gly Thr Leu Thr
    450                 455                 460
Leu Asn Gly Arg Asp Ser Lys Ile His Val Thr Asp Tyr Asn Val Ser
465                 470                 475                 480
Gly Thr Asn Ile Ile Tyr Ser Thr Ala Glu Val Phe Thr Trp Lys Lys
                485                 490                 495
Phe Ala Asp Gly Lys Val Leu Val Leu Tyr Gly Gly Ala Gly Glu His
            500                 505                 510
His Glu Leu Ala Ile Ser Thr Lys Ser Asn Val Thr Val Ile Glu Gly
        515                 520                 525
Ser Glu Ser Gly Ile Ser Ser Lys Gln Thr Ser Ser Ser Val Val Val
    530                 535                 540
Gly Trp Asp Val Ser Thr Thr Arg Arg Ile Ile Gln Val Gly Asp Leu
545                 550                 555                 560
Lys Ile Leu Leu Leu Asp Arg Asn Ser Ala Tyr Asn Tyr Trp Val Pro
                565                 570                 575
Gln Leu Ala Thr Asp Gly Thr Ser Pro Gly Phe Ser Thr Pro Glu Lys
            580                 585                 590
Val Ala Ser Ser Ile Ile Val Lys Ala Gly Tyr Leu Val Arg Thr Ala
        595                 600                 605
Tyr Leu Lys Gly Ser Gly Leu Tyr Leu Thr Ala Asp Phe Asn Ala Thr
    610                 615                 620
Thr Ser Val Glu Val Ile Gly Val Pro Ser Thr Ala Lys Asn Leu Phe
625                 630                 635                 640
Ile Asn Gly Asp Lys Thr Ser His Thr Val Asp Lys Asn Gly Ile Trp
                645                 650                 655
Ser Ala Thr Val Asp Tyr Asn Ala Pro Asp Ile Ser Leu Pro Ser Leu
            660                 665                 670
Lys Asp Leu Asp Trp Lys Tyr Val Asp Thr Leu Pro Glu Ile Gln Ser
        675                 680                 685
Ser Tyr Asp Asp Ser Leu Trp Pro Ala Ala Asp Leu Lys Gln Thr Lys
    690                 695                 700
Asn Thr Leu Arg Ser Leu Thr Thr Pro Thr Ser Leu Tyr Ser Ser Asp
705                 710                 715                 720
Tyr Gly Phe His Thr Gly Tyr Leu Leu Tyr Arg Gly His Phe Thr Ala
                725                 730                 735
Thr Gly Asn Glu Ser Thr Phe Ala Ile Asp Thr Gln Gly Gly Ser Ala
            740                 745                 750
Phe Gly Ser Ser Val Trp Leu Asn Gly Thr Tyr Leu Gly Ser Trp Thr
        755                 760                 765
Gly Leu Tyr Ala Asn Ser Asp Tyr Asn Ala Thr Tyr Asn Leu Pro Gln
    770                 775                 780
Leu Gln Ala Gly Lys Thr Tyr Val Ile Thr Val Val Ile Asp Asn Met
785                 790                 795                 800
Gly Leu Glu Glu Asn Trp Thr Val Gly Glu Asp Leu Met Lys Thr Pro
                805                 810                 815
Arg Gly Ile Leu Asn Phe Leu Leu Ala Gly Arg Pro Ser Ser Ala Ile
            820                 825                 830
Ser Trp Lys Leu Thr Gly Asn Leu Gly Gly Glu Asp Tyr Glu Asp Lys
        835                 840                 845
Val Arg Gly Pro Leu Asn Glu Gly Gly Leu Tyr Ala Glu Arg Gln Gly
```

```
    850                 855                 860
Phe His Gln Pro Glu Pro Pro Ser Gln Asn Trp Lys Ser Ser Ser Pro
865                 870                 875                 880
Leu Glu Gly Leu Ser Glu Ala Gly Ile Gly Phe Tyr Ser Ala Ser Phe
                885                 890                 895
Asp Leu Asp Leu Pro Lys Gly Trp Asp Val Pro Leu Phe Leu Asn Ile
            900                 905                 910
Gly Asn Ser Thr Thr Pro Ser Pro Tyr Arg Val Gln Val Tyr Val Asn
        915                 920                 925
Gly Tyr Gln Tyr Ala Lys Tyr Ile Ser Asn Ile Gly Pro Gln Thr Ser
    930                 935                 940
Phe Pro Val Pro Glu Gly Ile Leu Asn Tyr Arg Gly Thr Asn Trp Leu
945                 950                 955                 960
Ala Val Thr Leu Trp Ala Leu Asp Ser Ala Gly Gly Lys Leu Glu Ser
                965                 970                 975
Leu Glu Leu Ser Tyr Thr Thr Pro Val Leu Thr Ala Leu Gly Glu Val
            980                 985                 990
Glu Ser Val Asp Gln Pro Lys Tyr Lys Lys Arg Lys Gly Ala Tyr
        995                 1000                1005
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<210> 696
<211> 994
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase C;
AltName: Full=Lactase C; Flags: Precursor 994 aa
protein A2QL84.1 GI: 300680867

<400> 696

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

```
Ile Leu Asn Gln Ile Glu Asn Glu Leu Gln Glu Thr Thr His Ser Ala
            180                 185                 190
Ser Asn Thr Leu Val Glu Tyr Met Glu Gln Ile Glu Glu Ala Phe Arg
        195                 200                 205
Ala Ala Gly Val Asp Val Pro Phe Thr Ser Asn Glu Lys Gly Gln Arg
    210                 215                 220
Ser Arg Ser Trp Ser Thr Asp Tyr Glu Asp Val Gly Gly Ala Val Asn
225                 230                 235                 240
Val Tyr Gly Leu Asp Ser Tyr Pro Gly Gly Leu Ser Cys Thr Asn Pro
                245                 250                 255
Ser Thr Gly Phe Ser Val Leu Arg Asn Tyr Tyr Gln Trp Phe Gln Asn
            260                 265                 270
Thr Ser Tyr Thr Gln Pro Glu Tyr Leu Pro Glu Phe Glu Gly Gly Trp
        275                 280                 285
Phe Ser Ala Trp Gly Ala Asp Ser Phe Tyr Asp Gln Cys Thr Ser Glu
    290                 295                 300
Leu Ser Pro Gln Phe Ala Asp Val Tyr Tyr Lys Asn Asn Ile Gly Gln
305                 310                 315                 320
Arg Val Thr Leu Gln Asn Leu Tyr Met Leu Tyr Gly Gly Thr Asn Trp
                325                 330                 335
Gly His Leu Ala Ala Pro Val Val Tyr Thr Ser Tyr Asp Tyr Ser Ala
            340                 345                 350
Pro Leu Arg Glu Thr Arg Gln Ile Arg Asp Lys Leu Ser Gln Thr Lys
        355                 360                 365
Leu Val Gly Leu Phe Thr Arg Val Ser Ser Gly Leu Leu Gly Val Glu
    370                 375                 380
Met Glu Gly Asn Gly Thr Ser Tyr Thr Ser Thr Thr Ser Ala Tyr Thr
385                 390                 395                 400
Trp Val Leu Arg Asn Pro Asn Thr Thr Ala Gly Phe Tyr Val Val Gln
                405                 410                 415
Gln Asp Thr Thr Ser Ser Gln Thr Asp Ile Thr Phe Ser Leu Asn Val
            420                 425                 430
Asn Thr Ser Ala Gly Ala Phe Thr Leu Pro Asn Ile Asn Leu Gln Gly
        435                 440                 445
Arg Gln Ser Lys Val Ile Ser Thr Asp Tyr Pro Leu Gly His Ser Thr
    450                 455                 460
Leu Leu Tyr Val Ser Thr Asp Ile Ala Thr Tyr Gly Thr Phe Gly Asp
465                 470                 475                 480
Thr Asp Val Val Val Leu Tyr Ala Arg Ser Gly Gln Val Val Ser Phe
                485                 490                 495
Ala Phe Lys Asn Thr Thr Lys Leu Thr Phe Glu Glu Tyr Gly Asp Ser
            500                 505                 510
Val Asn Leu Thr Ser Ser Ser Gly Asn Arg Thr Ile Thr Ser Tyr Thr
        515                 520                 525
Tyr Thr Gln Gly Ser Gly Thr Ser Val Val Lys Phe Ser Asn Gly Ala
    530                 535                 540
Ile Phe Tyr Leu Val Glu Thr Glu Thr Ala Phe Arg Phe Trp Ala Pro
545                 550                 555                 560
Pro Thr Thr Thr Asp Pro Tyr Val Thr Ala Glu Gln Gln Ile Phe Val
                565                 570                 575
Leu Gly Pro Tyr Leu Val Arg Asn Val Ser Ile Ser Gly Ser Val Val
            580                 585                 590
Asp Leu Val Gly Asp Asn Asp Asn Ala Thr Thr Val Glu Val Phe Ala
        595                 600                 605
```

```
Gly Ser Pro Ala Lys Ala Val Lys Trp Asn Gly Lys Glu Ile Thr Val
    610                 615                 620
Thr Lys Thr Asp Tyr Gly Ser Leu Val Gly Ser Ile Gly Gly Ala Asp
625                 630                 635                 640
Ser Ser Ser Ile Thr Ile Pro Ser Leu Thr Gly Trp Lys Val Arg Asp
                645                 650                 655
Ser Leu Pro Glu Ile Gln Ser Ser Tyr Asp Asp Ser Lys Trp Thr Val
            660                 665                 670
Cys Asn Lys Thr Thr Thr Leu Ser Pro Val Asp Pro Leu Ser Leu Pro
        675                 680                 685
Val Leu Phe Ala Ser Asp Tyr Gly Tyr Tyr Thr Gly Ile Lys Ile Tyr
    690                 695                 700
Arg Gly Arg Phe Asp Gly Thr Asn Val Thr Gly Ala Asn Leu Thr Ala
705                 710                 715                 720
Gln Gly Gly Leu Ala Phe Gly Trp Asn Val Trp Leu Asn Gly Asp Leu
                725                 730                 735
Val Ala Ser Leu Pro Gly Asp Ala Asp Glu Thr Ser Ser Asn Ala Ala
            740                 745                 750
Ile Asp Phe Ser Asn His Thr Leu Lys Gln Thr Asp Asn Leu Leu Thr
        755                 760                 765
Val Val Ile Asp Tyr Thr Gly His Asp Glu Thr Ser Thr Gly Asp Gly
    770                 775                 780
Val Glu Asn Pro Arg Gly Leu Leu Gly Ala Thr Leu Asn Gly Gly Ser
785                 790                 795                 800
Phe Thr Ser Trp Lys Ile Gln Gly Asn Ala Gly Gly Ala Ala Gly Ala
                805                 810                 815
Tyr Glu Leu Asp Pro Val Arg Ala Pro Met Asn Glu Gly Gly Leu Leu
            820                 825                 830
Ala Glu Arg Gln Gly Trp His Leu Pro Gly Tyr Lys Ala Lys Ser Ser
        835                 840                 845
Asp Gly Trp Thr Asp Gly Ser Pro Leu Asp Gly Leu Asn Lys Ser Gly
    850                 855                 860
Val Ala Phe Tyr Leu Thr Thr Phe Thr Leu Asp Leu Pro Lys Lys Tyr
865                 870                 875                 880
Asp Val Pro Leu Gly Ile Gln Phe Thr Ser Pro Ser Thr Val Asp Pro
                885                 890                 895
Val Arg Ile Gln Leu Phe Ile Asn Gly Tyr Gln Tyr Gly Lys Tyr Val
            900                 905                 910
Pro Tyr Leu Gly Pro Gln Thr Thr Phe Pro Ile Pro Pro Gly Ile Ile
        915                 920                 925
Asn Asn Arg Asp Lys Asn Thr Ile Gly Leu Ser Leu Trp Ala Gln Thr
    930                 935                 940
Asp Ala Gly Ala Lys Leu Glu Asn Ile Glu Leu Ile Ser Tyr Gly Ala
945                 950                 955                 960
Tyr Glu Ser Gly Phe Asp Ala Gly Asn Gly Thr Gly Phe Asp Leu Asn
                965                 970                 975
Gly Ala Lys Leu Gly Tyr Gln Pro Glu Trp Thr Glu Ala Arg Ala Lys
            980                 985                 990
Tyr Thr
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<210> 697
<211> 1006

<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase A;
AltName: Full=Lactase A; Flags: Precursor 1006 aa
protein BXMP7.2 GI: 300681017

<400> 697

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

```
        355                 360                 365
Thr Glu Ser Arg Asn Val Thr Arg Glu Lys Tyr Ser Glu Leu Lys Leu
    370                 375                 380
Ile Gly Asn Phe Val Lys Ala Ser Pro Ser Tyr Leu Leu Ala Thr Pro
385                 390                 395                 400
Gly Asn Leu Thr Thr Ser Gly Tyr Ala Asp Thr Ala Asp Leu Thr Val
                405                 410                 415
Thr Pro Leu Leu Gly Asn Gly Thr Gly Ser Tyr Phe Val Val Arg His
            420                 425                 430
Thr Asp Tyr Thr Ser Gln Ala Ser Thr Pro Tyr Lys Leu Ser Leu Pro
        435                 440                 445
Thr Ser Ala Gly Arg Leu Thr Val Pro Gln Leu Gly Gly Thr Leu Thr
    450                 455                 460
Leu Asn Gly Arg Asp Ser Lys Ile His Val Val Asp Tyr Asn Val Ala
465                 470                 475                 480
Gly Thr Asn Ile Ile Tyr Ser Thr Ala Glu Val Phe Thr Trp Lys Asn
                485                 490                 495
Phe Gly Asp Ser Lys Val Leu Ile Leu Tyr Gly Gly Pro Gly Glu His
            500                 505                 510
His Glu Leu Ala Val Ser Phe Lys Ser Asp Val Gln Val Val Glu Gly
        515                 520                 525
Ser Asn Ser Glu Phe Lys Ser Lys Lys Val Gly Asp Val Ala Val Val
    530                 535                 540
Ala Trp Asp Val Ser Pro Ser Arg Arg Ile Val Gln Ile Gly Asp Leu
545                 550                 555                 560
Lys Ile Phe Leu Leu Asp Arg Asn Ser Val Tyr Asn Tyr Trp Val Pro
                565                 570                 575
Gln Leu Asp Lys Asp Asp Ser Ser Thr Gly Tyr Ser Ser Glu Lys Thr
            580                 585                 590
Thr Ala Ser Ser Ile Ile Val Lys Ala Gly Tyr Leu Val Arg Thr Ala
        595                 600                 605
Tyr Thr Lys Gly Ser Gly Leu Tyr Leu Thr Ala Asp Phe Asn Ala Thr
    610                 615                 620
Thr Pro Val Glu Val Ile Gly Ala Pro Ser Asn Val Arg Asn Leu Tyr
625                 630                 635                 640
Ile Asn Gly Glu Lys Thr Gln Phe Lys Thr Asp Lys Asn Gly Ile Trp
                645                 650                 655
Ser Thr Glu Val Lys Tyr Ser Ala Pro Lys Ile Lys Leu Pro Ser Met
            660                 665                 670
Lys Asp Leu Asp Trp Lys Tyr Leu Asp Thr Leu Gln Glu Val Gln Ser
        675                 680                 685
Thr Tyr Asp Asp Ser Ala Trp Pro Ala Ala Asp Leu Asp Thr Thr Pro
    690                 695                 700
Asn Thr Leu Arg Pro Leu Thr Thr Pro Lys Ser Leu Tyr Ser Ser Asp
705                 710                 715                 720
Tyr Gly Phe His Thr Gly Tyr Leu Ile Tyr Arg Gly His Phe Val Ala
                725                 730                 735
Asp Gly Ser Glu Thr Thr Phe Asp Val Arg Thr Gln Gly Gly Ser Ala
            740                 745                 750
Phe Gly Ser Ser Val Trp Leu Asn Glu Ser Phe Leu Gly Ser Trp Thr
        755                 760                 765
Gly Leu Asn Ala Asn Ala Asp Tyr Asn Ser Thr Tyr Lys Leu Pro Gln
    770                 775                 780
Val Glu Gln Gly Lys Asn Tyr Val Leu Thr Ile Leu Ile Asp Thr Met
```

785 790 795 800
Gly Leu Asn Glu Asn Trp Val Val Gly Thr Asp Glu Met Lys Asn Pro
805 810 815
Arg Gly Ile Leu Ser Tyr Lys Leu Ser Gly Arg Asp Ala Ser Ala Ile
820 825 830
Thr Trp Lys Leu Thr Gly Asn Leu Gly Gly Glu Asp Tyr Gln Asp Lys
835 840 845
Ile Arg Gly Pro Leu Asn Glu Gly Gly Leu Tyr Ala Glu Arg Gln Gly
850 855 860
Phe His Gln Pro Gln Pro Pro Ser Gln Lys Trp Lys Ser Ala Ser Pro
865 870 875 880
Leu Asp Gly Leu Ser Lys Pro Gly Ile Gly Phe Tyr Thr Ala Gln Phe
885 890 895
Asp Leu Asp Ile Pro Ser Gly Trp Asp Val Pro Leu Tyr Phe Asn Phe
900 905 910
Gly Asn Ser Thr Lys Ser Ala Tyr Arg Val Gln Leu Tyr Val Asn Gly
915 920 925
Tyr Gln Tyr Gly Lys Phe Val Ser Asn Ile Gly Pro Gln Thr Ser Phe
930 935 940
Pro Val Pro Gln Gly Ile Leu Asn Tyr Gln Gly Thr Asn Trp Val Ala
945 950 955 960
Leu Thr Leu Trp Ala Leu Glu Ser Asp Gly Ala Lys Leu Asp Asp Phe
965 970 975
Glu Leu Val Asn Thr Thr Pro Val Met Thr Ala Leu Ser Lys Ile Arg
980 985 990
Pro Ser Lys Gln Pro Asn Tyr Arg Gln Arg Lys Gly Ala Tyr
995 1000 1005

<210> 698
<211> 1015
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase B;
AltName: Full=Lactase B; Flags: Precursor 1015 aa
protein B0XNY2.1 GI: 300680860

<400> 698
Met Ala His Ile Tyr Arg Leu Leu Leu Leu Leu Leu Ser Asn Leu Trp
1 5 10 15
Phe Ser Thr Ala Ala Gln Asn Gln Ser Glu Thr Glu Trp Pro Leu His
20 25 30
Asp Asn Gly Leu Ser Lys Val Val Gln Trp Asp His Tyr Ser Phe Gln
35 40 45
Val Asn Gly Gln Arg Ile Phe Ile Phe Ser Gly Glu Phe His Tyr Trp
50 55 60
Arg Ile Pro Val Pro Glu Leu Trp Arg Asp Ile Leu Glu Lys Val Lys
65 70 75 80
Ala Thr Gly Phe Thr Ala Phe Ala Phe Tyr Ser Ser Trp Ala Tyr His
85 90 95
Ala Pro Asn Asn Ser Thr Val Asp Phe Ser Thr Gly Ala Arg Asp Ile
100 105 110

```
Thr Pro Ile Phe Glu Leu Ala Lys Glu Leu Gly Met Tyr Met Ile Val
        115                 120                 125
Arg Pro Gly Pro Tyr Val Asn Ala Glu Ala Ser Ala Gly Gly Phe Pro
    130                 135                 140
Leu Trp Leu Met Thr Gly Glu Tyr Gly Ser Leu Arg Asn Asp Asp Pro
145                 150                 155                 160
Arg Tyr Thr Ala Ala Trp Thr Pro Tyr Phe Ala Asn Met Ser Gln Ile
                165                 170                 175
Thr Ser Lys Tyr Gln Val Thr Asp Gly His Asn Thr Leu Val Tyr Gln
            180                 185                 190
Ile Glu Asn Glu Tyr Gly Gln Gln Trp Ile Gly Asp Pro Lys Asn Arg
        195                 200                 205
Asn Pro Asn Lys Thr Ala Val Ala Tyr Met Glu Leu Leu Glu Ala Ser
    210                 215                 220
Ala Arg Glu Asn Gly Ile Thr Val Pro Leu Thr Ser Asn Asp Pro Asn
225                 230                 235                 240
Met Asn Ser Lys Ser Trp Gly Ser Asp Trp Ser Asn Ala Gly Gly Asn
                245                 250                 255
Val Asp Val Ala Gly Leu Asp Ser Tyr Pro Ser Cys Trp Thr Cys Asp
            260                 265                 270
Val Ser Gln Cys Thr Ser Thr Asn Gly Glu Tyr Val Pro Tyr Lys Val
        275                 280                 285
Ile Asp Tyr Tyr Asp Tyr Phe Gln Glu Val Gln Pro Thr Leu Pro Ser
    290                 295                 300
Phe Met Pro Glu Phe Gln Gly Gly Ser Tyr Asn Pro Trp Ala Gly Pro
305                 310                 315                 320
Glu Gly Gly Cys Pro Gln Asp Thr Ser Ala Glu Phe Ala Asn Leu Phe
                325                 330                 335
Tyr Arg Trp Asn Ile Gly Gln Arg Val Thr Ala Met Ser Leu Tyr Met
            340                 345                 350
Leu Tyr Gly Gly Thr Asn Trp Gly Ala Ile Ala Ala Pro Val Thr Ala
        355                 360                 365
Thr Ser Tyr Asp Tyr Ser Ala Pro Ile Ser Glu Asp Arg Ser Ile Gly
    370                 375                 380
Ala Lys Tyr Ser Glu Thr Lys Leu Leu Ala Leu Phe Thr Arg Thr Ala
385                 390                 395                 400
Lys Asp Leu Thr Met Thr Glu Ala Ile Gly Asn Gly Thr Gln Tyr Thr
                405                 410                 415
Thr Asn Thr Ala Val Arg Ala Phe Glu Leu Arg Asn Pro Gln Thr Asn
            420                 425                 430
Ala Gly Phe Tyr Val Thr Phe His Thr Asp Thr Thr Val Gly Gly Asn
        435                 440                 445
Gln Ala Phe Lys Leu His Val Asn Thr Ser Val Gly Ala Leu Thr Val
    450                 455                 460
Pro Lys Asn Glu Gly Leu Ile Gln Leu Asn Gly His Gln Ser Lys Ile
465                 470                 475                 480
Ile Val Thr Asp Phe Thr Leu Gly Lys Arg Thr Leu Leu Tyr Ser Thr
                485                 490                 495
Ala Glu Val Leu Thr Tyr Ala Val Phe Glu Asn Arg Pro Thr Leu Val
            500                 505                 510
Leu Trp Val Pro Thr Gly Glu Ser Gly Glu Phe Ala Ile Lys Gly Ala
        515                 520                 525
Lys Ser Gly Lys Val Glu Asn Gly Asp Gly Cys Ser Gly Ile Lys Phe
    530                 535                 540
```

```
Lys Arg Glu Lys Asp Tyr Leu Val Val Asn Phe Ser Gln Ala Lys Gly
545                 550                 555                 560
Leu Ser Val Leu Arg Leu Asp Asn Gly Val Arg Val Val Leu Leu Asp
                565                 570                 575
Lys Ala Ala Ala Tyr Arg Phe Trp Ala Pro Ala Leu Thr Asp Asp Pro
            580                 585                 590
Asn Val Gln Glu Thr Glu Thr Val Leu Val His Gly Pro Tyr Leu Val
        595                 600                 605
Arg Ser Ala Ser Ile Ser Lys Thr Thr Leu Ala Leu Arg Gly Asp Ser
    610                 615                 620
Val Glu Lys Thr Thr Leu Glu Ile Phe Ala Pro His Ser Val Arg Lys
625                 630                 635                 640
Ile Thr Trp Asn Gly Lys Glu Val Gln Thr Ser His Thr Pro Tyr Gly
                645                 650                 655
Ser Leu Lys Ala Thr Leu Ala Ala Pro Pro Asp Ile Lys Leu Pro Ala
            660                 665                 670
Leu Thr Ser Trp Arg Ser Asn Asp Ser Leu Pro Glu Arg Leu Pro Ser
        675                 680                 685
Tyr Asp Asp Ser Gly Pro Ala Trp Ile Glu Ala Asn His Met Thr Thr
    690                 695                 700
Ser Asn Pro Ser Pro Pro Ala Thr Phe Pro Val Leu Tyr Ala Asp Glu
705                 710                 715                 720
Tyr Gly Phe His Asn Gly Val Arg Leu Trp Arg Gly Tyr Phe Asn Gly
                725                 730                 735
Ser Ala Ser Gly Val Phe Leu Asn Ile Gln Gly Gly Ser Ala Phe Gly
            740                 745                 750
Trp Ser Ala Trp Leu Asn Gly His Phe Leu Asp Ser His Leu Gly Thr
        755                 760                 765
Ala Thr Thr Ser Gln Ala Asn Lys Thr Leu Thr Phe Pro Ser Ser Ile
    770                 775                 780
Leu Asn Pro Thr Glu Asn Val Leu Leu Ile Val His Asp Asp Thr Gly
785                 790                 795                 800
His Asp Gln Thr Thr Gly Ala Leu Asn Pro Arg Gly Ile Leu Glu Ala
                805                 810                 815
Arg Leu Leu Ser Asn Asp Thr Ser Ser Pro Pro Pro Glu Phe Thr His
            820                 825                 830
Trp Arg Leu Ala Gly Thr Ala Gly Gly Glu Ser Asn Leu Asp Pro Ile
        835                 840                 845
Arg Gly Val Phe Asn Glu Asp Gly Leu Phe Ala Glu Arg Met Gly Trp
    850                 855                 860
His Leu Pro Gly Phe Asp Asp Ser Ala Trp Thr Ser Glu Asn Ser Ala
865                 870                 875                 880
Thr Ser Ala Ser Ser Ala Leu Ser Phe Thr Gly Ala Thr Val Arg Phe
                885                 890                 895
Phe Arg Ser Val Val Pro Leu Asn Ile Pro Ala Gly Leu Asp Val Ser
            900                 905                 910
Ile Ser Phe Val Leu Ser Thr Pro Thr Ala Ala Pro Lys Gly Tyr Arg
        915                 920                 925
Ala Gln Leu Phe Val Asn Gly Tyr Gln Tyr Gly Arg Tyr Asn Pro His
    930                 935                 940
Ile Gly Asn Gln Val Val Phe Pro Val Pro Pro Gly Ile Leu Asp Tyr
945                 950                 955                 960
Gln Gly Asp Asn Thr Ile Gly Leu Ala Val Trp Ala Gln Thr Glu Glu
                965                 970                 975
```

Gly Ala Gly Ile Gln Val Asp Trp Lys Val Asn Tyr Val Ala Asp Ser
980 985 990
Ser Leu Ser Val Ala Gly Phe Gly Lys Gly Leu Arg Pro Gly Trp Thr
995 1000 1005
Glu Glu Arg Leu Lys Phe Ala
1010 1015

<210> 699
<211> 1011
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase E;
AltName: Full=Lactase E; Flags: Precursor 1011 aa
protein B0XXE7.1 GI:300680872

<400> 699
Met Lys Ser Leu Leu Lys Arg Leu Ile Ala Leu Ala Ala Ala Tyr Ser
1 5 10 15
Val Ala Ala Ala Pro Ser Phe Ser His His Ser Ser Gln Asp Ala Ala
20 25 30
Asn Lys Arg Glu Leu Leu Gln Asp Leu Val Thr Trp Asp Gln His Ser
35 40 45
Leu Phe Val Arg Gly Glu Arg Leu Met Ile Phe Ser Gly Glu Phe His
50 55 60
Pro Phe Arg Leu Pro Val Pro Gly Leu Trp Phe Asp Val Phe Gln Lys
65 70 75 80
Ile Lys Ser Leu Gly Phe Asn Ala Val Ser Phe Tyr Thr Asp Trp Gly
85 90 95
Leu Met Glu Gly Asn Pro Gly His Val Val Thr Asp Gly Ile Trp Ser
100 105 110
Leu Asp Glu Phe Phe Thr Ala Ala Arg Glu Ala Gly Leu Tyr Leu Ile
115 120 125
Ala Arg Pro Gly Pro Tyr Ile Asn Ala Glu Thr Ser Ala Gly Gly Ile
130 135 140
Pro Gly Trp Val Leu Arg Arg Lys Gly Ile Ile Arg Ser Asn Ser Glu
145 150 155 160
Asp Tyr Leu Arg Ala Thr Asp Thr Tyr Met Ala Thr Leu Gly Lys Ile
165 170 175
Ile Ala Lys Ala Gln Ile Thr Asn Gly Gly Pro Val Ile Leu Val Gln
180 185 190
Pro Glu Asn Glu Tyr Thr Thr Trp Pro Asn Val Ser Glu Ser Glu Phe
195 200 205
Pro Thr Thr Met Asn Gln Glu Val Met Ala Tyr Ala Glu Lys Gln Leu
210 215 220
Arg Asp Ala Gly Val Val Val Pro Thr Val Val Asn Asp Asn Lys Asn
225 230 235 240
Leu Gly Tyr Phe Ala Pro Gly Thr Gly Leu Gly Glu Thr Asp Leu Tyr
245 250 255
Gly Ile Asp Ala Tyr Pro Met Arg Tyr Asp Cys Gly Asn Pro Tyr Val
260 265 270
Trp Pro Thr Tyr Arg Phe Pro Arg Asp Trp Gln His Glu His Arg Asn

```
        275                 280                 285
His Ser Pro Thr Thr Pro Phe Ala Ile Met Glu Phe Gln Gly Gly Ser
    290                 295                 300
Gly Asp Gly Trp Gly Gly Val Thr Glu Asp Gly Cys Ala Ile Leu Val
305                 310                 315                 320
Asn Asn Glu Ala Val Arg Val Val Tyr Lys Asn Asn Tyr Gly Phe Gly
                325                 330                 335
Val Arg Val Phe Asn Ile Tyr Met Thr Tyr Gly Gly Thr Asn Trp Gly
            340                 345                 350
Asn Leu Gly Tyr Tyr Gly Gly Tyr Thr Ser Tyr Asp Tyr Gly Ala Ala
        355                 360                 365
Ile Thr Glu Asp Arg Gln Ile Trp Arg Glu Lys Tyr Ser Glu Glu Lys
    370                 375                 380
Leu Gln Ala Asn Phe Leu Lys Val Ser Pro Ala Tyr Leu Thr Ser Thr
385                 390                 395                 400
Pro Gly Asn Gly Val Asn Gly Ser Tyr Thr Gly Asn Lys Asp Ile Thr
                405                 410                 415
Val Thr Pro Leu Phe Gly Asn Gly Thr Thr Thr Asn Leu Tyr Leu Val
            420                 425                 430
Arg His Ala Asp Phe Thr Ser Thr Gly Ser Ala Gln Tyr Asn Leu Ser
        435                 440                 445
Ile Ser Thr Ser Val Gly Asn Val Thr Ile Pro Gln Leu Gly Gly Ser
    450                 455                 460
Leu Ser Leu Asn Gly Arg Asp Ser Lys Phe His Ile Thr Asp Tyr Asp
465                 470                 475                 480
Val Gly Gly Phe Asn Leu Ile Tyr Ser Ser Ala Glu Val Phe Thr Trp
                485                 490                 495
Ala Lys Gly Asp Asn Lys Lys Arg Val Leu Val Leu Tyr Gly Gly Ala
            500                 505                 510
Gly Glu Leu His Glu Phe Ala Leu Pro Lys His Leu Pro Arg Pro Thr
        515                 520                 525
Val Val Glu Gly Ser Tyr Val Lys Ile Ala Lys Gln Gly Ser Ala Trp
    530                 535                 540
Val Val Gln Trp Glu Val Ala Ala Gln Arg Arg Val Leu Arg Ala Gly
545                 550                 555                 560
Lys Leu Glu Ile His Leu Leu Trp Arg Asn Asp Ala Tyr Gln His Trp
                565                 570                 575
Val Leu Glu Leu Pro Ala Lys Gln Pro Ile Ala Asn Tyr Ser Ser Pro
            580                 585                 590
Ser Lys Glu Thr Val Ile Val Lys Gly Gly Tyr Leu Leu Arg Ser Ala
        595                 600                 605
Trp Ile Thr Asp Asn Asp Leu His Leu Thr Gly Asp Val Asn Val Thr
    610                 615                 620
Thr Pro Leu Glu Val Ile Ser Ala Pro Lys Arg Phe Asp Gly Ile Val
625                 630                 635                 640
Phe Asn Gly Gln Ser Leu Lys Ser Thr Arg Ser Lys Ile Gly Asn Leu
                645                 650                 655
Ala Ala Thr Val His Tyr Gln Pro Pro Ala Ile Ser Leu Pro Asp Leu
            660                 665                 670
Lys Arg Leu Asp Trp Lys Tyr Ile Asp Ser Leu Pro Glu Ile Ser Thr
        675                 680                 685
Glu Tyr Asn Asp Glu Gly Trp Thr Pro Leu Thr Asn Thr Tyr Thr Asn
    690                 695                 700
Asn Thr Arg Glu Phe Thr Gly Pro Thr Cys Leu Tyr Ala Asp Asp Tyr
```

705 710 715 720
Gly Tyr His Gly Gly Ser Leu Ile Tyr Arg Gly His Phe Thr Ala Asn
725 730 735
Gly Asp Glu Ser Trp Val Phe Leu Asn Thr Ser Gly Gly Val Gly Phe
740 745 750
Ala Asn Ser Val Trp Leu Asn Gln Thr Phe Leu Gly Ser Trp Thr Gly
755 760 765
Ser Gly Arg Asn Met Thr Tyr Pro Arg Asn Ile Ser Leu Pro His Glu
770 775 780
Leu Ser Pro Gly Glu Pro Tyr Val Phe Thr Val Val Ile Asp His Met
785 790 795 800
Gly Gln Asp Glu Glu Ala Pro Gly Thr Asp Ala Ile Lys Phe Pro Arg
805 810 815
Gly Ile Leu Asp Tyr Ala Leu Ser Gly His Glu Leu Ser Asp Leu Arg
820 825 830
Trp Lys Met Thr Gly Asn Leu Gly Gly Glu Gln Tyr Gln Asp Leu Thr
835 840 845
Arg Gly Pro Leu Asn Glu Gly Ala Met Tyr Ala Glu Arg Gln Gly Tyr
850 855 860
His Leu Pro Ser Pro Pro Thr Ser Ser Trp Lys Ser Ser Asn Pro Ile
865 870 875 880
Lys Glu Gly Leu Thr Gly Ala Gly Ile Gly Phe Tyr Ala Thr Ser Phe
885 890 895
Ser Leu Asp Leu Pro Glu Gly Tyr Asp Ile Pro Leu Ser Phe Arg Phe
900 905 910
Asn Asn Ser Ala Ser Ala Ala Arg Ser Gly Thr Ser Tyr Arg Cys Gln
915 920 925
Leu Phe Val Asn Gly Tyr Gln Phe Gly Lys Tyr Val Asn Asp Leu Gly
930 935 940
Pro Gln Thr Lys Phe Pro Val Pro Glu Gly Ile Leu Asn Tyr Asn Gly
945 950 955 960
Val Asn Tyr Val Ala Val Ser Leu Trp Ala Leu Glu Ser Gln Gly Ala
965 970 975
Leu Ile Gly Gly Leu Asp Leu Val Ala Ser Thr Pro Ile Leu Ser Gly
980 985 990
Tyr Arg Lys Pro Ala Pro Ala Pro Gln Pro Gly Trp Lys Pro Arg Arg
995 1000 1005
Gly Ala Tyr
1010

<210> 700
<211> 983
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase C;
AltName: Full=Lactase C; Flags: Precursor 983 aa
protein B0Y752.1 GI:300680865

<400> 700
Met Arg Ile Phe Ser Phe Leu Phe Leu Leu Leu Leu Gly Ile Leu Thr
1 5 10 15

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

```
Leu Asn Gly Arg Gln Ser Lys Ile Ile Val Thr Asp Tyr Asn Phe Gly
    450                 455                 460
Thr Asn Ser Thr Leu Leu Phe Ser Ser Ala Glu Val Leu Thr Tyr Ala
465                 470                 475                 480
Asn Leu Asp Val Asn Val Leu Val Phe Tyr Leu Asn Val Gly Gln Lys
                485                 490                 495
Gly Thr Phe Val Phe Lys Asp Glu Pro Lys Leu Ala Phe Gln Thr Tyr
            500                 505                 510
Gly Asn Ser Asn Leu Thr Thr Ser Glu Ser Ser Tyr Gly Thr Gln Tyr
        515                 520                 525
Ser Tyr Thr Gln Gly Lys Gly Val Thr Ala Val Lys Phe Ser Asn Gly
    530                 535                 540
Val Leu Ala Tyr Phe Leu Asp Lys Glu Ser Ala Trp Asn Phe Phe Ala
545                 550                 555                 560
Pro Pro Thr Thr Ser Ser Pro Gln Val Ala Pro Asn Glu His Ile Leu
                565                 570                 575
Val Gln Gly Pro Tyr Leu Val Arg Gly Ala Ser Val Asn His Gly Thr
            580                 585                 590
Val Glu Ile Thr Gly Asp Asn Ala Asn Thr Thr Ser Ile Glu Val Tyr
        595                 600                 605
Thr Gly Asn Ser Gln Val Lys Lys Ile Lys Trp Asn Gly Lys Thr Ile
    610                 615                 620
Glu Thr Arg Lys Thr Ala Tyr Gly Ser Leu Ile Gly Thr Ala Pro Gly
625                 630                 635                 640
Ala Glu Asp Val Lys Ile Gln Leu Pro Ser Leu Asp Ser Trp Lys Ala
                645                 650                 655
Gln Asp Thr Leu Pro Glu Ile Gln Pro Asp Tyr Asp Asp Ser Lys Trp
            660                 665                 670
Thr Val Cys Asn Lys Thr Thr Ser Val Asn Ala Ile Ala Pro Leu Ser
        675                 680                 685
Leu Pro Val Leu Tyr Ser Gly Asp Tyr Gly Tyr His Ala Gly Thr Lys
    690                 695                 700
Val Tyr Arg Gly Arg Phe Asp Gly Arg Asn Val Thr Gly Ala Asn Val
705                 710                 715                 720
Thr Val Gln Asn Gly Ala Ala Ala Gly Trp Ala Ala Trp Val Asn Gly
                725                 730                 735
Gln Tyr Ala Gly Gly Ser Ala Gly Ser Pro Asn Leu Ala Ala Thr Ser
            740                 745                 750
Ala Val Leu Thr Phe Asn Ser Ser Ser Leu Lys Asp Gln Asp Asn Val
        755                 760                 765
Leu Thr Val Val Thr Asp Tyr Thr Gly His Asp Gln Asn Ser Val Arg
    770                 775                 780
Pro Lys Gly Thr Gln Asn Pro Arg Gly Ile Leu Gly Ala Thr Leu Ile
785                 790                 795                 800
Gly Gly Gly Asn Phe Thr Ser Trp Arg Ile Gln Gly Asn Ala Gly Gly
                805                 810                 815
Glu Lys Asn Ile Asp Pro Val Arg Gly Pro Met Asn Glu Gly Gly Leu
            820                 825                 830
Tyr Gly Glu Arg Met Gly Trp His Leu Pro Gly Tyr Lys Val Pro Lys
        835                 840                 845
Ser Ala Ser Lys Ser Ser Pro Leu Asp Gly Val Ser Gly Ala Glu Gly
    850                 855                 860
Arg Phe Tyr Thr Thr Thr Phe Lys Leu Lys Leu Asp Lys Asp Leu Asp
865                 870                 875                 880
```

```
Val Pro Ile Gly Leu Gln Leu Gly Ala Pro Glu Gly Thr Lys Ala Val
                885                 890                 895
Val Gln Val Phe Met Asn Gly Tyr Gln Phe Gly His Tyr Leu Pro His
            900                 905                 910
Thr Gly Pro Gln Ser Leu Phe Pro Phe Pro Pro Gly Val Ile Asn Asn
        915                 920                 925
Arg Gly Glu Asn Thr Leu Ala Ile Ser Met Trp Ala Leu Thr Asp Ala
    930                 935                 940
Gly Ala Lys Leu Asp Lys Val Glu Leu Val Ala Tyr Gly Lys Tyr Arg
945                 950                 955                 960
Ser Gly Phe Asp Phe Asn Gln Asp Trp Gly Tyr Leu Gln Pro Gly Trp
                965                 970                 975
Lys Asp Arg Ser Gln Tyr Ala
            980
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<210> 701
<211> 984
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase C;
AltName: Full=Lactase C; Flags: Precursor 984 aa
protein B8N2I5.1 GI:300680866

<400> 701

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Met Arg Leu Leu Ser Phe Ile Tyr Leu Val Trp Leu Ala Leu Leu Thr
 1               5                  10                  15
Gly Thr Pro Gln Val Ser Ala Thr Asp Asn Gly Lys Thr Ser Asp Val
            20                  25                  30
Ala Trp Asp Lys Tyr Ser Leu Ser Val Lys Gly Glu Arg Leu Phe Val
        35                  40                  45
Phe Ser Gly Glu Phe His Tyr Gln Arg Leu Pro Val Pro Glu Leu Trp
    50                  55                  60
Leu Asp Val Phe Gln Lys Leu Arg Ala Asn Gly Phe Asn Thr Ile Ser
65                  70                  75                  80
Val Tyr Phe Phe Trp Ser Tyr His Ser Ala Ser Glu Asp Val Phe Asp
                85                  90                  95
Phe Thr Thr Gly Ala His Asp Ile Gln Arg Leu Phe Asp Tyr Ala Lys
            100                 105                 110
Gln Ala Gly Leu Tyr Val Ile Ala Arg Ala Gly Pro Tyr Cys Asn Ala
        115                 120                 125
Glu Thr Ser Ala Gly Gly Phe Ala Leu Trp Ala Ala Asn Gly Gln Met
    130                 135                 140
Gly Ser Glu Arg Thr Ser Asp Glu Ala Tyr Tyr Lys Lys Trp Lys Pro
145                 150                 155                 160
Trp Ile Leu Glu Val Gly Lys Ile Ile Ala Ala Asn Gln Ile Thr Asn
                165                 170                 175
Gly Gly Pro Val Ile Leu Asn Gln His Glu Asn Glu Leu Gln Glu Thr
            180                 185                 190
Thr Tyr Asp Ser Asn Asp Thr Lys Val Ile Tyr Met Glu Gln Val Ala
        195                 200                 205
Lys Ala Phe Glu Glu Ala Gly Val Val Val Pro Ser Ser His Asn Glu
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    210                 215                 220
Lys Gly Met Arg Thr Val Ser Trp Ser Thr Asp Tyr Lys Asn Val Gly
225                 230                 235                 240
Gly Ala Val Asn Val Tyr Gly Leu Asp Ser Tyr Pro Gly Ser Leu Ser
                245                 250                 255
Cys Ala Asn Pro Asn Ser Gly Phe Asn Leu Leu Arg Thr Tyr Tyr Gln
            260                 265                 270
Trp Phe Gln Asn Tyr Ser Tyr Thr Gln Pro Glu Tyr Leu Ala Glu Phe
        275                 280                 285
Glu Gly Gly Trp Phe Gln Pro Trp Gly Gly Ser Phe Tyr Asp Ser Cys
    290                 295                 300
Ala Ser Glu Leu Ser Pro Glu Phe Ala Asp Val Tyr Tyr Lys Asn Asn
305                 310                 315                 320
Ile Gly Ser Arg Val Thr Leu His Asn Ile Tyr Met Thr Phe Gly Gly
                325                 330                 335
Thr Asn Trp Gly His Ser Ala Ala Pro Val Val Tyr Thr Ser Tyr Asp
            340                 345                 350
Tyr Gly Ser Pro Leu Arg Glu Thr Arg Glu Ile Arg Asp Lys Leu Lys
        355                 360                 365
Gln Thr Lys Leu Leu Gly Leu Phe Thr Arg Val Ser Lys Asp Leu Leu
    370                 375                 380
Lys Thr Tyr Met Glu Gly Asn Gly Thr Ser Tyr Thr Ser Asp Asp Ser
385                 390                 395                 400
Ile Tyr Thr Trp Ala Leu Arg Asn Pro Asp Ser Asp Ala Gly Phe Tyr
                405                 410                 415
Val Val Ala His Asn Thr Ser Ser Ser Arg Glu Val Thr Thr Phe Ser
            420                 425                 430
Leu Asn Ile Thr Thr Ser Ala Gly Ala Leu Thr Ile Pro Asp Ile Glu
        435                 440                 445
Leu Asp Gly Arg Gln Ser Lys Ile Ile Val Thr Asp Tyr Ser Ile Gly
    450                 455                 460
Ser Glu Ser Ser Leu Leu Tyr Ser Ser Ala Glu Val Leu Thr Tyr Ala
465                 470                 475                 480
Thr Leu Asp Val Asp Val Leu Val Phe Tyr Leu Asn Ala Gly Gln Lys
                485                 490                 495
Gly Ala Phe Val Phe Lys Asp Ala Pro Ala Asp Leu Lys Tyr Gln Thr
            500                 505                 510
Tyr Gly Asn Ser Asn Leu Ser Ala Leu Glu Thr Ser Gln Gly Thr Gln
        515                 520                 525
Tyr Ser Tyr Thr Gln Gly Glu Gly Val Thr Ala Val Lys Phe Ser Asn
    530                 535                 540
Gly Val Leu Val Tyr Leu Leu Asp Lys Glu Thr Ala Trp Asn Phe Phe
545                 550                 555                 560
Ala Pro Pro Thr Val Ser Ser Pro Thr Val Ala Pro Asn Glu His Ile
                565                 570                 575
Leu Val Phe Gly Pro Tyr Leu Val Arg Gly Ala Ser Ile Lys His Asp
            580                 585                 590
Thr Val Glu Ile Val Gly Asp Asn Ser Asn Ser Thr Ser Ile Glu Ile
        595                 600                 605
Tyr Thr Gly Asp Glu His Val Lys Lys Val Ser Trp Asn Gly Asn Leu
    610                 615                 620
Ile Asp Thr Arg Ala Thr Ala Tyr Gly Ser Leu Ile Gly Thr Val Pro
625                 630                 635                 640
Gly Ala Glu Asp Ile Glu Ile Ser Leu Pro Ser Leu Ser Ser Trp Lys
```

```
                645                 650                 655
Ala Gln Asp Thr Leu Pro Glu Ile Ser Pro Asp Tyr Asp Asp Ser Arg
            660                 665                 670
Trp Thr Ile Cys Asn Lys Thr Thr Ser Val Asn Ser Val Ala Pro Leu
        675                 680                 685
Ser Leu Pro Val Leu Tyr Ser Gly Asp Tyr Gly Tyr His Thr Gly Thr
    690                 695                 700
Lys Ile Tyr Arg Gly Arg Phe Asp Gly Gln Asn Ala Thr Gly Ala Asn
705                 710                 715                 720
Val Thr Val Gln Asn Gly Val Ala Ala Gly Trp Ala Ala Trp Leu Asn
                725                 730                 735
Gly Ala Tyr Val Gly Gly Phe Ser Gly Asp Pro Asp Lys Val Ala Ser
            740                 745                 750
Trp Glu Val Leu Lys Phe Asn His Ser Ser Leu Arg Ser Arg Asp Asn
        755                 760                 765
Val Leu Thr Ile Ile Thr Asp Tyr Thr Gly His Asp Gln Asn Ser Gln
    770                 775                 780
Lys Pro Ile Gly Thr Gln Asn Pro Arg Gly Ile Met Gly Ala Thr Leu
785                 790                 795                 800
Ile Gly Gly Gly Asn Phe Thr Leu Trp Arg Ile Gln Gly Asn Ala Gly
                805                 810                 815
Gly Glu Lys Asn Ile Asp Pro Val Arg Gly Pro Met Asn Glu Gly Gly
            820                 825                 830
Leu Tyr Gly Glu Arg Met Gly Trp His Leu Pro Gly Tyr Gln Val Pro
        835                 840                 845
Glu Ser Ala Leu Asp Ser Ser Pro Leu Glu Gly Val Ser Gly Ala Glu
    850                 855                 860
Gly Arg Phe Tyr Thr Thr Ser Phe Gln Leu Asp Leu Glu Glu Asp Leu
865                 870                 875                 880
Asp Val Pro Ile Gly Leu Gln Leu Ser Ala Pro Ala Gly Thr Glu Ala
                885                 890                 895
Val Val Gln Ile Phe Met Asn Gly Tyr Gln Phe Gly His Tyr Leu Pro
            900                 905                 910
His Ile Gly Pro Gln Ser Leu Phe Pro Phe Pro Pro Gly Val Ile Tyr
        915                 920                 925
Asn Arg Gly Gln Asn Ser Leu Ala Ile Ser Met Trp Ala Leu Thr Asp
    930                 935                 940
Ala Gly Ala Arg Leu Glu Gln Val Glu Leu Lys Ala Tyr Ala Lys Tyr
945                 950                 955                 960
Arg Ser Gly Phe Asp Phe Asn Arg Asp Trp Thr Tyr Leu Gln Pro Gly
                965                 970                 975
Trp Lys Asp Arg Thr Glu Tyr Ala
            980
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<210> 702
<211> 1005
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase A;
AltName: Full=Lactase A; Flags: Precursor 1005 aa
protein B8N6V7.1 GI:300680889

<400> 702
Met Lys Leu Leu Ser Val Ala Ala Val Ala Leu Leu Ala Ala Gln Ala
 1               5                  10                  15
Ala Gly Ala Ser Ile Lys His Arg Leu Asn Gly Phe Thr Ile Leu Glu
            20                  25                  30
His Pro Asp Pro Ala Lys Arg Asp Leu Leu Gln Asp Ile Val Thr Trp
        35                  40                  45
Asp Asp Lys Ser Leu Phe Ile Asn Gly Glu Arg Ile Met Leu Phe Ser
    50                  55                  60
Gly Glu Val His Pro Phe Arg Leu Pro Val Pro Ser Leu Trp Leu Asp
65                  70                  75                  80
Ile Phe His Lys Ile Arg Ala Leu Gly Phe Asn Cys Val Ser Phe Tyr
                85                  90                  95
Ile Asp Trp Ala Leu Leu Glu Gly Lys Pro Gly Asp Tyr Arg Ala Glu
            100                 105                 110
Gly Ile Phe Ala Leu Glu Pro Phe Phe Asp Ala Ala Lys Glu Ala Gly
        115                 120                 125
Ile Tyr Leu Ile Ala Arg Pro Gly Ser Tyr Ile Asn Ala Glu Val Ser
    130                 135                 140
Gly Gly Gly Phe Pro Gly Trp Leu Gln Arg Val Asn Gly Thr Leu Arg
145                 150                 155                 160
Ser Ser Asp Glu Pro Phe Leu Lys Ala Thr Asp Asn Tyr Ile Ala Asn
                165                 170                 175
Ala Ala Ala Ala Val Ala Lys Ala Gln Ile Thr Asn Gly Gly Pro Val
            180                 185                 190
Ile Leu Tyr Gln Pro Glu Asn Glu Tyr Ser Gly Gly Cys Cys Gly Val
        195                 200                 205
Lys Tyr Pro Asp Ala Asp Tyr Met Gln Tyr Val Met Asp Gln Ala Arg
    210                 215                 220
Lys Ala Asp Ile Val Val Pro Phe Ile Ser Asn Asp Ala Ser Pro Ser
225                 230                 235                 240
Gly His Asn Ala Pro Gly Ser Gly Thr Gly Ala Val Asp Ile Tyr Gly
                245                 250                 255
His Asp Ser Tyr Pro Leu Gly Phe Asp Cys Ala Asn Pro Ser Val Trp
            260                 265                 270
Pro Glu Gly Lys Leu Pro Asp Asn Phe Arg Thr Leu His Leu Glu Gln
        275                 280                 285
Ser Pro Ser Thr Pro Tyr Ser Leu Leu Glu Phe Gln Ala Gly Ala Phe
    290                 295                 300
Asp Pro Trp Gly Gly Pro Gly Phe Glu Lys Cys Tyr Ala Leu Val Asn
305                 310                 315                 320
His Glu Phe Ser Arg Val Phe Tyr Arg Asn Asp Leu Ser Phe Gly Val
                325                 330                 335
Ser Thr Phe Asn Leu Tyr Met Thr Phe Gly Gly Thr Asn Trp Gly Asn
            340                 345                 350
Leu Gly His Pro Gly Gly Tyr Thr Ser Tyr Asp Tyr Gly Ser Pro Ile
        355                 360                 365
Thr Glu Thr Arg Asn Val Thr Arg Glu Lys Tyr Ser Asp Ile Lys Leu
    370                 375                 380
Leu Ala Asn Phe Val Lys Ala Ser Pro Ser Tyr Leu Thr Ala Thr Pro
385                 390                 395                 400
Arg Asn Leu Thr Thr Gly Val Tyr Thr Asp Thr Ser Asp Leu Ala Val
                405                 410                 415

```
Thr Pro Leu Ile Gly Asp Ser Pro Gly Ser Phe Phe Val Val Arg His
            420                 425                 430
Thr Asp Tyr Ser Ser Gln Glu Ser Thr Ser Tyr Lys Leu Lys Leu Pro
        435                 440                 445
Thr Ser Ala Gly Asn Leu Thr Ile Pro Gln Leu Glu Gly Thr Leu Ser
    450                 455                 460
Leu Asn Gly Arg Asp Ser Lys Ile His Val Val Asp Tyr Asn Val Ser
465                 470                 475                 480
Gly Thr Asn Ile Ile Tyr Ser Thr Ala Glu Val Phe Thr Trp Lys Lys
                485                 490                 495
Phe Asp Gly Asn Lys Val Leu Val Leu Tyr Gly Gly Pro Lys Glu His
            500                 505                 510
His Glu Leu Ala Ile Ala Ser Lys Ser Asn Val Thr Ile Ile Glu Gly
        515                 520                 525
Ser Asp Ser Gly Ile Val Ser Thr Arg Lys Gly Ser Ser Val Ile Ile
    530                 535                 540
Gly Trp Asp Val Ser Ser Thr Arg Arg Ile Val Gln Val Gly Asp Leu
545                 550                 555                 560
Arg Val Phe Leu Leu Asp Arg Asn Ser Ala Tyr Asn Tyr Trp Val Pro
                565                 570                 575
Glu Leu Pro Thr Glu Gly Thr Ser Pro Gly Phe Ser Thr Ser Lys Thr
            580                 585                 590
Thr Ala Ser Ser Ile Ile Val Lys Ala Gly Tyr Leu Leu Arg Gly Ala
        595                 600                 605
His Leu Asp Gly Ala Asp Leu His Leu Thr Ala Asp Phe Asn Ala Thr
    610                 615                 620
Thr Pro Ile Glu Val Ile Gly Ala Pro Thr Gly Ala Lys Asn Leu Phe
625                 630                 635                 640
Val Asn Gly Glu Lys Ala Ser His Thr Val Asp Lys Asn Gly Ile Trp
                645                 650                 655
Ser Ser Glu Val Lys Tyr Ala Ala Pro Glu Ile Lys Leu Pro Gly Leu
            660                 665                 670
Lys Asp Leu Asp Trp Lys Tyr Leu Asp Thr Leu Pro Glu Ile Lys Ser
        675                 680                 685
Ser Tyr Asp Asp Ser Ala Trp Val Ser Ala Asp Leu Pro Lys Thr Lys
    690                 695                 700
Asn Thr His Arg Pro Leu Asp Thr Pro Thr Ser Leu Tyr Ser Ser Asp
705                 710                 715                 720
Tyr Gly Phe His Thr Gly Tyr Leu Ile Tyr Arg Gly His Phe Val Ala
                725                 730                 735
Asn Gly Lys Glu Ser Glu Phe Phe Ile Arg Thr Gln Gly Gly Ser Ala
            740                 745                 750
Phe Gly Ser Ser Val Trp Leu Asn Glu Thr Tyr Leu Gly Ser Trp Thr
        755                 760                 765
Gly Ala Asp Tyr Ala Met Asp Gly Asn Ser Thr Tyr Lys Leu Ser Gln
    770                 775                 780
Leu Glu Ser Gly Lys Asn Tyr Val Ile Thr Val Val Ile Asp Asn Leu
785                 790                 795                 800
Gly Leu Asp Glu Asn Trp Thr Val Gly Glu Glu Thr Met Lys Asn Pro
                805                 810                 815
Arg Gly Ile Leu Ser Tyr Lys Leu Ser Gly Gln Asp Ala Ser Ala Ile
            820                 825                 830
Thr Trp Lys Leu Thr Gly Asn Leu Gly Gly Glu Asp Tyr Gln Asp Lys
        835                 840                 845
```

```
Val Arg Gly Pro Leu Asn Glu Gly Gly Leu Tyr Ala Glu Arg Gln Gly
    850                 855                 860
Phe His Gln Pro Gln Pro Pro Ser Glu Ser Trp Glu Ser Gly Ser Pro
865                 870                 875                 880
Leu Glu Gly Leu Ser Lys Pro Gly Ile Gly Phe Tyr Thr Ala Gln Phe
                885                 890                 895
Asp Leu Asp Leu Pro Lys Gly Trp Asp Val Pro Leu Tyr Phe Asn Phe
            900                 905                 910
Gly Asn Asn Thr Gln Ala Ala Arg Ala Gln Leu Tyr Val Asn Gly Tyr
        915                 920                 925
Gln Tyr Gly Lys Phe Thr Gly Asn Val Gly Pro Gln Thr Ser Phe Pro
    930                 935                 940
Val Pro Glu Gly Ile Leu Asn Tyr Arg Gly Thr Asn Tyr Val Ala Leu
945                 950                 955                 960
Ser Leu Trp Ala Leu Glu Ser Asp Gly Ala Lys Leu Gly Ser Phe Glu
                965                 970                 975
Leu Ser Tyr Thr Thr Pro Val Leu Thr Gly Tyr Gly Asn Val Glu Ser
            980                 985                 990
Pro Glu Gln Pro Lys Tyr Glu Gln Arg Lys Gly Ala Tyr
        995                 1000                1005
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<210> 703
<211> 1020
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase B;
AltName: Full=Lactase B; Flags: Precursor 12 aa
protein B8NKI4.2 GI:68115

<400> 703

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

```
                165                 170                 175
Ile Ala Pro His Leu Ile Thr Asn Gly Gly Asn Val Ile Leu Tyr Gln
            180                 185                 190
Ile Glu Asn Glu Tyr Ala Glu Gln Trp Leu Asp Glu Glu Thr His Glu
        195                 200                 205
Pro Asn Thr Ser Gly Gln Glu Tyr Met Gln Tyr Leu Glu Asp Val Ala
    210                 215                 220
Arg Glu Asn Gly Ile Asp Ala Pro Leu Ile His Asn Leu Pro Asn Met
225                 230                 235                 240
Asn Gly His Ser Trp Ser Lys Asp Leu Ser Asn Ala Thr Gly Asn Val
                245                 250                 255
Asp Val Ile Gly Val Asp Ser Tyr Pro Thr Cys Trp Thr Cys Asn Val
            260                 265                 270
Ser Glu Cys Ala Ser Thr Asn Gly Glu Tyr Ile Pro Tyr Lys Thr Leu
        275                 280                 285
Ile Tyr Tyr Asp Tyr Phe Lys Glu Leu Ser Pro Thr Gln Pro Ser Phe
    290                 295                 300
Met Pro Glu Phe Gln Gly Gly Ser Tyr Asn Pro Trp Gly Gly Pro Gln
305                 310                 315                 320
Gly Gly Cys Pro Asp Asp Leu Gly Pro Asp Phe Ala Asn Leu Phe Tyr
                325                 330                 335
Arg Asn Leu Ile Ser Gln Arg Val Ser Ala Ile Ser Leu Tyr Met Leu
            340                 345                 350
Tyr Gly Gly Thr Asn Trp Gly Trp His Ala Ser Thr Asp Val Ala Thr
        355                 360                 365
Ser Tyr Asp Tyr Ser Ser Pro Ile Ser Glu Asn Arg Lys Leu Ile Glu
    370                 375                 380
Lys Tyr Tyr Glu Thr Lys Val Leu Thr Gln Phe Thr Lys Ile Ala Gln
385                 390                 395                 400
Asp Leu Ser Lys Val Asp Arg Leu Gly Asn Ser Thr Lys Tyr Ser Ser
                405                 410                 415
Asn Pro Ala Val Ser Val Ala Glu Leu Arg Asn Pro Asp Thr Gly Ala
            420                 425                 430
Ala Phe Tyr Val Thr Gln His Glu Tyr Thr Pro Ser Gly Thr Val Glu
        435                 440                 445
Lys Phe Thr Val Lys Val Asn Thr Ser Glu Gly Ala Leu Thr Ile Pro
    450                 455                 460
Gln Tyr Gly Ser Gln Ile Thr Leu Asn Gly His Gln Ser Lys Ile Ile
465                 470                 475                 480
Val Thr Asp Phe Lys Phe Gly Ser Lys Thr Leu Leu Tyr Ser Thr Ala
                485                 490                 495
Glu Val Leu Thr Tyr Ala Val Ile Asp Gly Lys Glu Val Leu Ala Leu
            500                 505                 510
Trp Val Pro Thr Gly Glu Ser Gly Glu Phe Thr Val Lys Gly Val Asn
        515                 520                 525
Ser Ala Lys Phe Ala Asp Lys Gly Arg Thr Ala Asn Ile Glu Ile His
    530                 535                 540
Pro Gly Ala Asn Asn Val Thr Val Ser Phe Met Gln Arg Ser Gly Met
545                 550                 555                 560
Ser Leu Val Glu Leu Gly Asp Gly Thr Arg Ile Val Leu Leu Asp Arg
                565                 570                 575
Ser Ala Ala His Val Phe Trp Ser Thr Pro Leu Asn Asn Asp Pro Ala
            580                 585                 590
Glu Ala Gly Asn Asn Thr Val Leu Val His Gly Pro Tyr Leu Val Arg
```

```
        595                 600                 605
Ser Ala Lys Leu Glu Gly Cys Asp Leu Lys Leu Thr Gly Asp Ile Gln
    610                 615                 620
Asn Ser Thr Glu Val Ser Ile Phe Ala Pro Lys Ser Val Cys Ser Val
625                 630                 635                 640
Asn Trp Asn Gly Lys Lys Thr Ser Val Lys Ser Ala Lys Gly Gly Val
                645                 650                 655
Ile Thr Thr Thr Leu Gly Gly Asp Ala Lys Phe Glu Leu Pro Thr Ile
            660                 665                 670
Ser Gly Trp Lys Ser Ala Asp Ser Leu Pro Glu Ile Ala Lys Asp Tyr
        675                 680                 685
Ser Ala Thr Ser Lys Ala Trp Val Val Ala Thr Lys Thr Asn Ser Ser
    690                 695                 700
Asn Pro Thr Pro Pro Ala Pro Asn Asn Pro Val Leu Tyr Val Asp Glu
705                 710                 715                 720
Asn Asp Ile His Val Gly Asn His Ile Tyr Arg Ala Thr Phe Pro Ser
                725                 730                 735
Thr Asp Glu Pro Pro Thr Asp Val Tyr Leu Asn Ile Thr Gly Gly Arg
            740                 745                 750
Ala Phe Ser Tyr Ser Val Trp Leu Asn Ser Asp Phe Ile Gly Ser Trp
        755                 760                 765
Leu Gly Thr Ala Thr Thr Glu Gln Asn Asp Gln Thr Phe Ser Phe Ser
    770                 775                 780
Asn Ala Thr Leu Ser Thr Asp Glu Asp Asn Ile Leu Val Val Val Met
785                 790                 795                 800
Asp Asn Ser Ala His Asp Leu Arg Asp Gly Ala Leu Asn Pro Arg Gly
                805                 810                 815
Ile Thr Asn Ala Thr Leu Ile Gly Pro Gly Ser Tyr Ser Phe Thr Glu
            820                 825                 830
Trp Lys Leu Ala Gly Asn Ala Gly Phe Glu Asp His Leu Asp Pro Val
        835                 840                 845
Arg Ala Pro Leu Asn Glu Gly Ser Leu Tyr Ala Glu Arg Val Gly Ile
    850                 855                 860
His Leu Pro Gly Tyr Glu Phe Asp Glu Ala Glu Glu Val Ser Ser Asn
865                 870                 875                 880
Ser Thr Ser Leu Thr Val Pro Gly Ala Gly Ile Arg Val Phe Arg Thr
                885                 890                 895
Val Val Pro Leu Ser Val Pro Gln Gly Leu Asp Val Ser Ile Ser Phe
            900                 905                 910
Arg Leu Thr Ala Pro Ser Asn Val Thr Phe Thr Ser Ala Glu Gly Tyr
        915                 920                 925
Thr Asn Gln Leu Arg Ala Leu Leu Phe Val Asn Gly Tyr Gln Tyr Gly
    930                 935                 940
Arg Phe Asn Pro Tyr Ile Gly His Gln Ile Asp Phe Pro Val Pro Pro
945                 950                 955                 960
Gly Val Leu Asp Tyr Asn Gly Asp Asn Thr Ile Ala Val Thr Val Trp
                965                 970                 975
Ser Gln Ser Val Asp Gly Ala Glu Ile Lys Val Asp Trp Asn Val Asp
            980                 985                 990
Tyr Val His Glu Thr Ser Phe Asp Met Asn Phe Asp Gly Ala Tyr Leu
        995                 1000                1005
Arg Pro Gly Trp Ile Glu Glu Arg Arg Glu Tyr Ala
    1010                1015                1020
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<210> 704
<211> 1022
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase B;
AltName: Full=Lactase B; Flags: Precursor 1022 aa
protein Q0CMF3.2 GI:300681013

<400> 704
Met Ala Arg Phe Pro Gln Leu Leu Phe Leu Leu Leu Ala Ser Ile Gly
1 5 10 15
Leu Leu Ser Ala Ala Gln Asn His Ser Asp Ser Glu Trp Pro Leu His
20 25 30
Asp Asn Gly Leu Ser Thr Val Val Gln Trp Asp His Tyr Ser Phe His
35 40 45
Val His Gly Gln Arg Ile Phe Val Phe Ser Gly Glu Phe His Tyr Trp
50 55 60
Arg Ile Pro Val Pro Gly Leu Trp Arg Asp Ile Leu Glu Lys Ile Lys
65 70 75 80
Ala Ala Gly Phe Thr Ala Phe Ala Phe Tyr Ser Ser Trp Gly Tyr His
85 90 95
Ala Pro Asn Asn His Thr Val Asp Phe Ser Thr Gly Ala Arg Asp Ile
100 105 110
Thr Pro Ile Tyr Glu Leu Ala Lys Glu Leu Gly Met Tyr Ile Ile Val
115 120 125
Arg Pro Gly Pro Tyr Val Asn Ala Glu Ala Ser Ala Gly Gly Tyr Pro
130 135 140
Leu Trp Val Thr Thr Gly Ala Tyr Gly Ser Leu Arg Asn Asp Asp Ala
145 150 155 160
Arg Tyr Thr Ala Ala Trp Lys Pro Tyr Phe Ala Lys Met Ser Glu Ile
165 170 175
Thr Ser Gln Tyr Gln Val Thr Asp Gly His Asn Thr Phe Cys Tyr Gln
180 185 190
Ile Glu Asn Glu Tyr Gly Gln Gln Trp Ile Gly Asp Pro Val Asp Arg
195 200 205
Asn Pro Asn Gln Thr Ala Val Ala Tyr Met Glu Leu Leu Glu Ala Ser
210 215 220
Ala Arg Glu Asn Gly Ile Val Val Pro Leu Thr Ala Asn Asp Pro Asn
225 230 235 240
Met Asn Thr Lys Ser Trp Gly Ser Asp Trp Ser His Ala Gly Gly Asn
245 250 255
Val Asp Val Val Gly Leu Asp Ser Tyr Pro Ser Cys Trp Thr Cys Asp
260 265 270
Val Thr Gln Cys Thr Ser Thr Asn Gly Glu Tyr Val Pro Tyr Lys Val
275 280 285
Met Gln Tyr Tyr Asp Tyr Phe Gln Glu Val Gln Pro Thr Met Pro Gly
290 295 300
Phe Met Pro Glu Phe Gln Gly Gly Ser Tyr Asn Pro Trp Ala Gly Pro
305 310 315 320
Glu Gly Gly Cys Pro Gly Asp Thr Gly Val Asp Phe Ala Asn Leu Phe
325 330 335

```
Tyr Arg Trp Asn Ile Ala Gln Arg Val Thr Ala Met Ser Leu Tyr Met
            340                 345                 350
Leu Tyr Gly Gly Thr Asn Trp Gly Ala Ile Ala Ala Pro Val Thr Ala
        355                 360                 365
Thr Ser Tyr Asp Tyr Ser Ser Pro Ile Ser Glu Asp Arg Ser Ile Gly
    370                 375                 380
Ser Lys Tyr Tyr Glu Thr Lys Leu Leu Ala Leu Phe Thr Arg Ser Ala
385                 390                 395                 400
Thr Asp Leu Thr Met Thr Asp Arg Ile Gly Asn Gly Thr His Tyr Thr
                405                 410                 415
Asn Asn Pro Ala Val Ala Ala Tyr Glu Leu Arg Asn Pro Val Thr Asn
            420                 425                 430
Gly Ala Phe Tyr Val Thr Ile His Ala Asp Ser Thr Val Gly Thr Asp
        435                 440                 445
Glu Ser Phe Arg Leu Asn Val Asn Thr Ser Ala Gly Ala Leu Thr Val
    450                 455                 460
Pro Ser Lys Gly Ser Ile Arg Leu Asn Gly His Gln Ser Lys Ile Ile
465                 470                 475                 480
Val Thr Asp Phe Arg Phe Gly Pro Ser His Thr Leu Leu Tyr Ser Thr
                485                 490                 495
Ala Glu Val Leu Thr His Ala Val Met Asp Lys Lys Ala Thr Leu Val
            500                 505                 510
Leu Trp Val Pro Thr Gly Glu Ser Gly Glu Phe Ala Val Lys Gly Ala
        515                 520                 525
Lys Ser Gly Lys Val Glu Arg Cys Pro Gln Cys Ser Asn Ala Thr Phe
    530                 535                 540
Thr Arg Lys Lys Asp Val Leu Val Val Asn Phe Thr Gln Ala Gly Gly
545                 550                 555                 560
Met Ser Val Leu Gln Leu Asn Asn Gly Val Arg Val Val Leu Leu Asp
                565                 570                 575
Arg Ala Ala Ala Tyr Lys Phe Trp Ala Pro Pro Leu Thr Asp Asp Pro
            580                 585                 590
Phe Ala Pro Glu Thr Asp Leu Val Leu Val Gln Gly Pro Tyr Leu Val
        595                 600                 605
Arg Ser Ala Ser Leu Ser Gly Ser Thr Leu Ala Leu Arg Gly Asp Ser
    610                 615                 620
Ala Asn Glu Thr Ala Leu Glu Val Phe Ala Ser Lys Lys Val His Thr
625                 630                 635                 640
Val Thr Trp Asn Gly Lys Arg Ile Lys Thr Ser Arg Ser Ser Tyr Gly
                645                 650                 655
Ser Leu Thr Ala Ser Leu Ala Ala Pro Pro Ala Val Ser Leu Pro Ala
            660                 665                 670
Leu Ser Ser Ala Gln Trp Lys Ser Gln Asp Ser Leu Pro Glu Arg Leu
        675                 680                 685
Pro Ser Tyr Asp Asp Ser Gly Pro Ala Trp Val Asp Ala Asn His Met
    690                 695                 700
Thr Thr Gln Asn Pro Arg Thr Pro Asp Thr Leu Pro Val Leu Tyr Ala
705                 710                 715                 720
Asp Glu Tyr Gly Phe His Asn Gly Ile Arg Leu Trp Arg Gly Ser Phe
                725                 730                 735
Thr Asp Ala Ala Ser Gly Val Tyr Leu Asn Val Gln Gly Gly Ala Ala
            740                 745                 750
Phe Gly Trp Ser Ala Tyr Leu Asn Gly His Phe Leu Gly Ser His Leu
        755                 760                 765
```

```
Gly Thr Ala Thr Thr Ser Gln Ala Asn Lys Thr Leu Leu Phe Pro Ala
    770                 775                 780
Gly Thr Leu Arg Lys Asn Thr Thr Asn Thr Ile Leu Val Ile His Asp
785                 790                 795                 800
Asp Thr Gly His Asp Gln Thr Thr Gly Ala Leu Asn Pro Arg Gly Ile
                805                 810                 815
Leu Ala Ala Arg Leu Leu Ala Pro Ser Asp Ser Ser Thr Ala Pro Asn
            820                 825                 830
Phe Thr Gln Trp Arg Val Ala Gly Thr Ala Gly Gly Glu Ser Asp Leu
        835                 840                 845
Asp Pro Val Arg Gly Val Tyr Asn Glu Asp Gly Leu Phe Ala Glu Arg
    850                 855                 860
Met Gly Trp His Leu Pro Gly Phe Asp Asp Ala Asp Trp Pro Ala Asn
865                 870                 875                 880
Asn Ser Thr Thr Thr Arg Gly Ala Gln Val Ser Leu Ser Val Thr Gly
                885                 890                 895
Ala Thr Val Arg Phe Phe Arg Ala Val Val Pro Leu His Leu Pro Arg
            900                 905                 910
Gly Val Asp Ala Ser Ile Ser Phe Met Leu Gly Thr Pro Ala Gly Ala
        915                 920                 925
Ser Thr Ala Tyr Arg Ala Gln Leu Phe Val Asn Gly Tyr Gln Tyr Gly
    930                 935                 940
Arg Phe Tyr Pro His Ile Gly Asn Gln Val Val Tyr Pro Val Pro Ala
945                 950                 955                 960
Gly Val Leu Asp Tyr Asp Gly Glu Asn Thr Ile Gly Val Ala Val Trp
                965                 970                 975
Ala Gln Ser Glu Ala Gly Ala Glu Met Ser Leu Asp Trp Arg Val Asn
            980                 985                 990
Tyr Val Ala Asp Ser Ser Leu Asp Ala Val Arg Val Ala Ala Glu Gly
        995                 1000                1005
Ala Leu Arg Pro Gly Trp Ser Glu Glu Arg Leu Gln Tyr Ala
    1010                1015                1020


<210> 705
<211> 1022
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase B;
      AltName: Full=Lactase B; Flags: Precursor 1022 aa
      protein Q2U6P1.2 GI:300681012

<400> 705
Met Leu Ile Ser Lys Thr Val Leu Ser Gly Leu Ala Leu Gly Ala Ser
 1               5                  10                  15
Phe Val Gly Val Ser Ala Gln Gln Asn Ser Thr Arg Trp Pro Leu His
            20                  25                  30
Asp Asn Gly Leu Thr Asp Thr Val Glu Trp Asp His Tyr Ser Phe Leu
        35                  40                  45
Ile Asn Gly Gln Arg His Phe Val Phe Ser Gly Glu Phe His Tyr Trp
    50                  55                  60
Arg Ile Pro Val Pro Glu Leu Trp Arg Asp Leu Leu Glu Lys Ile Lys
```

```
65                  70                  75                  80
Ala Ala Gly Phe Thr Ala Phe Ser Ile Tyr Asn His Trp Gly Tyr His
                85                  90                  95
Ser Pro Lys Pro Gly Val Leu Asp Phe Glu Asn Gly Ala His Asn Phe
            100                 105                 110
Thr Ser Ile Met Thr Leu Ala Lys Glu Ile Gly Leu Tyr Met Ile Ile
        115                 120                 125
Arg Pro Gly Pro Tyr Val Asn Ala Glu Ala Asn Ala Gly Gly Leu Pro
    130                 135                 140
Leu Trp Thr Thr Thr Gly Ala Tyr Gly Lys Leu Arg Asp Asn Asp Pro
145                 150                 155                 160
Arg Tyr Leu Glu Ala Leu Thr Pro Tyr Trp Ala Asn Ile Ser Lys Ile
                165                 170                 175
Ile Ala Pro His Leu Ile Thr Asn Asp Gly Asn Val Ile Leu Tyr Gln
            180                 185                 190
Ile Glu Asn Glu Tyr Ala Glu Gln Trp Leu Asp Glu Glu Thr His Glu
        195                 200                 205
Pro Asn Thr Ser Gly Gln Glu Tyr Met Gln Tyr Leu Glu Asp Val Ala
    210                 215                 220
Arg Glu Asn Gly Ile Asp Ala Pro Leu Ile His Asn Leu Pro Asn Met
225                 230                 235                 240
Asn Gly His Ser Trp Ser Lys Asp Leu Ser Asn Ala Thr Gly Asn Val
                245                 250                 255
Asp Val Ile Gly Val Asp Ser Tyr Pro Thr Cys Trp Thr Cys Asn Val
            260                 265                 270
Ser Glu Cys Ala Ser Thr Asn Gly Glu Tyr Ile Pro Tyr Leu Lys Leu
        275                 280                 285
Thr Tyr Pro Gln Ile Ser Tyr Phe Lys Glu Leu Ser Pro Thr Gln Pro
    290                 295                 300
Ser Phe Met Pro Glu Phe Gln Gly Gly Ser Tyr Asn Pro Trp Gly Gly
305                 310                 315                 320
Pro Gln Gly Gly Cys Pro Asp Asp Leu Gly Pro Asp Phe Ala Asn Leu
                325                 330                 335
Phe Tyr Arg Asn Leu Ile Ser Gln Arg Val Ser Ala Ile Ser Leu Tyr
            340                 345                 350
Met Leu Tyr Gly Gly Thr Asn Trp Gly Trp His Ala Ser Thr Asp Val
        355                 360                 365
Ala Thr Ser Tyr Asp Tyr Ser Ser Pro Ile Ser Glu Asn Arg Lys Leu
    370                 375                 380
Ile Glu Lys Tyr Tyr Glu Thr Lys Val Leu Thr Gln Phe Thr Lys Ile
385                 390                 395                 400
Ala Gln Asp Leu Ser Lys Val Asp Arg Leu Gly Asn Ser Thr Lys Tyr
                405                 410                 415
Ser Ser Asn Pro Ala Val Ser Val Ala Glu Leu Arg Asn Pro Asp Thr
            420                 425                 430
Gly Ala Ala Phe Tyr Val Thr Gln His Glu Tyr Thr Pro Ser Gly Thr
        435                 440                 445
Val Glu Lys Phe Thr Val Lys Val Asn Thr Ser Glu Gly Ala Leu Thr
    450                 455                 460
Ile Pro Gln Tyr Gly Ser Gln Ile Thr Leu Asn Gly His Gln Ser Lys
465                 470                 475                 480
Ile Ile Val Thr Asp Phe Lys Phe Gly Ser Lys Thr Leu Leu Tyr Ser
                485                 490                 495
Thr Ala Glu Val Leu Thr Tyr Ala Val Ile Asp Gly Lys Glu Val Leu
```

```
            500                 505                 510
Ala Leu Trp Val Pro Thr Gly Glu Ser Gly Glu Phe Thr Val Lys Gly
        515                 520                 525
Val Asn Ser Ala Lys Phe Ala Asp Lys Gly Arg Thr Ala Asn Ile Glu
    530                 535                 540
Ile His Pro Gly Thr Asn Asn Val Thr Val Ser Phe Met Gln Arg Ser
545                 550                 555                 560
Gly Met Ser Leu Val Glu Leu Gly Asp Gly Thr Arg Ile Val Leu Leu
                565                 570                 575
Asp Arg Ser Ala Ala His Val Phe Trp Ser Thr Pro Leu Asn Asn Asp
            580                 585                 590
Pro Ala Glu Ala Gly Asn Asn Thr Val Leu Val His Gly Pro Tyr Leu
        595                 600                 605
Val Arg Ser Ala Lys Leu Glu Gly Cys Asp Leu Lys Leu Thr Gly Asp
    610                 615                 620
Ile Gln Asn Ser Thr Glu Val Ser Ile Phe Ala Pro Lys Ser Val Cys
625                 630                 635                 640
Ser Val Asn Trp Asn Gly Lys Lys Thr Ser Val Lys Ser Ala Lys Gly
                645                 650                 655
Gly Val Ile Thr Thr Thr Leu Gly Gly Asp Ala Lys Phe Glu Leu Pro
            660                 665                 670
Thr Ile Ser Gly Trp Lys Ser Ala Asp Ser Leu Pro Glu Ile Ala Lys
        675                 680                 685
Asp Tyr Ser Ala Thr Ser Lys Ala Trp Val Val Ala Thr Lys Thr Asn
    690                 695                 700
Ser Ser Asn Pro Thr Pro Pro Ala Pro Asn Asn Pro Val Leu Tyr Val
705                 710                 715                 720
Asp Glu Asn Asp Ile His Val Gly Asn His Ile Tyr Arg Ala Thr Phe
                725                 730                 735
Pro Ser Thr Asp Glu Pro Pro Thr Asp Val Tyr Leu Asn Ile Thr Gly
            740                 745                 750
Gly Arg Ala Phe Gly Tyr Ser Val Trp Leu Asn Ser Asp Phe Ile Gly
        755                 760                 765
Ser Trp Leu Gly Thr Ala Thr Thr Glu Gln Asn Asp Gln Thr Phe Ser
    770                 775                 780
Phe Ser Asn Ala Thr Leu Ser Thr Asp Glu Asp Asn Ile Leu Val Val
785                 790                 795                 800
Val Met Asp Asn Ser Ala His Asp Leu Arg Asp Gly Ala Leu Asn Pro
                805                 810                 815
Arg Gly Ile Thr Asn Ala Thr Leu Ile Gly Pro Gly Ser Tyr Ser Phe
            820                 825                 830
Thr Glu Trp Lys Leu Ala Gly Asn Ala Gly Phe Glu Asp His Leu Asp
        835                 840                 845
Pro Val Arg Ala Pro Leu Asn Glu Gly Ser Leu Tyr Ala Glu Arg Val
    850                 855                 860
Gly Ile His Leu Pro Gly Tyr Glu Phe Asp Glu Ala Glu Glu Val Ser
865                 870                 875                 880
Ser Asn Ser Thr Ser Leu Thr Val Pro Gly Ala Gly Ile Arg Val Phe
                885                 890                 895
Arg Thr Val Val Pro Leu Ser Val Pro Gln Gly Leu Asp Val Ser Ile
            900                 905                 910
Ser Phe Arg Leu Thr Ala Pro Ser Asn Val Thr Phe Thr Ser Ala Glu
        915                 920                 925
Gly Tyr Thr Asn Gln Leu Arg Ala Leu Leu Phe Val Asn Gly Tyr Gln
```

```
    930                 935                 940
Tyr Gly Arg Phe Asn Pro Tyr Ile Gly His Gln Ile Asp Phe Pro Val
945                 950                 955                 960
Pro Pro Gly Val Leu Asp Tyr Asn Gly Asp Asn Thr Ile Ala Val Thr
                965                 970                 975
Val Trp Ser Gln Ser Val Asp Gly Ala Glu Ile Lys Val Asp Trp Asn
            980                 985                 990
Val Asp Tyr Val His Glu Thr Ser Phe Asp Met Asn Phe Asp Gly Ala
        995                 1000                1005
Tyr Leu Arg Pro Gly Trp Ile Glu Glu Arg Arg Glu Tyr Ala
    1010                1015                1020


<210> 706
<211> 1005
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase A;
      AltName: Full=Lactase A; Flags: Precursor 1005 aa
      protein Q2UCU3.1 GI:121801672

<400> 706
Met Lys Leu Leu Ser Val Ala Ala Val Ala Leu Leu Ala Ala Gln Ala
 1               5                  10                  15
Ala Gly Ala Ser Ile Lys His Arg Leu Asn Gly Phe Thr Ile Leu Glu
            20                  25                  30
His Pro Asp Pro Ala Lys Arg Asp Leu Leu Gln Asp Ile Val Thr Trp
        35                  40                  45
Asp Asp Lys Ser Leu Phe Ile Asn Gly Glu Arg Ile Met Leu Phe Ser
    50                  55                  60
Gly Glu Val His Pro Phe Arg Leu Pro Val Pro Ser Leu Trp Leu Asp
65                  70                  75                  80
Ile Phe His Lys Ile Arg Ala Leu Gly Phe Asn Cys Val Ser Phe Tyr
                85                  90                  95
Ile Asp Trp Ala Leu Leu Glu Gly Lys Pro Gly Asp Tyr Arg Ala Glu
            100                 105                 110
Gly Ile Phe Ala Leu Glu Pro Phe Phe Asp Ala Ala Lys Glu Ala Gly
        115                 120                 125
Ile Tyr Leu Ile Ala Arg Pro Gly Ser Tyr Ile Asn Ala Glu Val Ser
    130                 135                 140
Gly Gly Gly Phe Pro Gly Trp Leu Gln Arg Val Asn Gly Thr Leu Arg
145                 150                 155                 160
Ser Ser Asp Glu Pro Phe Leu Lys Ala Thr Asp Asn Tyr Ile Ala Asn
                165                 170                 175
Ala Ala Ala Ala Val Ala Lys Ala Gln Ile Thr Asn Gly Gly Pro Val
            180                 185                 190
Ile Leu Tyr Gln Pro Glu Asn Glu Tyr Ser Gly Gly Cys Cys Gly Val
        195                 200                 205
Lys Tyr Pro Asp Ala Asp Tyr Met Gln Tyr Val Met Asp Gln Ala Arg
    210                 215                 220
Lys Ala Asp Ile Val Val Pro Phe Ile Ser Asn Asp Ala Ser Pro Ser
225                 230                 235                 240
```

```
Gly His Asn Ala Pro Gly Ser Gly Thr Gly Ala Val Asp Ile Tyr Gly
                245                 250                 255
His Asp Ser Tyr Pro Leu Gly Phe Asp Cys Ala Asn Pro Ser Val Trp
            260                 265                 270
Pro Glu Gly Lys Leu Pro Asp Asn Phe Arg Thr Leu His Leu Glu Gln
        275                 280                 285
Ser Pro Ser Thr Pro Tyr Ser Leu Leu Glu Phe Gln Ala Gly Ala Phe
    290                 295                 300
Asp Pro Trp Gly Gly Pro Gly Phe Glu Lys Cys Tyr Ala Leu Val Asn
305                 310                 315                 320
His Glu Phe Ser Arg Val Phe Tyr Arg Asn Asp Leu Ser Phe Gly Val
                325                 330                 335
Ser Thr Phe Asn Leu Tyr Met Thr Phe Gly Gly Thr Asn Trp Gly Asn
            340                 345                 350
Leu Gly His Pro Gly Gly Tyr Thr Ser Tyr Asp Tyr Gly Ser Pro Ile
        355                 360                 365
Thr Glu Thr Arg Asn Val Thr Arg Glu Lys Tyr Ser Asp Ile Lys Leu
    370                 375                 380
Leu Ala Asn Phe Val Lys Ala Ser Pro Ser Tyr Leu Thr Ala Thr Pro
385                 390                 395                 400
Arg Asn Leu Thr Thr Gly Val Tyr Thr Asp Thr Ser Asp Leu Ala Val
                405                 410                 415
Thr Pro Leu Ile Gly Asp Ser Pro Gly Ser Phe Phe Val Val Arg His
            420                 425                 430
Thr Asp Tyr Ser Ser Gln Glu Ser Thr Ser Tyr Lys Leu Lys Leu Pro
        435                 440                 445
Thr Ser Ala Gly Asn Leu Thr Ile Pro Gln Leu Glu Gly Thr Leu Ser
    450                 455                 460
Leu Asn Gly Arg Asp Ser Lys Ile His Val Val Asp Tyr Asn Val Ser
465                 470                 475                 480
Gly Thr Asn Ile Ile Tyr Ser Thr Ala Glu Val Phe Thr Trp Lys Lys
                485                 490                 495
Phe Asp Gly Asn Lys Val Leu Val Leu Tyr Gly Gly Pro Lys Glu His
            500                 505                 510
His Glu Leu Ala Ile Ala Ser Lys Ser Asn Val Thr Ile Ile Glu Gly
        515                 520                 525
Ser Asp Ser Gly Ile Val Ser Thr Arg Lys Gly Ser Ser Val Ile Ile
    530                 535                 540
Gly Trp Asp Val Ser Ser Thr Arg Arg Ile Val Gln Val Gly Asp Leu
545                 550                 555                 560
Arg Val Phe Leu Leu Asp Arg Asn Ser Ala Tyr Asn Tyr Trp Val Pro
                565                 570                 575
Glu Leu Pro Thr Glu Gly Thr Ser Pro Gly Phe Ser Thr Ser Lys Thr
            580                 585                 590
Thr Ala Ser Ser Ile Ile Val Lys Ala Gly Tyr Leu Leu Arg Gly Ala
        595                 600                 605
His Leu Asp Gly Ala Asp Leu His Leu Thr Ala Asp Phe Asn Ala Thr
    610                 615                 620
Thr Pro Ile Glu Val Ile Gly Ala Pro Thr Gly Ala Lys Asn Leu Phe
625                 630                 635                 640
Val Asn Gly Glu Lys Ala Ser His Thr Val Asp Lys Asn Gly Ile Trp
                645                 650                 655
Ser Ser Glu Val Lys Tyr Ala Ala Pro Glu Ile Lys Leu Pro Gly Leu
            660                 665                 670
```

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Lys Asp Leu Asp Trp Lys Tyr Leu Asp Thr Leu Pro Glu Ile Lys Ser
        675                 680                 685
Ser Tyr Asp Asp Ser Ala Trp Val Ser Ala Asp Leu Pro Lys Thr Lys
    690                 695                 700
Asn Thr His Arg Pro Leu Asp Thr Pro Thr Ser Leu Tyr Ser Ser Asp
705                 710                 715                 720
Tyr Gly Phe His Thr Gly Tyr Leu Ile Tyr Arg Gly His Phe Val Ala
                725                 730                 735
Asn Gly Lys Glu Ser Glu Phe Phe Ile Arg Thr Gln Gly Gly Ser Ala
            740                 745                 750
Phe Gly Ser Ser Val Trp Leu Asn Glu Thr Tyr Leu Gly Ser Trp Thr
        755                 760                 765
Gly Ala Asp Tyr Ala Met Asp Gly Asn Ser Thr Tyr Lys Leu Ser Gln
    770                 775                 780
Leu Glu Ser Gly Lys Asn Tyr Val Ile Thr Val Val Ile Asp Asn Leu
785                 790                 795                 800
Gly Leu Asp Glu Asn Trp Thr Val Gly Glu Glu Thr Met Lys Asn Pro
                805                 810                 815
Arg Gly Ile Leu Ser Tyr Lys Leu Ser Gly Gln Asp Ala Ser Ala Ile
            820                 825                 830
Thr Trp Lys Leu Thr Gly Asn Leu Gly Gly Glu Asp Tyr Gln Asp Lys
        835                 840                 845
Val Arg Gly Pro Leu Asn Glu Gly Gly Leu Tyr Ala Glu Arg Gln Gly
    850                 855                 860
Phe His Gln Pro Gln Pro Pro Ser Glu Ser Trp Glu Ser Gly Ser Pro
865                 870                 875                 880
Leu Glu Gly Leu Ser Lys Pro Gly Ile Gly Phe Tyr Thr Ala Gln Phe
                885                 890                 895
Asp Leu Asp Leu Pro Lys Gly Trp Asp Val Pro Leu Tyr Phe Asn Phe
            900                 905                 910
Gly Asn Asn Thr Gln Ala Ala Arg Ala Gln Leu Tyr Val Asn Gly Tyr
        915                 920                 925
Gln Tyr Gly Lys Phe Thr Gly Asn Val Gly Pro Gln Thr Ser Phe Pro
    930                 935                 940
Val Pro Glu Gly Ile Leu Asn Tyr Arg Gly Thr Asn Tyr Val Ala Leu
945                 950                 955                 960
Ser Leu Trp Ala Leu Glu Ser Asp Gly Ala Lys Leu Gly Ser Phe Glu
                965                 970                 975
Leu Ser Tyr Thr Thr Pro Val Leu Thr Gly Tyr Gly Asn Val Glu Ser
            980                 985                 990
Pro Glu Gln Pro Lys Tyr Glu Gln Arg Lys Gly Ala Tyr
        995                 1000                1005


<210> 707
<211> 984
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase C;
      AltName: Full=Lactase C; Flags: Precursor 984 aa
      protein Q2UMD5.1 GI:121804415
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<400> 707
Met Arg Leu Leu Ser Phe Ile Tyr Leu Val Trp Leu Ala Leu Leu Thr
 1               5                  10                  15
Gly Thr Pro Gln Val Ser Ala Thr Asp Asn Gly Lys Thr Ser Asp Val
            20                  25                  30
Ala Trp Asp Lys Tyr Ser Leu Ser Val Lys Gly Glu Arg Leu Phe Val
        35                  40                  45
Phe Ser Gly Glu Phe His Tyr Gln Arg Leu Pro Val Pro Glu Leu Trp
    50                  55                  60
Leu Asp Val Phe Gln Lys Leu Arg Ala Asn Gly Phe Asn Thr Ile Ser
65                  70                  75                  80
Val Tyr Phe Phe Trp Ser Tyr His Ser Ala Ser Glu Asp Val Phe Asp
                85                  90                  95
Phe Thr Thr Gly Ala His Asp Ile Gln Arg Leu Phe Asp Tyr Ala Lys
            100                 105                 110
Gln Ala Gly Leu Tyr Val Ile Ala Arg Ala Gly Pro Tyr Cys Asn Ala
        115                 120                 125
Glu Thr Ser Ala Gly Gly Phe Ala Leu Trp Ala Ala Asn Gly Gln Met
    130                 135                 140
Gly Ser Glu Arg Thr Ser Asp Glu Ala Tyr Tyr Lys Lys Trp Lys Pro
145                 150                 155                 160
Trp Ile Leu Glu Val Gly Lys Ile Ile Ala Ala Asn Gln Ile Thr Asn
                165                 170                 175
Gly Gly Pro Val Ile Leu Asn Gln His Glu Asn Glu Leu Gln Glu Thr
            180                 185                 190
Thr Tyr Asp Ser Asn Asp Thr Lys Val Ile Tyr Met Glu Gln Val Ala
        195                 200                 205
Lys Ala Phe Glu Glu Ala Gly Val Val Val Pro Ser Ser His Asn Glu
    210                 215                 220
Lys Gly Met Arg Thr Val Ser Trp Ser Thr Asp Tyr Lys Asn Val Gly
225                 230                 235                 240
Gly Ala Val Asn Val Tyr Gly Leu Asp Ser Tyr Pro Gly Ser Leu Ser
                245                 250                 255
Cys Ala Asn Pro Asn Ser Gly Phe Asn Leu Leu Arg Thr Tyr Tyr Gln
            260                 265                 270
Trp Phe Gln Asn Tyr Ser Tyr Thr Gln Pro Glu Tyr Leu Ala Glu Phe
        275                 280                 285
Glu Gly Gly Trp Phe Gln Pro Trp Gly Gly Ser Phe Tyr Asp Ser Cys
    290                 295                 300
Ala Ser Glu Leu Ser Pro Glu Phe Ala Asp Val Tyr Tyr Lys Asn Asn
305                 310                 315                 320
Ile Gly Ser Arg Val Thr Leu His Asn Ile Tyr Met Thr Phe Gly Gly
                325                 330                 335
Thr Asn Trp Gly His Ser Ala Ala Pro Val Val Tyr Thr Ser Tyr Asp
            340                 345                 350
Tyr Gly Ser Pro Leu Arg Glu Thr Arg Glu Ile Arg Asp Lys Leu Lys
        355                 360                 365
Gln Thr Lys Leu Leu Gly Leu Phe Thr Arg Val Ser Lys Asp Leu Leu
    370                 375                 380
Lys Thr Tyr Met Glu Gly Asn Gly Thr Ser Tyr Thr Ser Asp Asp Ser
385                 390                 395                 400
Ile Tyr Thr Trp Ala Leu Arg Asn Pro Asp Ser Asp Ala Gly Phe Tyr
                405                 410                 415
Val Val Ala His Asn Thr Ser Ser Ser Arg Glu Val Thr Thr Phe Ser

```
            420                 425                 430
Leu Asn Ile Thr Thr Ser Ala Gly Ala Met Thr Ile Pro Asp Ile Glu
        435                 440                 445
Leu Asp Gly Arg Gln Ser Lys Ile Ile Val Thr Asp Tyr Ser Ile Gly
    450                 455                 460
Ser Glu Ser Ser Leu Leu Tyr Ser Ser Ala Glu Val Leu Thr Tyr Ala
465                 470                 475                 480
Thr Leu Asp Val Asp Val Leu Val Phe Tyr Leu Asn Ala Gly Gln Lys
                485                 490                 495
Gly Ala Phe Val Phe Lys Asp Ala Pro Ala Asp Leu Lys Tyr Gln Thr
            500                 505                 510
Tyr Gly Asn Ser Asn Leu Ser Ala Leu Glu Thr Ser Gln Gly Thr Gln
        515                 520                 525
Tyr Ser Tyr Thr Gln Gly Glu Gly Val Thr Ala Val Lys Phe Ser Asn
    530                 535                 540
Gly Val Leu Val Tyr Leu Leu Asp Lys Glu Thr Ala Trp Asn Phe Phe
545                 550                 555                 560
Ala Pro Pro Thr Val Ser Ser Pro Thr Val Ala Pro Asn Glu His Ile
                565                 570                 575
Leu Val Phe Gly Pro Tyr Leu Val Arg Gly Ala Ser Ile Lys His Asp
            580                 585                 590
Thr Val Glu Ile Val Gly Asp Asn Ser Asn Ser Thr Ser Ile Glu Ile
        595                 600                 605
Tyr Thr Gly Asp Glu His Val Lys Lys Val Ser Trp Asn Gly Asn Leu
    610                 615                 620
Ile Asp Thr Arg Ala Thr Ala Tyr Gly Ser Leu Ile Gly Thr Val Pro
625                 630                 635                 640
Gly Ala Glu Asp Ile Glu Ile Ser Leu Pro Ser Leu Ser Ser Trp Lys
                645                 650                 655
Ala Gln Asp Thr Leu Pro Glu Ile Ser Pro Asp Tyr Asp Asp Ser Arg
            660                 665                 670
Trp Thr Ile Cys Asn Lys Thr Thr Ser Val Asn Ser Val Ala Pro Leu
        675                 680                 685
Ser Leu Pro Val Leu Tyr Ser Gly Asp Tyr Gly Tyr His Thr Gly Thr
    690                 695                 700
Lys Ile Tyr Arg Gly Arg Phe Asp Gly Gln Asn Ala Thr Gly Ala Asn
705                 710                 715                 720
Val Thr Val Gln Asn Gly Val Ala Ala Gly Trp Ala Ala Trp Leu Asn
                725                 730                 735
Gly Ala Tyr Val Gly Gly Phe Ser Gly Asp Pro Asp Lys Val Ala Ser
            740                 745                 750
Trp Glu Val Leu Lys Phe Asn His Ser Ser Leu Arg Ser Arg Asp Asn
        755                 760                 765
Val Leu Thr Ile Ile Thr Asp Tyr Thr Gly His Asp Gln Asn Ser Gln
    770                 775                 780
Lys Pro Ile Gly Thr Gln Asn Pro Arg Gly Ile Met Gly Ala Thr Leu
785                 790                 795                 800
Ile Gly Gly Gly Asn Phe Thr Leu Trp Arg Ile Gln Gly Asn Ala Gly
                805                 810                 815
Gly Glu Lys Asn Ile Asp Pro Val Arg Gly Pro Met Asn Glu Gly Gly
            820                 825                 830
Leu Tyr Gly Glu Arg Met Gly Trp His Leu Pro Gly Tyr Gln Val Pro
        835                 840                 845
Glu Ser Ala Leu Asp Ser Ser Pro Leu Glu Gly Val Ser Gly Ala Glu
```

```
    850                 855                 860
Gly Arg Phe Tyr Thr Thr Ser Phe Gln Leu Asp Leu Glu Glu Asp Leu
865                 870                 875                 880
Asp Val Pro Ile Gly Leu Gln Leu Ser Ala Pro Ala Gly Thr Glu Ala
                885                 890                 895
Val Val Gln Ile Phe Met Asn Gly Tyr Gln Phe Gly His Tyr Leu Pro
            900                 905                 910
His Ile Gly Pro Gln Ser Leu Phe Pro Phe Pro Pro Gly Val Ile Lys
        915                 920                 925
Asn Arg Gly Gln Asn Ser Leu Ala Ile Ser Met Trp Ala Leu Thr Asp
    930                 935                 940
Ala Gly Ala Arg Leu Glu Gln Val Glu Leu Lys Ala Tyr Ala Lys Tyr
945                 950                 955                 960
Arg Ser Gly Phe Asp Phe Asn Arg Asp Trp Thr Tyr Leu Gln Pro Gly
                965                 970                 975
Trp Lys Asp Arg Thr Glu Tyr Ala
            980


<210> 708
<211> 960
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase E;
      AltName: Full=Lactase E; Flags: Precursor 1011 aa
      protein Q4WG05.1 GI:74668464

<400> 708
Met Lys Ser Leu Leu Lys Arg Leu Ile Ala Leu Ala Ala Ala Tyr Ser
 1               5                  10                  15
Val Ala Ala Ala Pro Ser Phe Ser His His Ser Ser Gln Asp Ala Ala
            20                  25                  30
Asn Lys Arg Glu Leu Leu Gln Asp Leu Val Thr Trp Asp Gln His Ser
        35                  40                  45
Leu Phe Val Arg Gly Glu Arg Leu Met Ile Phe Ser Gly Glu Phe His
    50                  55                  60
Pro Phe Arg Leu Pro Val Pro Gly Leu Trp Phe Asp Val Phe Gln Lys
65                  70                  75                  80
Ile Lys Ser Leu Gly Phe Asn Ala Val Ser Phe Tyr Thr Asp Trp Gly
                85                  90                  95
Leu Met Glu Gly Asn Pro Gly His Val Val Thr Asp Gly Ile Trp Ser
            100                 105                 110
Leu Asp Glu Phe Phe Thr Ala Ala Arg Glu Ala Gly Leu Tyr Leu Ile
        115                 120                 125
Ala Arg Pro Gly Pro Tyr Ile Asn Ala Glu Thr Ser Ala Gly Gly Ile
    130                 135                 140
Pro Gly Trp Val Leu Arg Arg Lys Gly Ile Ile Arg Ser Asn Ser Glu
145                 150                 155                 160
Asp Tyr Leu Arg Ala Thr Asp Thr Tyr Met Ala Thr Leu Gly Lys Ile
                165                 170                 175
Ile Ala Lys Ala Gln Ile Thr Asn Gly Gly Pro Val Ile Leu Val Gln
            180                 185                 190
```

```
Pro Glu Asn Glu Tyr Thr Thr Trp Pro Asn Val Ser Glu Ser Glu Phe
        195                 200                 205
Pro Thr Thr Met Asn Gln Glu Val Met Ala Tyr Ala Glu Lys Gln Leu
    210                 215                 220
Arg Asp Ala Gly Val Val Val Pro Thr Val Val Asn Asp Asn Lys Asn
225                 230                 235                 240
Leu Gly Tyr Phe Ala Pro Gly Thr Gly Leu Gly Glu Thr Asp Leu Tyr
                245                 250                 255
Gly Ile Asp Ala Tyr Pro Met Arg Tyr Asp Cys Gly Asn Pro Tyr Val
            260                 265                 270
Trp Pro Thr Tyr Arg Phe Pro Arg Asp Trp Gln His Glu His Arg Asn
        275                 280                 285
His Ser Pro Thr Thr Pro Phe Ala Ile Met Glu Phe Gln Gly Gly Ser
    290                 295                 300
Gly Asp Gly Trp Gly Gly Val Thr Glu Asp Gly Cys Ala Ile Leu Val
305                 310                 315                 320
Asn Asn Glu Ala Val Arg Val Val Tyr Lys Asn Asn Tyr Gly Phe Gly
                325                 330                 335
Val Arg Val Phe Asn Ile Tyr Met Thr Tyr Gly Gly Thr Asn Trp Gly
            340                 345                 350
Asn Leu Gly Tyr Tyr Gly Gly Tyr Thr Ser Tyr Asp Tyr Gly Ala Ala
        355                 360                 365
Ile Thr Glu Asp Arg Gln Ile Trp Arg Glu Lys Tyr Ser Glu Glu Lys
    370                 375                 380
Leu Gln Ala Asn Phe Leu Lys Val Ser Pro Ala Tyr Leu Thr Ser Thr
385                 390                 395                 400
Pro Gly Asn Gly Val Asn Gly Ser Tyr Thr Gly Asn Lys Asp Ile Thr
                405                 410                 415
Val Thr Pro Leu Phe Gly Asn Gly Thr Thr Thr Asn Leu Tyr Leu Val
            420                 425                 430
Arg His Ala Asp Phe Thr Ser Thr Gly Ser Ala Gln Tyr Asn Leu Ser
        435                 440                 445
Ile Ser Thr Ser Val Gly Asn Val Thr Ile Pro Gln Leu Gly Gly Ser
    450                 455                 460
Leu Ser Leu Asn Gly Arg Asp Ser Lys Phe His Ile Thr Asp Tyr Asp
465                 470                 475                 480
Val Gly Gly Phe Asn Leu Ile Tyr Ser Ser Ala Glu Val Phe Thr Trp
                485                 490                 495
Ala Lys Gly Asp Asn Lys Lys Arg Val Leu Val Leu Tyr Gly Gly Ala
            500                 505                 510
Gly Glu Leu His Glu Phe Ala Leu Pro Lys His Leu Pro Arg Pro Thr
        515                 520                 525
Val Val Glu Gly Ser Tyr Val Lys Ile Ala Lys Gln Gly Ser Ala Trp
    530                 535                 540
Val Val Gln Trp Glu Val Ala Ala Gln Arg Arg Val Leu Arg Ala Gly
545                 550                 555                 560
Lys Leu Glu Ile His Leu Leu Trp Arg Asn Asp Ala Tyr Gln His Trp
                565                 570                 575
Val Leu Glu Leu Pro Ala Lys Gln Pro Ile Ala Asn Tyr Ser Ser Pro
            580                 585                 590
Ser Lys Glu Thr Val Ile Val Lys Gly Gly Tyr Leu Leu Arg Ser Ala
        595                 600                 605
Trp Ile Thr Asp Asn Asp Leu His Leu Thr Gly Asp Val Asn Val Thr
    610                 615                 620
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Thr Pro Leu Glu Val Ile Ser Ala Pro Lys Arg Phe Asp Gly Ile Val
625                 630                 635                 640
Phe Asn Gly Gln Ser Leu Lys Ser Thr Arg Ser Lys Ile Gly Asn Leu
                645                 650                 655
Ala Ala Thr Val His Tyr Gln Pro Pro Ala Ile Ser Leu Pro Asp Leu
            660                 665                 670
Lys Arg Leu Asp Trp Lys Tyr Ile Asp Ser Leu Pro Glu Ile Ser Thr
        675                 680                 685
Glu Tyr Asn Asp Glu Gly Trp Thr Pro Leu Thr Asn Thr Tyr Thr Asn
    690                 695                 700
Asn Thr Arg Glu Phe Thr Gly Pro Thr Cys Leu Tyr Ala Asp Asp Tyr
705                 710                 715                 720
Gly Tyr His Gly Gly Ser Leu Ile Tyr Arg Gly His Phe Thr Ala Asn
                725                 730                 735
Gly Asp Glu Ser Trp Val Phe Leu Asn Thr Ser Gly Gly Val Gly Phe
            740                 745                 750
Ala Asn Ser Val Trp Leu Asn Gln Thr Phe Leu Gly Ser Trp Thr Gly
        755                 760                 765
Ser Gly Arg Asn Met Thr Tyr Pro Arg Asn Ile Ser Leu Pro His Glu
    770                 775                 780
Leu Ser Pro Gly Glu Pro Tyr Val Phe Thr Val Val Ile Asp His Met
785                 790                 795                 800
Gly Gln Asp Glu Glu Ala Pro Gly Thr Asp Ala Ile Lys Phe Pro Arg
                805                 810                 815
Gly Ile Leu Asp Tyr Ala Leu Ser Gly His Glu Leu Ser Asp Leu Arg
            820                 825                 830
Trp Lys Met Thr Gly Asn Leu Gly Gly Glu Gln Tyr Gln Asp Leu Thr
        835                 840                 845
Arg Gly Pro Leu Asn Glu Gly Ala Met Tyr Ala Glu Arg Gln Gly Tyr
    850                 855                 860
His Leu Pro Ser Pro Pro Thr Ser Ser Trp Lys Ser Ser Asn Pro Ile
865                 870                 875                 880
Lys Glu Gly Leu Thr Gly Ala Gly Ile Gly Phe Tyr Ala Thr Ser Phe
                885                 890                 895
Ser Leu Asp Leu Pro Glu Gly Tyr Asp Ile Pro Leu Ser Phe Arg Phe
            900                 905                 910
Asn Asn Ser Ala Ser Ala Ala Arg Ser Gly Thr Ser Tyr Arg Cys Gln
        915                 920                 925
Leu Phe Val Asn Gly Tyr Gln Phe Gly Lys Tyr Val Asn Asp Leu Gly
    930                 935                 940
Pro Gln Thr Lys Phe Pro Val Pro Glu Gly Ile Leu Asn Tyr Asn Gly
945                 950                 955                 960
```

<210> 709
<211> 983
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase C;
AltName: Full=Lactase C; Flags: Precursor 983 aa
protein Q4WNE4.1 GI:74671041

<400> 709
Met Arg Ile Phe Ser Phe Leu Phe Leu Leu Leu Leu Gly Ile Leu Thr
 1               5                  10                  15
Gly Gln Gly Leu Val Ser Gly Thr Asp Asn Gly Lys Thr Thr Asp Val
            20                  25                  30
Thr Trp Asp Lys Tyr Ser Leu Ser Val Lys Gly Gln Arg Leu Phe Val
        35                  40                  45
Phe Ser Gly Glu Phe His Tyr Gln Arg Leu Pro Val Pro Glu Leu Trp
    50                  55                  60
Leu Asp Val Phe Gln Lys Leu Arg Ala Asn Gly Phe Asn Ala Ile Ser
65                  70                  75                  80
Val Tyr Phe Phe Trp Ser Phe His Ser Ala Ser Glu Gly Glu Phe Asp
                85                  90                  95
Phe Glu Asn Gly Ala His Asp Ile Gln Arg Leu Phe Asp Tyr Ala Lys
            100                 105                 110
Glu Ala Gly Leu Tyr Val Ile Ala Arg Ala Gly Pro Tyr Cys Asn Ala
        115                 120                 125
Glu Thr Ser Ala Gly Gly Phe Ala Leu Trp Ala Ala Asn Gly Gln Met
    130                 135                 140
Gly Asn Glu Arg Thr Ser Asp Glu Ala Tyr Tyr Glu Lys Trp Arg Pro
145                 150                 155                 160
Trp Ile Leu Glu Val Gly Lys Ile Ile Ala Lys Asn Gln Ile Thr Asn
                165                 170                 175
Gly Gly Pro Val Ile Leu Asn Gln His Glu Asn Glu Leu Val Glu Thr
            180                 185                 190
Thr Tyr Asp Pro Asn His Thr Leu Val Val Tyr Met Lys Gln Ile Ala
        195                 200                 205
Gln Val Phe Glu Glu Ala Gly Ile Val Val Pro Ser Ser His Asn Glu
    210                 215                 220
Lys Gly Met Arg Gly Val Ser Trp Ser Thr Asp Tyr His Asn Val Gly
225                 230                 235                 240
Gly Ala Val Asn Ile Tyr Gly Leu Asp Ser Tyr Pro Gly Gly Leu Ser
                245                 250                 255
Cys Thr Asn Pro Asn Ser Gly Phe Asn Leu Val Arg Thr Tyr His Gln
            260                 265                 270
Trp Phe Gln Asn Tyr Ser Phe Thr Gln Pro Ser Tyr Leu Pro Glu Phe
        275                 280                 285
Glu Gly Gly Trp Phe Gln Pro Trp Gly Gly Ser Phe Tyr Asp Thr Cys
    290                 295                 300
Ala Thr Glu Leu Ser Pro Glu Phe Pro Asp Val Tyr Tyr Lys Asn Asn
305                 310                 315                 320
Ile Gly Ser Arg Val Thr Leu His Ser Ile Tyr Met Thr Tyr Gly Gly
                325                 330                 335
Thr Asn Trp Gly His Ser Ala Ala Pro Val Val Tyr Thr Ser Tyr Asp
            340                 345                 350
Tyr Ala Ala Pro Leu Arg Glu Thr Arg Glu Ile Arg Asp Lys Leu Lys
        355                 360                 365
Gln Thr Lys Leu Ile Gly Leu Phe Thr Arg Val Ser Lys Asp Leu Leu
    370                 375                 380
Lys Thr Tyr Met Glu Gly Asn Gly Thr Gly Tyr Thr Ser Asp Ser Ser
385                 390                 395                 400
Ile Tyr Thr Trp Ser Leu Arg Asn Pro Asp Thr Asn Ala Gly Phe Tyr
                405                 410                 415
Val Leu Ala His Ser Thr Ser Ser Thr Arg Asp Val Thr Thr Phe Thr

```
            420                 425                 430
Leu Asn Val Thr Thr Ser Ala Gly Ala Ile Ser Ile Pro Asp Ile Glu
        435                 440                 445
Leu Asn Gly Arg Gln Ser Lys Ile Ile Val Thr Asp Tyr Asn Phe Gly
    450                 455                 460
Thr Asn Ser Thr Leu Leu Phe Ser Ser Ala Glu Val Leu Thr Tyr Ala
465                 470                 475                 480
Asn Leu Asp Val Asn Val Leu Val Phe Tyr Leu Asn Val Gly Gln Lys
                485                 490                 495
Gly Thr Phe Val Phe Lys Asp Glu Pro Lys Leu Ala Phe Gln Thr Tyr
            500                 505                 510
Gly Asn Ser Asn Leu Thr Thr Ser Glu Ser Ser Tyr Gly Thr Gln Tyr
        515                 520                 525
Ser Tyr Thr Gln Gly Lys Gly Val Thr Ala Val Lys Phe Ser Asn Gly
    530                 535                 540
Val Leu Ala Tyr Phe Leu Asp Lys Glu Ser Ala Trp Asn Phe Phe Ala
545                 550                 555                 560
Pro Pro Thr Thr Ser Ser Pro Gln Val Ala Pro Asn Glu His Ile Leu
                565                 570                 575
Val Gln Gly Pro Tyr Leu Val Arg Gly Ala Ser Val Asn His Gly Thr
            580                 585                 590
Val Glu Ile Thr Gly Asp Asn Ala Asn Thr Thr Ser Ile Glu Val Tyr
        595                 600                 605
Thr Gly Asn Ser Gln Val Lys Lys Ile Lys Trp Asn Gly Lys Thr Ile
    610                 615                 620
Glu Thr Arg Lys Thr Ala Tyr Gly Ser Leu Ile Gly Thr Ala Pro Gly
625                 630                 635                 640
Ala Glu Asp Val Lys Ile Gln Leu Pro Ser Leu Asp Ser Trp Lys Ala
                645                 650                 655
Gln Asp Thr Leu Pro Glu Ile Gln Pro Asp Tyr Asp Asp Ser Lys Trp
            660                 665                 670
Thr Val Cys Asn Lys Thr Thr Ser Val Asn Ala Ile Ala Pro Leu Ser
        675                 680                 685
Leu Pro Val Leu Tyr Ser Gly Asp Tyr Gly Tyr His Ala Gly Thr Lys
    690                 695                 700
Val Tyr Arg Gly Arg Phe Asp Gly Arg Asn Val Thr Gly Ala Asn Val
705                 710                 715                 720
Thr Val Gln Asn Gly Ala Ala Ala Gly Trp Ala Ala Trp Val Asn Gly
                725                 730                 735
Gln Tyr Ala Gly Gly Ser Ala Gly Ser Pro Asn Leu Ala Ala Thr Ser
            740                 745                 750
Ala Val Leu Thr Phe Asn Ser Ser Ser Leu Lys Asp Gln Asp Asn Val
        755                 760                 765
Leu Thr Val Val Thr Asp Tyr Thr Gly His Asp Gln Asn Ser Val Arg
    770                 775                 780
Pro Lys Gly Thr Gln Asn Pro Arg Gly Ile Leu Gly Ala Thr Leu Ile
785                 790                 795                 800
Gly Gly Gly Asn Phe Thr Ser Trp Arg Ile Gln Gly Asn Ala Gly Gly
                805                 810                 815
Glu Lys Asn Ile Asp Pro Val Arg Gly Pro Met Asn Glu Gly Gly Leu
            820                 825                 830
Tyr Gly Glu Arg Met Gly Trp His Leu Pro Gly Tyr Lys Val Pro Lys
        835                 840                 845
Ser Ala Ser Lys Ser Ser Pro Leu Asp Gly Val Ser Gly Ala Glu Gly
```

```
    850                 855                 860
Arg Phe Tyr Thr Thr Thr Phe Lys Leu Lys Leu Asp Lys Asp Leu Asp
865                 870                 875                 880
Val Pro Ile Gly Leu Gln Leu Gly Ala Pro Glu Gly Thr Lys Ala Val
                885                 890                 895
Val Gln Val Phe Met Asn Gly Tyr Gln Phe Gly His Tyr Leu Pro His
            900                 905                 910
Thr Gly Pro Gln Ser Leu Phe Pro Phe Pro Pro Gly Val Ile Asn Asn
        915                 920                 925
Arg Gly Glu Asn Thr Leu Ala Ile Ser Met Trp Ala Leu Thr Asp Ala
    930                 935                 940
Gly Ala Lys Leu Asp Lys Val Glu Leu Val Ala Tyr Gly Lys Tyr Arg
945                 950                 955                 960
Ser Gly Phe Asp Phe Asn Gln Asp Trp Gly Tyr Leu Gln Pro Gly Trp
                965                 970                 975
Lys Asp Arg Ser Gln Tyr Ala
            980
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<210> 710
<211> 1015
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase B;
AltName: Full=Lactase B; Flags: Precursor 1015 aa
protein Q4WRD3.1 GI:74672078

<400> 710

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

```
Ile Glu Asn Glu Tyr Gly Gln Gln Trp Ile Gly Asp Pro Lys Asn Arg
        195                 200                 205
Asn Pro Asn Lys Thr Ala Val Ala Tyr Met Glu Leu Leu Glu Ala Ser
    210                 215                 220
Ala Arg Glu Asn Gly Ile Thr Val Pro Leu Thr Ser Asn Asp Pro Asn
225                 230                 235                 240
Met Asn Ser Lys Ser Trp Gly Ser Asp Trp Ser Asn Ala Gly Gly Asn
                245                 250                 255
Val Asp Val Ala Gly Leu Asp Ser Tyr Pro Ser Cys Trp Thr Cys Asp
            260                 265                 270
Val Ser Gln Cys Thr Ser Thr Asn Gly Glu Tyr Val Pro Tyr Lys Val
        275                 280                 285
Ile Asp Tyr Tyr Asp Tyr Phe Gln Glu Val Gln Pro Thr Leu Pro Ser
    290                 295                 300
Phe Met Pro Glu Phe Gln Gly Gly Ser Tyr Asn Pro Trp Ala Gly Pro
305                 310                 315                 320
Glu Gly Gly Cys Pro Gln Asp Thr Ser Ala Glu Phe Ala Asn Leu Phe
                325                 330                 335
Tyr Arg Trp Asn Ile Gly Gln Arg Val Thr Ala Met Ser Leu Tyr Met
            340                 345                 350
Leu Tyr Gly Gly Thr Asn Trp Gly Ala Ile Ala Ala Pro Val Thr Ala
        355                 360                 365
Thr Ser Tyr Asp Tyr Ser Ala Pro Ile Ser Glu Asp Arg Ser Ile Gly
    370                 375                 380
Ala Lys Tyr Ser Glu Thr Lys Leu Leu Ala Leu Phe Thr Arg Thr Ala
385                 390                 395                 400
Lys Asp Leu Thr Met Thr Glu Ala Ile Gly Asn Gly Thr Gln Tyr Thr
                405                 410                 415
Thr Asn Thr Ala Val Arg Ala Phe Glu Leu Arg Asn Pro Gln Thr Asn
            420                 425                 430
Ala Gly Phe Tyr Val Thr Phe His Thr Asp Thr Thr Val Gly Gly Asn
        435                 440                 445
Gln Ala Phe Lys Leu His Val Asn Thr Ser Val Gly Ala Leu Thr Val
    450                 455                 460
Pro Lys Asn Glu Gly Leu Ile Gln Leu Asn Gly His Gln Ser Lys Ile
465                 470                 475                 480
Ile Val Thr Asp Phe Thr Leu Gly Lys Arg Thr Leu Leu Tyr Ser Thr
                485                 490                 495
Ala Glu Val Leu Thr Tyr Ala Val Phe Glu Asn Arg Pro Thr Leu Val
            500                 505                 510
Leu Trp Val Pro Thr Gly Glu Ser Gly Glu Phe Ala Ile Lys Gly Ala
        515                 520                 525
Lys Ser Gly Lys Val Glu Asn Gly Asp Gly Cys Ser Gly Ile Lys Phe
    530                 535                 540
Lys Arg Glu Lys Asp Tyr Leu Val Val Asn Phe Ser Gln Ala Lys Gly
545                 550                 555                 560
Leu Ser Val Leu Arg Leu Asp Asn Gly Val Arg Val Val Leu Leu Asp
                565                 570                 575
Lys Ala Ala Ala Tyr Arg Phe Trp Ala Pro Ala Leu Thr Asp Asp Pro
            580                 585                 590
Asn Val Gln Glu Thr Glu Thr Val Leu Val His Gly Pro Tyr Leu Val
        595                 600                 605
Arg Ser Ala Ser Ile Ser Lys Thr Thr Leu Ala Leu Arg Gly Asp Ser
    610                 615                 620
```

```
Val Glu Lys Thr Thr Leu Glu Ile Phe Ala Pro His Ser Val Arg Lys
625                 630                 635                 640
Ile Thr Trp Asn Gly Lys Glu Val Gln Thr Ser His Thr Pro Tyr Gly
                645                 650                 655
Ser Leu Lys Ala Thr Leu Ala Ala Pro Pro Asp Ile Lys Leu Pro Ala
            660                 665                 670
Leu Thr Ser Trp Arg Ser Asn Asp Ser Leu Pro Glu Arg Leu Pro Ser
        675                 680                 685
Tyr Asp Asp Ser Gly Pro Ala Trp Ile Glu Ala Asn His Met Thr Thr
    690                 695                 700
Ser Asn Pro Ser Pro Pro Ala Thr Phe Pro Val Leu Tyr Ala Asp Glu
705                 710                 715                 720
Tyr Gly Phe His Asn Gly Val Arg Leu Trp Arg Gly Tyr Phe Asn Gly
                725                 730                 735
Ser Ala Ser Gly Val Phe Leu Asn Ile Gln Gly Gly Ser Ala Phe Gly
            740                 745                 750
Trp Ser Ala Trp Leu Asn Gly His Phe Leu Asp Ser His Leu Gly Thr
        755                 760                 765
Ala Thr Thr Ser Gln Ala Asn Lys Thr Leu Thr Phe Pro Ser Ser Ile
    770                 775                 780
Leu Asn Pro Thr Glu Asn Val Leu Leu Ile Val His Asp Asp Thr Gly
785                 790                 795                 800
His Asp Gln Thr Thr Gly Ala Leu Asn Pro Arg Gly Ile Leu Glu Ala
                805                 810                 815
Arg Leu Leu Ser Asn Asp Thr Ser Ser Pro Pro Pro Glu Phe Thr His
            820                 825                 830
Trp Arg Leu Ala Gly Thr Ala Gly Gly Glu Ser Asn Leu Asp Pro Ile
        835                 840                 845
Arg Gly Val Phe Asn Glu Asp Gly Leu Phe Ala Glu Arg Met Gly Trp
    850                 855                 860
His Leu Pro Gly Phe Asp Asp Ser Ala Trp Thr Ser Glu Asn Ser Ala
865                 870                 875                 880
Thr Ser Ala Ser Ser Ala Leu Ser Phe Thr Gly Ala Thr Val Arg Phe
                885                 890                 895
Phe Arg Ser Val Val Pro Leu Asn Ile Pro Ala Gly Leu Asp Val Ser
            900                 905                 910
Ile Ser Phe Val Leu Ser Thr Pro Thr Ala Ala Pro Lys Gly Tyr Arg
        915                 920                 925
Ala Gln Leu Phe Val Asn Gly Tyr Gln Tyr Gly Arg Tyr Asn Pro His
    930                 935                 940
Ile Gly Asn Gln Val Val Phe Pro Val Pro Pro Gly Ile Leu Asp Tyr
945                 950                 955                 960
Gln Gly Asp Asn Thr Ile Gly Leu Ala Val Trp Ala Gln Thr Glu Glu
                965                 970                 975
Gly Ala Gly Ile Gln Val Asp Trp Lys Val Asn Tyr Val Ala Asp Ser
            980                 985                 990
Ser Leu Ser Val Ala Gly Phe Gly Lys Gly Leu Arg Pro Gly Trp Thr
        995                 1000                1005
Glu Glu Arg Leu Lys Phe Ala
    1010                1015
```

<210> 711
<211> 1006

<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase A;
AltName: Full=Lactase A; Flags: Precursor 1006 aa
protein Q4WS33.2 GI:300681010

<400> 711
Met Lys Leu Leu Ser Val Cys Ala Ile Ala Leu Leu Ala Ala Gln Ala
1 5 10 15
Ala Gly Ala Ser Ile Lys His Met Leu Asn Gly Phe Thr Leu Met Glu
20 25 30
His Ser Asp Pro Ala Lys Arg Glu Leu Leu Gln Lys Tyr Val Thr Trp
35 40 45
Asp Glu Lys Ser Leu Phe Val Asn Gly Glu Arg Ile Met Ile Phe Ser
50 55 60
Gly Glu Val His Pro Phe Arg Leu Pro Val Pro Ser Leu Trp Leu Asp
65 70 75 80
Val Phe Gln Lys Ile Lys Ala Leu Gly Phe Asn Cys Val Ser Phe Tyr
85 90 95
Val Asp Trp Ala Leu Leu Glu Gly Lys Pro Gly Glu Tyr Arg Ala Glu
100 105 110
Gly Asn Phe Ala Leu Glu Pro Phe Phe Asp Val Ala Lys Gln Ala Gly
115 120 125
Ile Tyr Leu Leu Ala Arg Pro Gly Pro Tyr Ile Asn Ala Glu Ala Ser
130 135 140
Gly Gly Gly Phe Pro Gly Trp Leu Gln Arg Val Asn Gly Thr Leu Arg
145 150 155 160
Thr Ser Asp Pro Ala Tyr Leu Lys Ala Thr Asp Asn Tyr Ile Ala His
165 170 175
Val Ala Ala Thr Ile Ala Lys Gly Gln Ile Thr Asn Gly Gly Pro Val
180 185 190
Ile Leu Tyr Gln Pro Glu Asn Glu Tyr Ser Gly Ala Cys Cys Asp Ala
195 200 205
Thr Phe Pro Asp Gly Asp Tyr Met Gln Tyr Val Ile Asp Gln Ala Arg
210 215 220
Asn Ala Gly Ile Val Val Pro Leu Ile Asn Asn Asp Ala Trp Thr Gly
225 230 235 240
Gly His Asn Ala Pro Gly Thr Gly Lys Gly Glu Val Asp Ile Tyr Gly
245 250 255
His Asp Ser Tyr Pro Leu Gly Phe Asp Cys Gly His Pro Ser Val Trp
260 265 270
Pro Lys Gly Asn Leu Pro Thr Thr Phe Arg Thr Asp His Leu Lys Gln
275 280 285
Ser Pro Thr Thr Pro Tyr Ser Leu Ile Glu Phe Gln Ala Gly Ser Phe
290 295 300
Asp Pro Trp Gly Gly Pro Gly Phe Ala Ala Cys Ala Ala Leu Val Asn
305 310 315 320
His Glu Phe Glu Arg Val Phe Tyr Lys Asn Asp Leu Ser Phe Gly Ala
325 330 335
Ala Ile Leu Asn Leu Tyr Met Thr Phe Gly Gly Thr Asn Trp Gly Asn
340 345 350
Leu Gly His Pro Gly Gly Tyr Thr Ser Tyr Asp Tyr Gly Ser Pro Leu

```
        355                 360                 365
Thr Glu Ser Arg Asn Val Thr Arg Glu Lys Tyr Ser Glu Leu Lys Leu
    370                 375                 380
Ile Gly Asn Phe Val Lys Ala Ser Pro Ser Tyr Leu Leu Ala Thr Pro
385                 390                 395                 400
Gly Asn Leu Thr Thr Ser Gly Tyr Ala Asp Thr Ala Asp Leu Thr Val
                405                 410                 415
Thr Pro Leu Leu Gly Asn Gly Thr Gly Ser Tyr Phe Val Val Arg His
            420                 425                 430
Thr Asp Tyr Thr Ser Gln Ala Ser Thr Pro Tyr Lys Leu Ser Leu Pro
        435                 440                 445
Thr Ser Ala Gly Arg Leu Thr Val Pro Gln Leu Gly Gly Thr Leu Thr
    450                 455                 460
Leu Asn Gly Arg Asp Ser Lys Ile His Val Val Asp Tyr Asn Val Ala
465                 470                 475                 480
Gly Thr Asn Ile Ile Tyr Ser Thr Ala Glu Val Phe Thr Trp Lys Asn
                485                 490                 495
Phe Gly Asp Ser Lys Val Leu Ile Leu Tyr Gly Gly Pro Gly Glu His
            500                 505                 510
His Glu Leu Ala Val Ser Leu Lys Ser Asp Val Gln Val Val Glu Gly
        515                 520                 525
Ser Asn Ser Glu Phe Lys Ser Lys Lys Val Gly Asp Val Val Val Val
    530                 535                 540
Ala Trp Asp Val Ser Pro Ser Arg Arg Ile Val Gln Ile Gly Asp Leu
545                 550                 555                 560
Lys Ile Phe Leu Leu Asp Arg Asn Ser Val Tyr Asn Tyr Trp Val Pro
                565                 570                 575
Gln Leu Asp Lys Asp Asp Ser Ser Thr Gly Tyr Ser Ser Glu Lys Thr
            580                 585                 590
Thr Ala Ser Ser Ile Ile Val Lys Ala Gly Tyr Leu Val Arg Thr Ala
        595                 600                 605
Tyr Thr Lys Gly Ser Gly Leu Tyr Leu Thr Ala Asp Phe Asn Ala Thr
    610                 615                 620
Thr Pro Val Glu Val Ile Gly Ala Pro Ser Asn Val Arg Asn Leu Tyr
625                 630                 635                 640
Ile Asn Gly Glu Lys Thr Gln Phe Lys Thr Asp Lys Asn Gly Ile Trp
                645                 650                 655
Ser Thr Glu Val Lys Tyr Ser Ala Pro Lys Ile Lys Leu Pro Ser Met
            660                 665                 670
Lys Asp Leu Asp Trp Lys Tyr Leu Asp Thr Leu Gln Glu Val Gln Ser
        675                 680                 685
Thr Tyr Asp Asp Ser Ala Trp Pro Ala Ala Asp Leu Asp Thr Thr Pro
    690                 695                 700
Asn Thr Leu Arg Pro Leu Thr Thr Pro Lys Ser Leu Tyr Ser Ser Asp
705                 710                 715                 720
Tyr Gly Phe His Thr Gly Tyr Leu Ile Tyr Arg Gly His Phe Val Ala
                725                 730                 735
Asp Gly Ser Glu Thr Thr Phe Asp Val Arg Thr Gln Gly Gly Ser Ala
            740                 745                 750
Phe Gly Ser Ser Val Trp Leu Asn Glu Ser Phe Leu Gly Ser Trp Thr
        755                 760                 765
Gly Leu Asn Ala Asn Ala Asp Tyr Asn Ser Thr Tyr Lys Leu Pro Gln
    770                 775                 780
Val Glu Gln Gly Lys Asn Tyr Val Leu Thr Ile Leu Ile Asp Thr Met
```

785 790 795 800
Gly Leu Asn Glu Asn Trp Val Val Gly Thr Asp Glu Met Lys Asn Pro
805 810 815
Arg Gly Ile Leu Ser Tyr Lys Leu Ser Gly Arg Asp Ala Ser Ala Ile
820 825 830
Thr Trp Lys Leu Thr Gly Asn Leu Gly Gly Glu Asp Tyr Gln Asp Lys
835 840 845
Ile Arg Gly Pro Leu Asn Glu Gly Gly Leu Tyr Ala Glu Arg Gln Gly
850 855 860
Phe His Gln Pro Gln Pro Pro Ser Gln Lys Trp Lys Ser Ala Ser Pro
865 870 875 880
Leu Asp Gly Leu Ser Lys Pro Gly Ile Gly Phe Tyr Thr Ala Gln Phe
885 890 895
Asp Leu Asp Ile Pro Ser Gly Trp Asp Val Pro Leu Tyr Phe Asn Phe
900 905 910
Gly Asn Ser Thr Lys Ser Ala Tyr Arg Val Gln Leu Tyr Val Asn Gly
915 920 925
Tyr Gln Tyr Gly Lys Phe Val Ser Asn Ile Gly Pro Gln Thr Ser Phe
930 935 940
Pro Val Pro Gln Gly Ile Leu Asn Tyr Gln Gly Thr Asn Trp Val Ala
945 950 955 960
Leu Thr Leu Trp Ala Leu Glu Ser Asp Gly Ala Lys Leu Asp Asp Phe
965 970 975
Glu Leu Val Asn Thr Thr Pro Val Met Thr Ala Leu Ser Lys Ile Arg
980 985 990
Pro Ser Lys Gln Pro Asn Tyr Arg Gln Arg Lys Gly Ala Tyr
995 1000 1005

<210> 712
<211> 1007
<212> PRT
<213> MKLSSACAIALLAAQAAGASIKHRINGFTLTEHSDPAKRELLQKYVTWDG

<220>
<223> RecName: Full=Probable beta-galactosidase A;
AltName: Full=Lactase A; Flags: Precursor 1007 aa
protein Q4ZHV7.1 GI:74645200

<400> 712
Met Lys Leu Ser Ser Ala Cys Ala Ile Ala Leu Leu Ala Ala Gln Ala
1 5 10 15
Ala Gly Ala Ser Ile Lys His Arg Ile Asn Gly Phe Thr Leu Thr Glu
20 25 30
His Ser Asp Pro Ala Lys Arg Glu Leu Leu Gln Lys Tyr Val Thr Trp
35 40 45
Asp Asp Lys Ser Leu Phe Ile Asn Gly Glu Arg Ile Met Ile Phe Ser
50 55 60
Gly Glu Phe His Pro Phe Arg Leu Pro Val Lys Glu Leu Gln Leu Asp
65 70 75 80
Ile Phe Gln Lys Val Lys Ala Leu Gly Phe Asn Cys Val Ser Phe Tyr
85 90 95
Val Asp Trp Ala Leu Val Glu Gly Glu Pro Gly Glu Tyr Arg Ala Asp
100 105 110

```
Gly Ile Phe Asp Leu Glu Pro Phe Phe Asp Ala Ala Ser Glu Ala Gly
        115                 120                 125
Ile Tyr Leu Leu Ala Arg Pro Gly Pro Tyr Ile Asn Ala Glu Ser Ser
    130                 135                 140
Gly Gly Gly Phe Pro Gly Trp Leu Gln Arg Val Asn Gly Thr Leu Arg
145                 150                 155                 160
Ser Ser Asp Lys Ala Tyr Leu Asp Ala Thr Asp Asn Tyr Val Ser His
                165                 170                 175
Val Ala Ala Thr Ile Ala Lys Tyr Gln Ile Thr Asn Gly Gly Pro Ile
            180                 185                 190
Ile Leu Tyr Gln Pro Glu Asn Glu Tyr Thr Ser Gly Cys Cys Gly Val
        195                 200                 205
Glu Phe Pro Asp Pro Val Tyr Met Gln Tyr Val Glu Asp Gln Ala Arg
    210                 215                 220
Asn Ala Gly Val Val Ile Pro Leu Ile Asn Asn Asp Ala Ser Ala Ser
225                 230                 235                 240
Gly Asn Asn Ala Pro Gly Thr Gly Lys Gly Ala Val Asp Ile Tyr Gly
                245                 250                 255
His Asp Ser Tyr Pro Leu Gly Phe Asp Cys Ala Asn Pro Thr Val Trp
            260                 265                 270
Pro Ser Gly Asp Leu Pro Thr Asn Phe Arg Thr Leu His Leu Glu Gln
        275                 280                 285
Ser Pro Thr Thr Pro Tyr Ala Ile Val Glu Phe Gln Gly Gly Ser Tyr
    290                 295                 300
Asp Pro Trp Gly Gly Pro Gly Phe Ala Ala Cys Ser Glu Leu Leu Asn
305                 310                 315                 320
Asn Glu Phe Glu Arg Val Ser Tyr Lys Asn Asp Phe Ser Phe Gln Ile
                325                 330                 335
Ala Ile Met Asn Leu Tyr Met Ile Phe Gly Gly Thr Asn Trp Gly Asn
            340                 345                 350
Leu Gly Tyr Pro Asn Gly Tyr Thr Ser Tyr Asp Tyr Gly Ser Ala Val
        355                 360                 365
Thr Glu Ser Arg Asn Ile Thr Arg Glu Lys Tyr Ser Glu Leu Lys Leu
    370                 375                 380
Leu Gly Asn Phe Ala Lys Val Ser Pro Gly Tyr Leu Thr Ala Ser Pro
385                 390                 395                 400
Gly Asn Leu Thr Thr Ser Gly Tyr Ala Asp Thr Thr Asp Leu Thr Val
                405                 410                 415
Thr Pro Leu Leu Gly Asn Ser Thr Gly Ser Phe Phe Val Val Arg His
            420                 425                 430
Ser Asp Tyr Ser Ser Glu Glu Ser Thr Ser Tyr Lys Leu Arg Leu Pro
        435                 440                 445
Thr Ser Ala Ser Ser Val Thr Ile Pro Gln Leu Gly Gly Thr Leu Thr
    450                 455                 460
Leu Asn Gly Arg Asp Ser Lys Ile His Val Thr Asp Tyr Asn Val Ser
465                 470                 475                 480
Gly Thr Asn Ile Ile Tyr Ser Thr Ala Glu Val Phe Thr Trp Lys Lys
                485                 490                 495
Phe Ala Asp Gly Lys Val Leu Val Leu Tyr Gly Gly Ala Gly Glu His
            500                 505                 510
His Glu Leu Ala Ile Ser Thr Lys Ser Asn Val Thr Val Ile Glu Gly
        515                 520                 525
Ser Glu Ser Gly Ile Ser Ser Lys Gln Thr Ser Ser Ser Val Val Val
    530                 535                 540
```

```
Gly Trp Asp Val Ser Thr Thr Arg Arg Ile Ile Gln Val Gly Asp Leu
545                 550                 555                 560
Lys Ile Leu Leu Leu Asp Arg Asn Ser Ala Tyr Asn Tyr Trp Val Pro
                565                 570                 575
Gln Leu Ala Thr Asp Gly Thr Ser Pro Gly Phe Ser Thr Pro Glu Lys
            580                 585                 590
Val Ala Ser Ser Ile Ile Val Lys Ala Gly Tyr Leu Val Arg Thr Ala
        595                 600                 605
Tyr Leu Lys Gly Ser Gly Leu Tyr Leu Thr Ala Asp Phe Asn Ala Thr
    610                 615                 620
Thr Ser Val Glu Val Ile Gly Val Pro Ser Thr Ala Lys Asn Leu Phe
625                 630                 635                 640
Ile Asn Gly Asp Lys Thr Ser His Thr Val Asp Lys Asn Gly Ile Trp
                645                 650                 655
Ser Ala Thr Val Asp Tyr Asn Ala Pro Asp Ile Ser Leu Pro Ser Leu
            660                 665                 670
Lys Asp Leu Asp Trp Lys Tyr Val Asp Thr Leu Pro Glu Ile Gln Ser
        675                 680                 685
Ser Tyr Asp Asp Ser Leu Trp Pro Ala Ala Asp Leu Lys Gln Thr Lys
    690                 695                 700
Asn Thr Leu Arg Ser Leu Thr Thr Pro Thr Ser Leu Tyr Ser Ser Asp
705                 710                 715                 720
Tyr Gly Phe His Thr Gly Tyr Leu Leu Tyr Arg Gly His Phe Thr Ala
                725                 730                 735
Thr Gly Asn Glu Ser Thr Phe Ala Ile Asp Thr Gln Gly Gly Ser Ala
            740                 745                 750
Phe Gly Ser Ser Val Trp Leu Asn Gly Thr Tyr Leu Gly Ser Trp Thr
        755                 760                 765
Gly Leu Tyr Ala Asn Ser Asp Tyr Asn Ala Thr Tyr Asn Leu Pro Gln
    770                 775                 780
Leu Gln Ala Gly Lys Thr Tyr Val Ile Thr Val Val Ile Asn Asn Met
785                 790                 795                 800
Gly Leu Glu Glu Asn Trp Thr Val Gly Glu Asp Leu Met Lys Thr Pro
                805                 810                 815
Arg Gly Ile Leu Asn Phe Leu Leu Ala Gly Arg Pro Ser Ser Ala Ile
            820                 825                 830
Ser Trp Lys Leu Thr Gly Asn Leu Gly Gly Glu Asp Tyr Glu Asp Lys
        835                 840                 845
Val Arg Gly Pro Leu Asn Glu Gly Gly Leu Tyr Ala Glu Arg Gln Gly
    850                 855                 860
Phe His Gln Pro Glu Pro Pro Ser Gln Asp Trp Lys Ser Ser Ser Pro
865                 870                 875                 880
Leu Glu Gly Leu Ser Glu Ala Gly Ile Gly Phe Tyr Ser Ala Ser Phe
                885                 890                 895
Asp Leu Asp Leu Pro Lys Gly Trp Asp Val Pro Leu Phe Leu Asn Ile
            900                 905                 910
Gly Asn Ser Thr Thr Pro Ser Pro Tyr Arg Val Gln Val Tyr Val Asn
        915                 920                 925
Gly Tyr Gln Tyr Ala Lys Tyr Ile Ser Asn Ile Gly Pro Gln Thr Ser
    930                 935                 940
Phe Pro Val Pro Glu Gly Ile Leu Asn Tyr Arg Gly Thr Asn Trp Leu
945                 950                 955                 960
Ala Val Thr Leu Trp Ala Leu Asp Ser Ala Gly Gly Lys Leu Glu Ser
                965                 970                 975
```

```
Leu Glu Leu Ser Tyr Thr Thr Pro Val Leu Thr Ala Leu Gly Glu Val
            980                 985                 990
Glu Ser Val Asp Gln Pro Lys Tyr Lys Lys Arg Lys Gly Ala Tyr
        995                 1000                1005


<210> 713
<211> 1025
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase B;
      AltName: Full=Lactase B; Flags: Precursor 1025 aa
      protein Q5BEQ0.2 GI:300681009

<400> 713
Met Ala Thr Ala Phe Trp Leu Leu Leu Phe Leu Leu Gly Ser Leu His
 1               5                  10                  15
Val Leu Thr Ala Ala Gln Asn Ser Ser Gln Ser Glu Trp Pro Ile His
            20                  25                  30
Asp Asn Gly Leu Ser Lys Val Val Gln Trp Asp His Tyr Ser Phe Tyr
        35                  40                  45
Ile Asn Gly Gln Arg Ile Phe Leu Phe Ser Gly Glu Phe His Tyr Trp
    50                  55                  60
Arg Ile Pro Val Pro Ala Leu Trp Arg Asp Ile Leu Glu Lys Ile Lys
65                  70                  75                  80
Ala Ile Gly Phe Thr Gly Phe Ala Phe Tyr Ser Ser Trp Ala Tyr His
                85                  90                  95
Ala Pro Asn Asn Gln Thr Val Asp Phe Ser Thr Gly Ala Arg Asp Ile
            100                 105                 110
Thr Pro Ile Tyr Asp Leu Ala Lys Glu Leu Gly Met Tyr Ile Ile Val
        115                 120                 125
Arg Pro Gly Pro Tyr Val Asn Ala Glu Ala Ser Ala Gly Gly Phe Pro
    130                 135                 140
Leu Trp Leu Thr Thr Gly Ala Tyr Gly Ser Thr Arg Asn Asp Asp Pro
145                 150                 155                 160
Arg Tyr Thr Ala Ala Trp Glu Pro Tyr Phe Ala Glu Val Ser Glu Ile
                165                 170                 175
Thr Ser Lys Tyr Gln Val Thr Asp Gly His Tyr Thr Leu Cys Tyr Gln
            180                 185                 190
Ile Glu Asn Glu Tyr Gly Gln Gln Trp Ile Gly Asp Pro Arg Asp Arg
        195                 200                 205
Asn Pro Asn Gln Thr Ala Ile Ala Tyr Met Glu Leu Leu Gln Ala Ser
    210                 215                 220
Ala Arg Glu Asn Gly Ile Thr Val Pro Leu Thr Gly Asn Asp Pro Asn
225                 230                 235                 240
Met Asn Thr Lys Ser Trp Gly Ser Asp Trp Ser Asp Ala Gly Gly Asn
                245                 250                 255
Leu Asp Thr Val Gly Leu Asp Ser Tyr Pro Ser Cys Trp Ser Cys Asp
            260                 265                 270
Val Ser Val Cys Thr Gly Thr Asn Gly Glu Tyr Val Pro Tyr Lys Val
        275                 280                 285
Leu Asp Tyr Tyr Asp Tyr Phe Gln Glu Val Gln Pro Thr Met Pro Phe
```

```
    290                 295                 300
Phe Met Pro Glu Phe Gln Gly Gly Ser Tyr Asn Pro Trp Asp Gly Pro
305                 310                 315                 320
Glu Gly Gly Cys Thr Glu Asp Thr Gly Ala Asp Phe Ala Asn Leu Phe
                325                 330                 335
Tyr Arg Trp Asn Ile Gly Gln Arg Val Ser Ala Met Ser Leu Tyr Met
            340                 345                 350
Met Phe Gly Gly Thr Asn Trp Gly Gly Ile Ala Ala Pro Val Thr Ala
        355                 360                 365
Ser Ser Tyr Asp Tyr Ser Ala Pro Ile Ser Glu Asp Arg Ser Ile Gly
    370                 375                 380
Ser Lys Tyr Tyr Glu Thr Lys Leu Leu Ala Leu Phe Thr Arg Cys Ala
385                 390                 395                 400
Lys Asp Leu Thr Met Thr Asp Arg Leu Gly Asn Gly Thr Gln Tyr Thr
                405                 410                 415
Asp Asn Glu Ala Val Ile Ala Ser Glu Leu Arg Asn Pro Asp Thr Asn
            420                 425                 430
Ala Ala Phe Tyr Val Thr Thr His Leu Asp Thr Thr Val Gly Thr Asp
        435                 440                 445
Glu Ser Phe Lys Leu His Val Asn Thr Ser Lys Gly Ala Leu Thr Ile
    450                 455                 460
Pro Arg His Gly Gly Thr Ile Arg Leu Asn Gly His His Ser Lys Ile
465                 470                 475                 480
Ile Val Thr Asp Phe Asn Phe Gly Ser Glu Thr Leu Leu Tyr Ser Thr
                485                 490                 495
Ala Glu Val Leu Thr Tyr Ala Val Phe Asp Arg Lys Pro Thr Leu Val
            500                 505                 510
Leu Trp Val Pro Thr Gly Glu Ser Gly Glu Phe Ala Ile Lys Gly Ala
        515                 520                 525
Lys Ser Gly Ser Val Ala Lys Cys Ser Gly Cys Ser Asn Ile Lys Phe
    530                 535                 540
His Arg Asp Ser Gly Ser Leu Thr Val Ala Phe Thr Gln Gly Glu Gly
545                 550                 555                 560
Ile Ser Val Leu Gln Leu Asp Asn Gly Val Arg Val Val Leu Leu Asp
                565                 570                 575
Arg Gln Lys Ala Tyr Thr Phe Trp Ala Pro Ala Leu Thr Asp Asn Pro
            580                 585                 590
Leu Val Pro Glu Gly Glu Ser Val Leu Val Ser Gly Pro Tyr Leu Val
        595                 600                 605
Arg Thr Ala Arg Leu Ala Arg Ser Thr Leu Thr Leu Arg Gly Asp Ser
    610                 615                 620
Lys Gly Glu Thr Leu Glu Ile Phe Ala Pro Arg Lys Ile Lys Lys Val
625                 630                 635                 640
Thr Trp Asn Gly Lys Ala Val Glu Ala Thr Arg Thr Ser Tyr Gly Ser
                645                 650                 655
Leu Lys Ala Ile Leu Ala Lys Pro Pro Ser Val Glu Leu Pro Thr Leu
            660                 665                 670
Asn Gly Trp Lys Tyr Ser Asp Ser Leu Pro Glu Arg Phe Pro Thr Tyr
        675                 680                 685
Asp Asp Ser Gly Ala Ala Trp Val Glu Ile Asp Ala Asn His Met Thr
    690                 695                 700
Thr Pro Asn Pro Asn Lys Pro Ala Thr Leu Pro Val Leu Tyr Ala Asp
705                 710                 715                 720
Glu Tyr Gly Phe His Asn Gly Val Arg Leu Trp Arg Gly Tyr Phe Asn
```

```
                725                 730                 735
Ser Ser Ala Ser Gly Val Tyr Leu Asn Ile Gln Gly Gly Ala Ala Phe
            740                 745                 750
Gly Trp Ser Ala Trp Leu Asn Gly His Phe Leu Gly Ser His Leu Gly
        755                 760                 765
Ser Ala Ser Ile Gln Gln Ala Asn Gly Thr Leu Asp Phe Pro Ala Asn
    770                 775                 780
Thr Leu Asn Thr Glu Gly Thr Pro Asn Val Leu Leu Val Val His Asp
785                 790                 795                 800
Asp Thr Gly His Asp Gln Thr Thr Gly Val Leu Asn Pro Arg Gly Ile
                805                 810                 815
Leu Glu Ala Arg Leu Leu Ser Glu Ala Ser Asp Asn Asn Asp Asp Asp
            820                 825                 830
Ser Pro Gly Phe Thr His Trp Arg Val Ala Gly Thr Ala Gly Gly Glu
        835                 840                 845
Ser Asp Leu Asp Pro Val Arg Gly Val Tyr Asn Glu Asp Gly Leu Tyr
    850                 855                 860
Ala Glu Arg Val Gly Trp His Leu Pro Gly Phe Asp Asp Ser Lys Trp
865                 870                 875                 880
Ala Thr Val Asn Gly Thr Ser Leu Ser Phe Thr Gly Ala Thr Val Arg
                885                 890                 895
Phe Phe Arg Thr Val Ile Pro Pro Leu Ser Ile Pro Glu Asn Thr Asp
            900                 905                 910
Val Ser Ile Ser Phe Val Phe Ser Thr Pro Asn Val Asn Asn Thr Ser
        915                 920                 925
Ala Gly Asn Thr Ser Ala Phe Arg Ala Gln Leu Phe Val Asn Gly Tyr
    930                 935                 940
Gln Tyr Gly Arg Tyr Asn Pro Tyr Val Gly Asn Gln Val Val Tyr Pro
945                 950                 955                 960
Val Pro Pro Gly Ile Leu Asp Tyr Asn Gly Glu Asn Thr Ile Gly Val
                965                 970                 975
Ala Val Trp Ala Gln Thr Glu Ala Gly Ala Arg Leu Asn Leu Asp Trp
            980                 985                 990
Arg Val Asn Tyr Val Leu Gly Ser Ser Leu Asp Ala Gly Arg Leu Asp
        995                 1000                1005
Leu Ser Phe Val Ala Ile Ala Tyr Val Tyr Ile Phe Glu Cys Leu Gln
    1010                1015                1020
Leu
1025


<210> 714
<211> 1007
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Probable beta-galactosidase A;
      AltName: Full=Lactase A; Flags: Precursor 1007 aa
      protein Q5BFC4.2 GI:300681016

<400> 714
Met Arg Leu Leu Pro Val Trp Thr Ala Ala Leu Leu Ala Ala Gln Ala
 1               5                  10                  15
```

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

```
Thr Ser Ala Gly Gln Leu Thr Ile Pro Gln Leu Gly Gly Ser Leu Val
    450                 455                 460
Leu Asn Gly Arg Asp Ser Lys Val His Leu Val Asp Tyr Asp Val Ala
465                 470                 475                 480
Gly Thr Lys Ile Leu Tyr Ser Thr Ala Glu Val Phe Thr Trp Lys Lys
                485                 490                 495
Phe His Asp Gly Lys Val Leu Val Leu Tyr Gly Gly Pro Gly Glu His
            500                 505                 510
His Glu Leu Ala Val Ser Ser Lys Ala Lys Val Lys Val Val Glu Gly
        515                 520                 525
Leu Gly Ser Gly Ile Ser Ser Lys Gln Ile Arg Gly Ala Val Val Val
    530                 535                 540
Ala Trp Asp Val Glu Pro Ala Arg Arg Ile Val Gln Ile Gly Asp Leu
545                 550                 555                 560
Lys Ile Phe Leu Leu Asp Arg Asn Ser Ala Tyr Asn Tyr Trp Val Pro
                565                 570                 575
Gln Leu Gly Thr Glu Thr Ser Ile Pro Tyr Ala Thr Glu Lys Ala Val
            580                 585                 590
Ala Ala Ser Val Ile Val Lys Ala Gly Tyr Leu Val Arg Thr Ala Tyr
        595                 600                 605
Val Lys Gly Arg Asp Leu His Leu Thr Ala Asp Phe Asn Ala Thr Thr
    610                 615                 620
Pro Val Glu Val Ile Gly Ala Pro Lys Thr Ala Glu Asn Leu Phe Ile
625                 630                 635                 640
Asn Gly Lys Lys Ala His His Thr Val Asp Lys Asn Gly Ile Trp Ser
                645                 650                 655
Thr Glu Val Gly Tyr Ser Pro Pro Lys Ile Val Leu Pro Val Leu Glu
            660                 665                 670
Asp Leu Lys Trp Lys Ser Ile Asp Thr Leu Pro Glu Ile Gln Pro Ser
        675                 680                 685
Tyr Asp Asp Ser Pro Trp Pro Asp Ala Asn Leu Pro Thr Lys Asn Thr
    690                 695                 700
Ile Tyr Pro Leu Arg Thr Pro Thr Ser Leu Tyr Ala Ser Asp Tyr Gly
705                 710                 715                 720
Phe His Thr Gly Tyr Leu Leu Phe Arg Gly His Phe Thr Ala Asn Gly
                725                 730                 735
Arg Glu Ser Asn Phe Ser Ile Gln Thr Gln Gly Gly Gln Ala Phe Gly
            740                 745                 750
Ser Ser Val Trp Leu Ser Gly Thr Tyr Leu Gly Ser Trp Thr Gly Asp
        755                 760                 765
Asn Asp Tyr Gln Asp Tyr Asn Ala Thr Tyr Thr Leu Pro Ser Leu Lys
    770                 775                 780
Ala Gly Lys Glu Tyr Val Phe Thr Val Val Val Asp Asn Met Gly Leu
785                 790                 795                 800
Asn Glu Asn Trp Ile Val Gly Gln Asp Glu Met Lys Lys Pro Arg Gly
                805                 810                 815
Ile Leu Asn Tyr Glu Leu Ser Gly His Glu Ala Ser Asp Ile Thr Trp
            820                 825                 830
Lys Leu Thr Gly Asn Phe Gly Gly Glu Asp Tyr Val Asp Lys Val Arg
        835                 840                 845
Gly Pro Leu Asn Glu Gly Gly Leu Tyr Ala Glu Arg His Gly Tyr His
    850                 855                 860
Gln Pro Tyr Pro Pro Thr Lys Ser Lys Asp Trp Lys Ser Ser Thr Pro
865                 870                 875                 880
```

```
Leu Thr Gly Leu Ser Lys Pro Gly Ile Ser Phe Tyr Thr Ala Ser Phe
                885                 890                 895
Asp Leu Asp Ile Lys Ser Gly Trp Asp Val Pro Ile Tyr Phe Glu Phe
            900                 905                 910
Gly Asn Ser Thr Thr Pro Ala Pro Ala Tyr Arg Val Gln Leu Tyr Val
        915                 920                 925
Asn Gly Trp Gln Tyr Gly Lys Tyr Val Asn Asn Ile Gly Pro Gln Thr
    930                 935                 940
Arg Phe Pro Val Pro Glu Gly Ile Leu Asn Tyr Lys Gly Thr Asn Trp
945                 950                 955                 960
Val Ala Val Thr Leu Trp Ala Leu Glu Gly Ser Gly Ala Lys Leu Asp
                965                 970                 975
Ser Phe Lys Leu Val His Gly Ile Pro Val Arg Thr Ala Leu Asp Val
            980                 985                 990
Glu Gly Val Glu Leu Pro Arg Tyr Gln Ser Arg Lys Gly Val Tyr
        995                 1000                1005


<210> 715
<211> 988
<212> PRT
<213> Artificial Sequence

<220>
<223> lactase, partial [Aspergillus niger] 988 aa
      protein ABL07484.1 GI:118582212

<400> 715
Ser Ile Lys His Arg Ile Asn Gly Phe Thr Leu Thr Glu His Ser Asp
 1               5                  10                  15
Pro Ala Lys Arg Glu Leu Leu Gln Lys Tyr Val Thr Trp Asp Asp Lys
            20                  25                  30
Ser Leu Phe Ile Asn Gly Glu Arg Ile Met Ile Phe Ser Gly Glu Phe
        35                  40                  45
His Pro Phe Arg Leu Pro Val Lys Glu Leu Gln Leu Asp Ile Phe Gln
    50                  55                  60
Lys Val Lys Ala Leu Gly Phe Asn Cys Val Ser Phe Tyr Val Asp Trp
65                  70                  75                  80
Ala Leu Val Glu Gly Lys Pro Gly Glu Tyr Gly Ala Asp Gly Ile Phe
                85                  90                  95
Asp Leu Glu Pro Phe Phe Asp Ala Ala Ser Glu Ala Gly Ile Tyr Leu
            100                 105                 110
Leu Ala Arg Pro Gly Pro Tyr Ile Asn Ala Glu Ser Ser Gly Gly Gly
        115                 120                 125
Phe Pro Gly Trp Leu Gln Arg Val Asn Gly Thr Leu Arg Thr Ser Asp
    130                 135                 140
Lys Ala Tyr Leu Glu Ala Thr Asp Asn Tyr Val Ser His Ile Ala Ala
145                 150                 155                 160
Thr Ile Ala Lys Tyr Gln Ile Thr Asn Gly Gly Pro Ile Ile Leu Tyr
                165                 170                 175
Gln Pro Glu Asn Glu Tyr Thr Gly Gly Cys Cys Gly Val Glu Phe Pro
            180                 185                 190
Asp Pro Val Tyr Met Gln Tyr Val Glu Asp Gln Ala Arg Asn Ala Gly
        195                 200                 205
```

```
Val Val Ile Pro Leu Ile Asn Asn Asp Ala Ser Ala Ser Gly His Asn
    210                 215                 220
Ala Pro Gly Thr Gly Glu Gly Ala Val Asp Ile Tyr Gly His Asp Ser
225                 230                 235                 240
Tyr Pro Leu Gly Phe Asp Cys Ala Asn Pro Thr Val Trp Pro Ser Gly
                245                 250                 255
Asp Leu Pro Thr Asn Phe Arg Thr Leu His Leu Val Gln Ser Pro Thr
            260                 265                 270
Thr Pro Tyr Ala Ile Val Glu Phe Gln Gly Gly Ser Tyr Asp Pro Trp
        275                 280                 285
Gly Gly Pro Gly Phe Ala Ala Cys Ser Glu Leu Leu Asn Asn Glu Phe
    290                 295                 300
Glu Arg Val Phe Tyr Lys Asn Asp Phe Ser Phe Gln Ile Ala Ile Met
305                 310                 315                 320
Asn Leu Tyr Met Ile Phe Gly Gly Thr Asn Trp Gly Asn Leu Gly Tyr
                325                 330                 335
Pro Asn Gly Tyr Thr Ser Tyr Asp Tyr Gly Ser Ala Val Thr Glu Ser
            340                 345                 350
Arg Asn Ile Thr Arg Glu Lys Tyr Ser Glu Leu Lys Leu Leu Gly Asn
        355                 360                 365
Phe Ala Lys Val Ser Pro Gly Tyr Leu Thr Ala Ser Pro Gly Asn Leu
    370                 375                 380
Thr Thr Ser Gly Tyr Ala Asp Thr Thr Asp Leu Thr Val Thr Pro Leu
385                 390                 395                 400
Leu Gly Asn Ser Thr Gly Ser Phe Phe Val Val Arg His Ser Asp Tyr
                405                 410                 415
Ser Ser Glu Asp Ser Thr Ser Tyr Lys Leu Arg Leu Pro Thr Ser Ala
            420                 425                 430
Gly Thr Val Thr Ile Pro Gln Leu Gly Gly Thr Leu Thr Leu Asn Gly
        435                 440                 445
Arg Asp Ser Lys Ile His Val Thr Asp Tyr Asn Val Ser Gly Thr Asn
    450                 455                 460
Ile Ile Tyr Ser Thr Ala Glu Val Phe Thr Trp Lys Lys Phe Ala Asp
465                 470                 475                 480
Gly Lys Val Leu Val Leu Tyr Gly Gly Ala Gly Glu His His Glu Leu
                485                 490                 495
Ala Ile Ser Thr Lys Ser Asn Val Thr Val Ile Glu Gly Ser Glu Ser
            500                 505                 510
Gly Ile Ser Ser Lys Gln Thr Ser Ser Ser Val Ile Val Gly Trp Asp
        515                 520                 525
Val Ser Thr Thr Arg Arg Ile Ile Gln Val Gly Asp Leu Lys Val Leu
    530                 535                 540
Leu Leu Asp Arg Asn Ser Ala Tyr Asn Tyr Trp Val Pro Gln Leu Ala
545                 550                 555                 560
Thr Asp Gly Thr Ser Pro Gly Phe Ser Thr Ser Glu Thr Val Ala Ser
                565                 570                 575
Ser Ile Ile Val Lys Ala Gly Tyr Leu Val Arg Thr Ala Tyr Leu Lys
            580                 585                 590
Gly Ser Gly Leu Tyr Leu Thr Ala Asp Phe Asn Ala Thr Thr Ser Val
        595                 600                 605
Glu Val Ile Gly Val Pro Ser Thr Ala Lys Asn Leu Phe Ile Asn Gly
    610                 615                 620
Asp Lys Thr Ser His Thr Val Asp Lys Asn Gly Ile Trp Ser Ala Thr
625                 630                 635                 640
```

```
Val Glu Tyr Asn Ala Pro Asp Ile Ser Leu Pro Ser Leu Lys Asp Leu
                645                 650                 655
Asp Trp Lys Tyr Val Asp Thr Leu Pro Glu Ile Gln Ser Ser Tyr Asp
            660                 665                 670
Asp Ser Leu Trp Pro Ala Ala Asp Leu Lys Gln Thr Lys Asn Thr Leu
        675                 680                 685
Arg Ser Leu Thr Thr Pro Thr Ser Leu Tyr Ser Ser Asp Tyr Gly Phe
    690                 695                 700
His Thr Gly Tyr Leu Leu Tyr Arg Gly His Phe Thr Ala Thr Gly Asn
705                 710                 715                 720
Glu Ser Thr Phe Ser Ile Asp Thr Gln Gly Gly Ser Ala Phe Gly Ser
                725                 730                 735
Ser Val Trp Leu Asn Gly Thr Tyr Leu Gly Ser Trp Thr Gly Leu Tyr
            740                 745                 750
Val Asn Ser Asp Tyr Asn Ala Thr Tyr Lys Leu Pro Gln Leu Gln Ala
        755                 760                 765
Gly Lys Ser Tyr Val Ile Thr Val Val Ile Asp Asn Met Gly Leu Glu
    770                 775                 780
Glu Asn Trp Thr Val Gly Glu Asp Leu Met Lys Thr Pro Arg Gly Ile
785                 790                 795                 800
Leu Asn Phe Leu Leu Ala Gly Arg Pro Gly Ser Ala Ile Ser Trp Lys
                805                 810                 815
Leu Thr Gly Asn Leu Gly Gly Glu Asp Tyr Glu Asp Lys Val Arg Gly
            820                 825                 830
Pro Leu Asn Glu Gly Gly Leu Tyr Ala Glu Arg Gln Gly Phe His Gln
        835                 840                 845
Pro Glu Pro Pro Ser Gly Asn Trp Lys Ser Ser Ser Pro Leu Glu Gly
    850                 855                 860
Leu Ser Glu Ala Gly Ile Gly Phe Tyr Ser Ala Lys Phe Asp Leu Asp
865                 870                 875                 880
Leu Pro Lys Gly Trp Asp Val Pro Leu Phe Leu Asn Ile Gly Asn Ser
                885                 890                 895
Thr Thr Pro Ser Pro Tyr Arg Val Gln Val Tyr Val Asn Gly Tyr Gln
            900                 905                 910
Tyr Ala Lys Tyr Ile Ser Asn Asn Gly Pro Gln Thr Ser Phe Pro Val
        915                 920                 925
Pro Glu Gly Ile Leu Asn Tyr Arg Gly Thr Asn Trp Leu Ala Val Thr
    930                 935                 940
Leu Trp Ala Leu Asp Ser Ala Gly Gly Lys Leu Glu Ser Leu Glu Leu
945                 950                 955                 960
Ser Tyr Thr Thr Pro Val Leu Thr Ala Leu Gly Glu Val Glu Ser Val
                965                 970                 975
Asp Gln Pro Lys Tyr Lys Lys Arg Lys Gly Ala Tyr
            980                 985
```

<210> 716
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<223> unnamed protein product [Aspergillus oryzae RIB40]
438 aa protein BAE57671.1 GI:83767532

<400> 716
Met Gly Ser Thr Ser Thr Ser Thr Leu Pro Pro Asp Phe Leu Trp Gly
 1               5                  10                  15
Phe Ala Thr Ala Ser Tyr Gln Ile Glu Gly Ala Val Asn Glu Asp Gly
            20                  25                  30
Arg Gly Pro Ser Ile Trp Asp Thr Phe Cys Lys Ile Pro Gly Lys Ile
        35                  40                  45
Ala Gly Gly Ala Asn Gly Asp Val Ala Cys Asp Ser Tyr His Arg Thr
    50                  55                  60
His Glu Asp Ile Ala Leu Leu Lys Ala Cys Gly Ala Lys Ala Tyr Arg
65                  70                  75                  80
Phe Ser Leu Ser Trp Ser Arg Ile Ile Pro Leu Gly Gly Arg Asn Asp
                85                  90                  95
Pro Ile Asn Glu Lys Gly Leu Gln Tyr Tyr Ile Lys Phe Val Asp Asp
            100                 105                 110
Leu His Ala Ala Gly Ile Thr Pro Leu Val Thr Leu Phe His Trp Asp
        115                 120                 125
Leu Pro Asp Glu Leu Asp Lys Arg Tyr Gly Gly Leu Leu Asn Lys Glu
    130                 135                 140
Glu Phe Val Ala Asp Phe Ala His Tyr Ala Arg Ile Val Phe Lys Ala
145                 150                 155                 160
Phe Gly Ser Lys Val Lys His Trp Ile Thr Phe Asn Glu Pro Trp Cys
                165                 170                 175
Ser Ser Val Leu Gly Tyr Asn Val Gly Gln Phe Ala Pro Gly Arg Thr
            180                 185                 190
Ser Asp Arg Ser Lys Ser Pro Val Gly Asp Ser Ser Arg Glu Cys Trp
        195                 200                 205
Ile Val Gly His Ser Leu Leu Val Ala His Gly Ala Ala Val Lys Ile
    210                 215                 220
Tyr Arg Asp Glu Phe Lys Ala Ser Asp Gly Gly Glu Ile Gly Ile Thr
225                 230                 235                 240
Leu Asn Gly Asp Trp Ala Glu Pro Trp Asp Pro Glu Asn Pro Ala Asp
                245                 250                 255
Val Glu Ala Cys Asp Arg Lys Ile Glu Phe Ala Ile Ser Trp Phe Ala
            260                 265                 270
Asp Pro Ile Tyr His Gly Lys Tyr Pro Asp Ser Met Val Lys Gln Leu
        275                 280                 285
Gly Asp Arg Leu Pro Lys Trp Thr Pro Glu Asp Ile Ala Leu Val His
    290                 295                 300
Gly Ser Asn Asp Phe Tyr Gly Met Asn His Tyr Cys Ala Asn Phe Ile
305                 310                 315                 320
Lys Ala Lys Thr Gly Glu Ala Asp Pro Asn Asp Thr Ala Gly Asn Leu
                325                 330                 335
Glu Ile Leu Leu Gln Asn Lys Lys Gly Glu Trp Val Gly Pro Glu Thr
            340                 345                 350
Gln Ser Pro Trp Leu Arg Pro Ser Ala Ile Gly Phe Arg Lys Leu Leu
        355                 360                 365
Lys Trp Leu Ser Glu Arg Tyr Asn Tyr Pro Lys Ile Tyr Val Thr Glu
    370                 375                 380
Asn Gly Thr Ser Leu Lys Gly Glu Asn Asp Leu Pro Leu Glu Gln Leu
385                 390                 395                 400
Leu Gln Asp Asp Phe Arg Thr Gln Tyr Phe Arg Asp Tyr Ile Gly Ala
                405                 410                 415

Met Ala Asp Ala Tyr Thr Leu Asp Gly Val Asn Val Arg Ala Tyr Met
420 425 430
Ala Trp Ser Leu Met Glu
435

<210> 717
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> unnamed protein product [Aspergillus oryzae RIB40]
458 aa protein BAE62705.1 GI:83772577

<400> 717
Met Ala Arg Val Arg Leu Lys Leu Pro Ala Asp Phe Ile Trp Gly Val
1 5 10 15
Ser Ser Ser Ser Trp Gln Ile Glu Gly Gly Leu Gln Leu Glu Gly Arg
20 25 30
Gly Pro Ser Val Leu Asp Thr Ile Gly Asn Val Leu Ser Pro Glu Ala
35 40 45
Ala Asp Arg Ser Asp Ala Asn Val Ala Asn Met His Tyr Phe Met Tyr
50 55 60
Glu Gln Asp Ile Ala Arg Leu Ala Ala Ala Gly Ile Pro Tyr Tyr Ser
65 70 75 80
Phe Ser Leu Ser Trp Pro Arg Ile Val Pro Phe Gly Val Ala Gly Ser
85 90 95
Pro Val Asn Thr Gln Gly Leu Asp His Tyr Asp Asp Leu Ile Asn Thr
100 105 110
Cys Ile Lys Tyr Gly Val Thr Pro Ile Val Thr Leu Asn His Val Asp
115 120 125
Ala Pro Thr Ala Val Gln Ala Asp Leu Asp Ser Leu Pro Glu His Phe
130 135 140
Leu Tyr Tyr Ala Lys Ile Val Met Thr Arg Tyr Ala Asp Arg Val Pro
145 150 155 160
Tyr Trp Val Thr Phe Asn Glu Pro Asn Ile Gly Val Gly Thr Leu Phe
165 170 175
Gln Lys Tyr Gln Asp Leu Thr Ser Ala Leu Ile Ala His Ala Asp Val
180 185 190
Tyr Asp Trp Tyr Lys Asn Thr Leu Gly Gly Thr Gly Lys Ile Thr Met
195 200 205
Lys Phe Ala Asn Asn Leu Ala Met Pro Leu Asp Thr Gln Asp Ser Ser
210 215 220
His Ile Ala Ala Ala Ser Arg Tyr Gln Asp Ile Leu Leu Gly Ile Met
225 230 235 240
Ser Asn Pro Leu Phe Leu Gly Lys Gln Tyr Pro Asp Ala Ala Ile Asp
245 250 255
Thr Val Asp Met Met Gln Pro Leu Thr Asp Asp Gln Ile Lys His Ile
260 265 270
His Gly Lys Ile Asp Phe Trp Ser Phe Asp Pro Tyr Thr Ala Gln Tyr
275 280 285
Ala Ser Pro Leu Pro Gln Gly Thr Glu Ala Cys Ala Ser Asn Ser Ser
290 295 300

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


<210> 718
<211> 506
<212> PRT
<213> Artificial Sequence

<220>
<223> unnamed protein product [Aspergillus oryzae RIB40]
      506 aa protein BAE63197.1 GI:83773069

<400> 718
Met Asn Val Asn Met Phe Lys Ala Gly Asp Asp Ile Leu Gln Asp Val
 1               5                  10                  15
Asp Gln Ser Cys Lys Asp Arg Leu Pro Ala Val Glu Glu Leu Pro Leu
            20                  25                  30
Pro Pro Ser Phe Thr Trp Gly Thr Ala Thr Ala Ala Tyr Gln Val Glu
        35                  40                  45
Gly Gly Ala Phe Gln Asp Gly Lys Gly Lys Ser Ile Trp Asp Thr Phe
    50                  55                  60
Thr His Leu Asp Pro Ser Arg Thr Asn Gly Glu Asn Gly Asp Ile Ala
65                  70                  75                  80
Cys Asp His Tyr Asn Arg Met Ala Glu Asp Val Val Leu Met Ala Ser
                85                  90                  95
Tyr Gly Val Asp Val Tyr Arg Phe Ser Ile Ala Trp Ala Arg Ile Leu
            100                 105                 110
Pro Leu Gly Gly Arg Gly Asp Pro Ile Asn Glu Lys Gly Ile Ala Phe
        115                 120                 125
Tyr Asn Asn Leu Ile Asp Cys Leu Leu Glu His Asn Ile Glu Pro Val
    130                 135                 140
Val Thr Leu Tyr His Trp Asp Val Pro Gln Gly Leu Tyr Asp Arg Tyr
145                 150                 155                 160
Gly Ala Phe Leu Asp Thr Thr Glu Phe Arg Ala Asp Phe Glu His Phe
                165                 170                 175
```

```
Ala Arg Leu Cys Phe Ser Arg Phe Gly Asp Arg Val Lys Arg Trp Ile
            180                 185                 190
Thr Phe Asn Glu Pro Tyr Ile Ile Ser Ile Phe Gly His His Ser Gly
        195                 200                 205
Val Leu Ala Pro Gly Arg Ser Ser Ala Thr Gly Gly Asp Ser Arg Thr
    210                 215                 220
Glu Pro Trp Arg Val Gly His Thr Ile Ile Leu Ala His Thr Ala Ala
225                 230                 235                 240
Val Gln Ala Tyr Ala Thr Asp Phe Gln Pro Thr Gln Lys Gly Asp Ile
                245                 250                 255
Ser Ile Val Leu Asn Gly His Tyr Tyr Glu Pro Trp Asp Ala Gly Ser
            260                 265                 270
Glu Glu His Arg Leu Ala Ala Gln Arg Arg Leu Glu Phe Tyr Ile Gly
        275                 280                 285
Trp Phe Gly Asp Pro Ile Phe Leu Gly Lys Asp Tyr Pro Ala Pro Met
    290                 295                 300
Arg Ala Gln Leu Gly Ser Arg Leu Pro Glu Phe Thr Ser Glu Glu Leu
305                 310                 315                 320
Asp Leu Leu Arg Arg Ser Ala Pro Ile Asn Ser Phe Tyr Gly Met Asn
                325                 330                 335
His Tyr Thr Thr Lys Tyr Ala Arg Ala Leu Pro Asp Pro Pro Ala Glu
            340                 345                 350
Asp Asp Cys Thr Gly Asn Val Glu Glu Gly Pro Thr Asn Ser Glu Gly
        355                 360                 365
Lys Thr Met Gly Pro Leu Ser Gly Met Ser Trp Leu Arg Val Thr Pro
    370                 375                 380
Ala Gly Phe Arg Lys Leu Leu Asn Trp Val Trp Asp Arg Tyr Arg Arg
385                 390                 395                 400
Pro Ile Val Val Thr Glu Asn Gly Cys Pro Cys Pro Gly Glu Ser Gln
                405                 410                 415
Met Thr Lys Glu Gln Ala Leu Asp Asp Gln Phe Arg Ile Arg Tyr Phe
            420                 425                 430
Gly Leu Tyr Leu Asp Ala Ile Ser Arg Ala Ile Tyr Asp Asp Gly Val
        435                 440                 445
Lys Val Glu Gly Tyr Tyr Val Trp Ser Leu Met Asp Asn Phe Glu Trp
    450                 455                 460
Ser Ala Gly Tyr Gly Pro Arg Tyr Gly Ile Thr His Val Asp Phe Thr
465                 470                 475                 480
Thr Leu Val Arg Thr Pro Lys Gln Ser Ala Lys Tyr Leu His His Ser
                485                 490                 495
Phe Asn Lys Arg Arg Ala Thr Ser Leu Arg
            500                 505
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<210> 719
<211> 1055
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-galactosidase [Aspergillus fumigatus Af293]
1055 aa protein XP_753202.1 GI:70996895

<400> 719

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

```
Tyr Glu Glu Arg Lys Lys Leu Thr Phe Gly Gln Ala Ala Gln Phe Thr
        435                 440                 445
Thr Asn Asn Pro Glu Trp Lys Glu Ala Tyr Val Asp Arg Met Ala Gln
    450                 455                 460
Met Val Gln Arg Asp Lys Asn His Ser Cys Ile Val Ile Trp Ser Leu
465                 470                 475                 480
Gly Asn Glu Ala Phe Tyr Gly Ser Asn His Gln Ala Met Tyr Asp Tyr
                485                 490                 495
Val Lys Gln Val Asp Pro Ser Arg Pro Val His Tyr Glu Gly Asp Met
            500                 505                 510
Glu Ala Lys Thr Val Asp Met Tyr Ser Tyr Met Tyr Pro Ser Leu Glu
        515                 520                 525
Arg Leu Val Gly Phe Ala Thr Ala Glu Gly Asp Glu Phe Lys Lys Pro
    530                 535                 540
Ile Val Leu Cys Glu Tyr Ala His Ala Met Gly Asn Ala Pro Gly Gly
545                 550                 555                 560
Leu Glu Glu Tyr Met Glu Ala Phe Arg Thr His Arg Arg Leu Gln Gly
                565                 570                 575
Gly Trp Val Trp Glu Trp Ala Asn His Gly Leu Trp Asp Glu Lys Lys
            580                 585                 590
Gly Trp Tyr Gly Tyr Gly Gly Asp Phe Gly Asp Thr Pro His Asp Gly
        595                 600                 605
Asn Phe Val Leu Asp Gly Leu Leu Phe Ser Asp His Thr Pro Thr Pro
    610                 615                 620
Gly Ile Thr Glu Leu Lys Lys Ala Tyr Ala Pro Val Arg Val Trp Pro
625                 630                 635                 640
Gly Glu Asp Gly Thr Leu Val Val Ala Asn Asp Tyr Asn Phe Val Gly
                645                 650                 655
Leu Glu Gly Leu Gln Ala Ser Tyr Lys Ile Glu Val Leu Gly Asp Ser
            660                 665                 670
Gly Arg Ile Ile Ala Thr Gly Ile Ile Glu Leu Pro Pro Ile Pro Ala
        675                 680                 685
Gly Gln Asn Gly Thr Ile Lys Leu Pro Ser Ala Pro Ala Thr Ala Ile
    690                 695                 700
Pro Gly Glu Val Trp Leu Thr Ile Ser Phe Leu Gln Lys Gly Glu Thr
705                 710                 715                 720
Ala Trp Ala Gly Asn Asn Tyr Glu Val Ala Trp Tyr Gln Gln Cys Leu
                725                 730                 735
Lys Ser Ser Ser Pro Arg Phe Ser Leu Ala Val Pro Ala Glu Ala Leu
            740                 745                 750
Thr His Ser Ser Thr Lys Thr Ser His Arg Ile Ser Gly Ala Ser Phe
        755                 760                 765
Ser Leu Glu Phe Ser Arg Glu Thr Gly Ser Leu Tyr Ala Trp Thr Ala
    770                 775                 780
Gly Gly Leu Ser Leu Leu Asp Gln Ser Ser Ser Thr Gly Ala Ile Ser
785                 790                 795                 800
Pro Gly Phe Trp Arg Pro Pro Thr Asp Asn Asp Met Ser His Asp Leu
                805                 810                 815
Leu Glu Trp Arg Arg Phe Gly Leu Asp Thr Leu Thr Ser Gln Leu Arg
            820                 825                 830
Lys Met His Val Val Gln His Thr Pro Thr Ser Val Glu Val Thr Thr
        835                 840                 845
Glu Thr Tyr Ile Ser Ala Pro Ile Leu Gly Trp Gly Phe Phe Ala Ser
    850                 855                 860
```

```
Thr Ser Tyr Thr Ile Ser Gly Asn Gly Ala Leu Thr Val Asn Val His
865                 870                 875                 880
Leu Lys Pro His Gly Pro Met Pro Ala Asp Leu Pro Arg Leu Gly Leu
                885                 890                 895
Asp Val Leu Leu Ala Asp Glu Leu Asp Asn Thr Ser Trp Phe Gly Leu
            900                 905                 910
Gly Pro Gly Glu Ala Tyr Pro Asp Lys Lys Arg Ala Gln Lys Val Gly
        915                 920                 925
Ile Tyr Asn Ala Ala Thr Ala Glu Leu His Thr Pro Tyr Glu Val Pro
    930                 935                 940
Gln Glu Gly Gly Asn Arg Met Asp Thr Arg Trp Leu Arg Val His Asp
945                 950                 955                 960
Ser Arg Gly Trp Gly Leu Arg Val Thr Arg Val Lys Asp Glu Ser Asp
                965                 970                 975
Lys Gln Pro Thr Glu Leu Phe Gln Trp Leu Ala Thr Arg Tyr Ser Pro
            980                 985                 990
Glu Ala Ile Glu Ala Ala Lys His Ala Pro Glu Leu Val Pro Glu Lys
        995                 1000                1005
Arg Ile Arg Leu Arg Leu Asp Val Glu Ser Cys Gly Val Gly Thr Gly
    1010                1015                1020
Ala Cys Gly Pro Arg Thr Leu Asp Lys Tyr Arg Val Lys Cys Glu Glu
1025                1030                1035                1040
Arg Lys Phe Gly Phe Thr Leu Gln Pro Val Leu Ala Glu Leu Cys
                1045                1050                1055
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<210> 720
<211> 1055
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-galactosidase, putative [Aspergillus
fumigatus Af293]
1055 aa protein EAL91164.1 GI:66850838

<400> 720

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

```
    130                 135                 140
Phe Asp Gly Val Asp Ser Ala Tyr His Val Trp Val Asn Gly Val Pro
145                 150                 155                 160
Ile Gly Tyr Ser Gln Gly Ser Arg Asn Pro Ala Glu Phe Asp Val Ser
                165                 170                 175
Gln Val Val Asp Arg Asp Gly Ala Asn Glu Leu Phe Val Arg Val Tyr
            180                 185                 190
Gln Trp Ser Asp Gly Ser Tyr Ile Glu Asp Gln Asp Gln Trp Trp Leu
        195                 200                 205
Ser Gly Ile Phe Arg Asp Val Thr Leu Leu Ala Phe Pro Gly Gln Ala
    210                 215                 220
Arg Ile Glu Asp Phe Phe Val Arg Thr Ala Leu Asp Lys Asp Tyr Val
225                 230                 235                 240
Asp Ala Thr Leu Arg Leu Ser Val Asp Leu Ala Leu Ala Thr Ala Ala
                245                 250                 255
Ile Val Gln Val Thr Leu Ser Asn Pro Ser Thr Gly Ser Thr Leu Gln
            260                 265                 270
Thr Glu Lys Tyr Ser Leu Gly Glu Lys Gln Asp Lys Leu Glu Ala Glu
        275                 280                 285
Leu Ser Val Ser Asn Pro Asn Lys Trp Thr Ala Glu Thr Pro Asn Leu
    290                 295                 300
Tyr Asn Leu Cys Ile Ala Leu Tyr Val Asp Gly Ala Lys Asp Pro Val
305                 310                 315                 320
Gln Thr Ile Asn His Arg Val Gly Phe Arg Gln Val Glu Ile Lys Asn
                325                 330                 335
Gly Asn Ile Thr Val Asn Gly Val Pro Val Met Phe Arg Gly Val Asn
            340                 345                 350
Arg His Asp His His Pro Arg Phe Gly Arg Ala Val Pro Leu Ser Phe
        355                 360                 365
Leu Arg Glu Asp Leu Leu Ile Met Lys Arg His Asn Val Asn Ala Leu
    370                 375                 380
Arg Cys Ser His Tyr Pro Ser His Pro Arg Leu Tyr Glu Leu Cys Asp
385                 390                 395                 400
Glu Leu Gly Leu Trp Val Met Asp Glu Ala Asp Leu Glu Cys His Gly
                405                 410                 415
Phe Tyr Asp Ala Ile Ala Arg Pro Leu Asp Ile Pro Glu Ser Met Asp
            420                 425                 430
Tyr Glu Glu Arg Lys Lys Leu Thr Phe Gly Gln Ala Ala Gln Phe Thr
        435                 440                 445
Thr Asn Asn Pro Glu Trp Lys Glu Ala Tyr Val Asp Arg Met Ala Gln
    450                 455                 460
Met Val Gln Arg Asp Lys Asn His Ser Cys Ile Val Ile Trp Ser Leu
465                 470                 475                 480
Gly Asn Glu Ala Phe Tyr Gly Ser Asn His Gln Ala Met Tyr Asp Tyr
                485                 490                 495
Val Lys Gln Val Asp Pro Ser Arg Pro Val His Tyr Glu Gly Asp Met
            500                 505                 510
Glu Ala Lys Thr Val Asp Met Tyr Ser Tyr Met Tyr Pro Ser Leu Glu
        515                 520                 525
Arg Leu Val Gly Phe Ala Thr Ala Glu Gly Asp Glu Phe Lys Lys Pro
    530                 535                 540
Ile Val Leu Cys Glu Tyr Ala His Ala Met Gly Asn Ala Pro Gly Gly
545                 550                 555                 560
Leu Glu Glu Tyr Met Glu Ala Phe Arg Thr His Arg Arg Leu Gln Gly
```

```
                565                 570                 575
Gly Trp Val Trp Glu Trp Ala Asn His Gly Leu Trp Asp Glu Lys Lys
            580                 585                 590
Gly Trp Tyr Gly Tyr Gly Gly Asp Phe Gly Asp Thr Pro His Asp Gly
        595                 600                 605
Asn Phe Val Leu Asp Gly Leu Leu Phe Ser Asp His Thr Pro Thr Pro
    610                 615                 620
Gly Ile Thr Glu Leu Lys Lys Ala Tyr Ala Pro Val Arg Val Trp Pro
625                 630                 635                 640
Gly Glu Asp Gly Thr Leu Val Val Ala Asn Asp Tyr Asn Phe Val Gly
                645                 650                 655
Leu Glu Gly Leu Gln Ala Ser Tyr Lys Ile Glu Val Leu Gly Asp Ser
            660                 665                 670
Gly Arg Ile Ile Ala Thr Gly Ile Ile Glu Leu Pro Pro Ile Pro Ala
        675                 680                 685
Gly Gln Asn Gly Thr Ile Lys Leu Pro Ser Ala Pro Ala Thr Ala Ile
    690                 695                 700
Pro Gly Glu Val Trp Leu Thr Ile Ser Phe Leu Gln Lys Gly Glu Thr
705                 710                 715                 720
Ala Trp Ala Gly Asn Asn Tyr Glu Val Ala Trp Tyr Gln Gln Cys Leu
                725                 730                 735
Lys Ser Ser Ser Pro Arg Phe Ser Leu Ala Val Pro Ala Glu Ala Leu
            740                 745                 750
Thr His Ser Ser Thr Lys Thr Ser His Arg Ile Ser Gly Ala Ser Phe
        755                 760                 765
Ser Leu Glu Phe Ser Arg Glu Thr Gly Ser Leu Tyr Ala Trp Thr Ala
    770                 775                 780
Gly Gly Leu Ser Leu Leu Asp Gln Ser Ser Ser Thr Gly Ala Ile Ser
785                 790                 795                 800
Pro Gly Phe Trp Arg Pro Pro Thr Asp Asn Asp Met Ser His Asp Leu
                805                 810                 815
Leu Glu Trp Arg Arg Phe Gly Leu Asp Thr Leu Thr Ser Gln Leu Arg
            820                 825                 830
Lys Met His Val Val Gln His Thr Pro Thr Ser Val Glu Val Thr Thr
        835                 840                 845
Glu Thr Tyr Ile Ser Ala Pro Ile Leu Gly Trp Gly Phe Phe Ala Ser
    850                 855                 860
Thr Ser Tyr Thr Ile Ser Gly Asn Gly Ala Leu Thr Val Asn Val His
865                 870                 875                 880
Leu Lys Pro His Gly Pro Met Pro Ala Asp Leu Pro Arg Leu Gly Leu
                885                 890                 895
Asp Val Leu Leu Ala Asp Glu Leu Asp Asn Thr Ser Trp Phe Gly Leu
            900                 905                 910
Gly Pro Gly Glu Ala Tyr Pro Asp Lys Lys Arg Ala Gln Lys Val Gly
        915                 920                 925
Ile Tyr Asn Ala Ala Thr Ala Glu Leu His Thr Pro Tyr Glu Val Pro
    930                 935                 940
Gln Glu Gly Gly Asn Arg Met Asp Thr Arg Trp Leu Arg Val His Asp
945                 950                 955                 960
Ser Arg Gly Trp Gly Leu Arg Val Thr Arg Val Lys Asp Glu Ser Asp
                965                 970                 975
Lys Gln Pro Thr Glu Leu Phe Gln Trp Leu Ala Thr Arg Tyr Ser Pro
            980                 985                 990
Glu Ala Ile Glu Ala Ala Lys His Ala Pro Glu Leu Val Pro Glu Lys
```

```
        995                 1000                1005
Arg Ile Arg Leu Arg Leu Asp Val Glu Ser Cys Gly Val Gly Thr Gly
    1010                1015                1020
Ala Cys Gly Pro Arg Thr Leu Asp Lys Tyr Arg Val Lys Cys Glu Glu
1025                1030                1035                1040
Arg Lys Phe Gly Phe Thr Leu Gln Pro Val Leu Ala Glu Leu Cys
                1045                1050                1055


<210> 721
<211> 1005
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-galactosidase [Aspergillus candidus] 1005 aa
      protein CAD24293.1 GI:18958133

<400> 721
Met Lys Leu Leu Ser Val Ala Ala Val Ala Leu Leu Ala Ala Gln Ala
 1               5                  10                  15
Ala Gly Ala Ser Ile Lys His Arg Leu Asn Gly Phe Thr Ile Leu Glu
            20                  25                  30
His Pro Asp Pro Ala Lys Arg Asp Leu Leu Gln Asp Ile Val Thr Trp
        35                  40                  45
Asp Asp Lys Ser Leu Phe Ile Asn Gly Glu Arg Ile Met Leu Phe Ser
    50                  55                  60
Gly Glu Val His Pro Phe Arg Leu Pro Val Pro Ser Leu Trp Leu Asp
65                  70                  75                  80
Ile Phe His Lys Ile Arg Ala Leu Gly Phe Asn Cys Val Ser Phe Tyr
                85                  90                  95
Ile Asp Trp Ala Leu Leu Glu Gly Lys Pro Gly Asp Tyr Arg Ala Glu
            100                 105                 110
Gly Ile Phe Ala Leu Glu Pro Phe Phe Asp Ala Ala Lys Glu Ala Gly
        115                 120                 125
Ile Tyr Leu Ile Ala Arg Pro Gly Ser Tyr Ile Asn Ala Glu Val Ser
    130                 135                 140
Gly Gly Gly Phe Pro Gly Trp Leu Gln Arg Val Asn Gly Thr Leu Arg
145                 150                 155                 160
Ser Ser Asp Glu Pro Phe Leu Lys Ala Thr Asp Asn Tyr Ile Ala Asn
                165                 170                 175
Ala Ala Ala Ala Val Ala Lys Ala Gln Ile Thr Asn Gly Gly Pro Val
            180                 185                 190
Ile Leu Tyr Gln Pro Glu Asn Glu Tyr Ser Gly Gly Cys Cys Gly Val
        195                 200                 205
Lys Tyr Pro Asp Ala Asp Tyr Met Gln Tyr Val Met Asp Gln Ala Arg
    210                 215                 220
Lys Ala Asp Ile Val Val Pro Phe Ile Ser Asn Asp Ala Ser Pro Ser
225                 230                 235                 240
Gly His Asn Ala Pro Gly Ser Gly Thr Gly Ala Val Asp Ile Tyr Gly
                245                 250                 255
His Asp Ser Tyr Pro Leu Gly Phe Asp Cys Ala Asn Pro Ser Val Trp
            260                 265                 270
Pro Glu Gly Lys Leu Pro Asp Asn Phe Arg Thr Leu His Leu Glu Gln
```

```
        275                 280                 285
Ser Pro Ser Thr Pro Tyr Ser Leu Leu Glu Phe Gln Ala Gly Ala Phe
    290                 295                 300
Asp Pro Trp Gly Gly Pro Gly Phe Glu Lys Cys Tyr Ala Leu Val Asn
305                 310                 315                 320
His Glu Phe Ser Arg Val Phe Tyr Arg Asn Asp Leu Ser Phe Gly Val
                325                 330                 335
Ser Thr Phe Asn Leu Tyr Met Thr Phe Gly Gly Thr Asn Trp Gly Asn
            340                 345                 350
Leu Gly His Pro Gly Gly Tyr Thr Ser Tyr Asp Tyr Gly Ser Pro Ile
        355                 360                 365
Thr Glu Thr Arg Asn Val Thr Arg Glu Lys Tyr Ser Asp Ile Lys Leu
    370                 375                 380
Leu Ala Asn Phe Val Lys Ala Ser Pro Ser Tyr Leu Thr Ala Thr Pro
385                 390                 395                 400
Arg Asn Leu Thr Thr Gly Val Tyr Thr Asp Thr Ser Asp Leu Ala Val
                405                 410                 415
Thr Pro Leu Met Gly Asp Ser Pro Gly Ser Phe Phe Val Val Arg His
            420                 425                 430
Thr Asp Tyr Ser Ser Gln Glu Ser Thr Ser Tyr Lys Leu Lys Leu Pro
        435                 440                 445
Thr Ser Ala Gly Asn Leu Thr Ile Pro Gln Leu Glu Gly Thr Leu Ser
    450                 455                 460
Leu Asn Gly Arg Asp Ser Lys Ile His Val Val Asp Tyr Asn Val Ser
465                 470                 475                 480
Gly Thr Asn Ile Ile Tyr Ser Thr Ala Glu Val Phe Thr Trp Lys Lys
                485                 490                 495
Phe Asp Gly Asn Lys Val Leu Val Leu Tyr Gly Gly Pro Lys Glu His
            500                 505                 510
His Glu Leu Ala Ile Ala Ser Lys Ser Asn Val Thr Ile Ile Glu Gly
        515                 520                 525
Ser Asp Ser Gly Ile Val Ser Thr Arg Lys Gly Ser Ser Val Ile Ile
    530                 535                 540
Gly Trp Asp Val Ser Ser Thr Arg Arg Ile Val Gln Val Gly Asp Leu
545                 550                 555                 560
Arg Val Phe Leu Leu Asp Arg Asn Ser Ala Tyr Asn Tyr Trp Val Pro
                565                 570                 575
Glu Leu Pro Thr Glu Gly Thr Ser Pro Gly Phe Ser Thr Ser Lys Thr
            580                 585                 590
Thr Ala Ser Ser Ile Ile Val Lys Ala Gly Tyr Leu Leu Arg Gly Ala
        595                 600                 605
His Leu Asp Gly Ala Asp Leu His Leu Thr Ala Asp Phe Asn Ala Thr
    610                 615                 620
Thr Pro Ile Glu Val Ile Gly Ala Pro Thr Gly Ala Lys Asn Leu Phe
625                 630                 635                 640
Val Asn Gly Glu Lys Ala Ser His Thr Val Asp Lys Asn Gly Ile Trp
                645                 650                 655
Ser Ser Glu Val Lys Tyr Ala Ala Pro Glu Ile Lys Leu Pro Gly Leu
            660                 665                 670
Lys Asp Leu Asp Trp Lys Tyr Leu Asp Thr Leu Pro Glu Ile Lys Ser
        675                 680                 685
Ser Tyr Asp Asp Ser Ala Trp Val Ser Ala Asp Leu Pro Lys Thr Lys
    690                 695                 700
Asn Thr His Arg Pro Leu Asp Thr Pro Thr Ser Leu Tyr Ser Ser Asp
```

```
705                 710                 715                 720
Tyr Gly Phe His Thr Gly Tyr Leu Ile Tyr Arg Gly His Phe Val Ala
                725                 730                 735
Asn Gly Lys Glu Ser Glu Phe Phe Ile Arg Thr Gln Gly Gly Ser Ala
            740                 745                 750
Phe Gly Ser Ser Val Trp Leu Asn Glu Thr Tyr Leu Gly Ser Trp Thr
        755                 760                 765
Gly Ala Asp Tyr Ala Met Asp Gly Asn Ser Thr Tyr Lys Leu Ser Gln
    770                 775                 780
Leu Glu Ser Gly Lys Asn Tyr Val Ile Thr Val Val Ile Asp Asn Leu
785                 790                 795                 800
Gly Leu Asp Glu Asn Trp Thr Val Gly Glu Glu Thr Met Lys Asn Pro
                805                 810                 815
Arg Gly Ile Leu Ser Tyr Lys Leu Ser Gly Gln Asp Ala Ser Ala Ile
            820                 825                 830
Thr Trp Lys Leu Thr Gly Asn Leu Gly Gly Glu Asp Tyr Gln Asp Lys
        835                 840                 845
Val Arg Gly Pro Leu Asn Glu Gly Gly Leu Tyr Ala Glu Arg Gln Gly
    850                 855                 860
Phe His Gln Pro Gln Pro Pro Ser Glu Ser Trp Glu Ser Gly Ser Pro
865                 870                 875                 880
Leu Glu Gly Leu Ser Lys Pro Gly Ile Gly Phe Tyr Thr Ala Gln Phe
                885                 890                 895
Asp Leu Asp Leu Pro Lys Gly Trp Asp Val Pro Leu Tyr Phe Asn Phe
            900                 905                 910
Gly Asn Asn Thr Gln Ala Ala Arg Ala Gln Leu Tyr Val Asn Gly Tyr
        915                 920                 925
Gln Tyr Gly Lys Phe Thr Gly Asn Val Gly Pro Gln Thr Ser Phe Pro
    930                 935                 940
Val Pro Glu Gly Ile Leu Asn Tyr Arg Gly Thr Asn Tyr Val Ala Leu
945                 950                 955                 960
Ser Leu Trp Ala Leu Glu Ser Asp Gly Ala Lys Leu Gly Ser Phe Glu
                965                 970                 975
Leu Ser Tyr Thr Thr Pro Val Leu Thr Gly Tyr Gly Asp Val Glu Ser
            980                 985                 990
Pro Glu Gln Pro Lys Tyr Glu Gln Arg Lys Gly Ala Tyr
        995                 1000                1005
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<210> 722
<211> 1006
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Beta-galactosidase; AltName:
Full=Lactase-N; Short=Lactase; AltName:
INN=Tilactase; Flags: Precursor 1006 aa protein
P29853.2 GI:461623

<400> 722

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Met Lys Leu Ser Ser Ala Cys Ala Ile Ala Leu Leu Ala Ala Gln Ala
 1               5                  10                  15
Ala Gly Ala Ser Ile Lys His Arg Ile Asn Gly Phe Thr Leu Thr Glu
```

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

```
    450                 455                 460
Leu Asn Gly Arg Asp Ser Lys Ile His Val Thr Asp His Asn Val Ser
465                 470                 475                 480
Gly Thr Asn Ile Ile Tyr Ser Thr Ala Glu Val Phe Thr Trp Lys Lys
                485                 490                 495
Phe Ala Asp Gly Lys Val Leu Val Leu Tyr Gly Gly Ala Gly Glu His
            500                 505                 510
His Glu Leu Ala Ile Ser Thr Lys Ser Asn Val Thr Val Ile Glu Gly
        515                 520                 525
Ser Glu Ser Gly Ile Ser Ser Lys Gln Thr Ser Ser Ser Val Val Val
    530                 535                 540
Gly Trp Asp Val Ser Thr Thr Arg Arg Ile Ile Gln Val Gly Asp Leu
545                 550                 555                 560
Lys Ile Leu Leu Leu Asp Arg Asn Ser Ala Tyr Asn Tyr Trp Val Pro
                565                 570                 575
Gln Leu Ala Thr Asp Gly Thr Ser Pro Gly Phe Ser Thr Pro Glu Lys
            580                 585                 590
Val Ala Ser Ser Ile Ile Val Lys Ala Gly Tyr Leu Val Arg Thr Ala
        595                 600                 605
Tyr Leu Lys Gly Ser Gly Leu Tyr Leu Thr Ala Asp Phe Asn Ala Thr
    610                 615                 620
Thr Ser Val Glu Val Ile Gly Val Pro Ser Thr Ala Lys Asn Leu Phe
625                 630                 635                 640
Ile Asn Gly Asp Lys Thr Ser His Thr Val Asp Lys Asn Gly Ile Trp
                645                 650                 655
Ser Ala Thr Val Asp Tyr Asn Ala Pro Asp Ile Ser Leu Pro Ser Leu
            660                 665                 670
Lys Asp Leu Asp Trp Lys Tyr Val Asp Thr Leu Pro Glu Ile Gln Ser
        675                 680                 685
Ser Tyr Asp Asp Ser Leu Trp Pro Ala Ala Asp Leu Lys Gln Thr Lys
    690                 695                 700
Asn Thr Leu Arg Ser Leu Thr Thr Pro Thr Ser Leu Tyr Ser Ser Asp
705                 710                 715                 720
Tyr Gly Phe His Thr Gly Tyr Leu Leu Tyr Arg Gly His Phe Thr Ala
                725                 730                 735
Thr Gly Asn Glu Ser Thr Phe Ala Ile Asp Thr Gln Gly Gly Ser Ala
            740                 745                 750
Phe Gly Ser Ser Val Trp Leu Asn Gly Thr Tyr Leu Gly Ser Trp Thr
        755                 760                 765
Gly Leu Tyr Ala Asn Ser Asp Tyr Asn Ala Thr Tyr Asn Leu Pro Gln
    770                 775                 780
Leu Gln Ala Gly Lys Thr Tyr Val Ile Thr Val Val Ile Asp Asn Met
785                 790                 795                 800
Gly Leu Glu Glu Asn Trp Thr Val Gly Glu Asp Leu Met Lys Ser Pro
                805                 810                 815
Arg Gly Ile Ser Thr Ser Cys Leu Pro Asp Gly Gln Ala Ala Pro Ile
            820                 825                 830
Ser Trp Lys Leu Thr Gly Asn Leu Gly Gly Glu Asp Tyr Glu Asp Lys
        835                 840                 845
Val Arg Gly Pro Leu Asn Glu Gly Gly Leu Tyr Ala Glu Arg Gln Gly
    850                 855                 860
Phe His Gln Pro Glu Pro Pro Ser Gln Asn Trp Lys Ser Ser Ser Pro
865                 870                 875                 880
Leu Glu Gly Leu Ser Glu Ala Gly Ile Gly Phe Tyr Ser Ala Ser Phe
```

```
                885                 890                 895
Asp Leu Asp Leu Pro Lys Asp Gly Met Ser His Cys Ser Ser Thr Ser
            900                 905                 910
Val Thr Ala Leu Arg His Pro Arg Thr Ala Cys Arg Ser Thr Ser Thr
        915                 920                 925
Asp Ile Val Cys Glu Ile His Lys Gln His Arg Thr Ser Asp Gln Leu
    930                 935                 940
Pro Cys Pro Arg Gly Asn Pro Glu Leu Ser Arg Asn Glu Leu Val Gly
945                 950                 955                 960
Gly Asp Pro Val Ala Leu Asp Ser Ala Gly Gly Lys Leu Glu Ser Leu
                965                 970                 975
Glu Leu Ser Tyr Thr Thr Pro Val Leu Thr Ala Leu Gly Glu Val Glu
            980                 985                 990
Ser Val Asp Gln Pro Lys Tyr Lys Lys Arg Lys Gly Ala Tyr
        995                 1000                1005


<210> 723
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Alpha-glucosidase P1 subunit, ANP P1 subunit
      Aspergillus niger, Peptide, 227 aa AAB2358.1
      GI:257186 (transglucosidase)

<220>
<221> VARIANT
<222> 11, 99, 118, 193
<223> Xaa = Any Amino Acid

<400> 723
Ser Leu Leu Ala Pro Ser Gln Pro Gln Phe Xaa Ile Pro Ala Ser Ala
 1               5                  10                  15
Ala Val Gly Ala Gln Leu Ile Ala Asn Ile Asp Asp Pro Gln Ala Ala
            20                  25                  30
Asp Ala Gln Ser Val Cys Pro Gly Tyr Lys Ala Ser Lys Val Gln His
        35                  40                  45
Asn Ser Arg Gly Phe Thr Ala Ser Leu Gln Leu Ala Gly Arg Pro Cys
    50                  55                  60
Asn Val Tyr Gly Thr Asp Val Glu Ser Leu Thr Leu Ser Val Glu Tyr
65                  70                  75                  80
Gln Asp Ser Asp Arg Leu Asn Ile Gln Ile Leu Pro Thr His Val Asp
                85                  90                  95
Ser Thr Xaa Ala Ser Trp Tyr Phe Leu Ser Glu Asn Leu Val Pro Arg
            100                 105                 110
Pro Lys Ala Ser Leu Xaa Ala Ser Val Ser Gln Ser Asp Leu Phe Val
        115                 120                 125
Ser Trp Ser Asn Glu Pro Ser Phe Asn Phe Lys Val Ile Arg Lys Ala
    130                 135                 140
Thr Gly Asp Ala Leu Phe Ser Thr Glu Gly Thr Val Leu Val Tyr Glu
145                 150                 155                 160
Asn Gln Phe Ile Glu Phe Val Thr Ala Leu Pro Glu Glu Tyr Asn Leu
```

```
                165                 170                 175
Tyr Gly Leu Gly Glu His Ile Thr Gln Phe Arg Leu Gln Arg Asn Ala
            180                 185                 190
Xaa Leu Thr Ile Tyr Pro Ser Asp Asp Gly Thr Pro Ile Asp Gln Asn
        195                 200                 205
Leu Tyr Gly Gln His Pro Phe Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly
    210                 215                 220
Asp Arg Gln
225
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<210> 724
<211> 834
<212> PRT
<213> Artificial Sequence

<220>
<223> Celluclast hypothetical protein M419DRAFT_125268
[Trichoderma reesei RUT C-3] 834 aa protein
ETR97394.1 GI:57227381

<400> 724

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

```
Phe Asn Val Ser Asn Gly Lys Pro Phe Ile His Val Ile Asp Gln Arg
            260                 265                 270
Ala Arg Glu Val Leu Gln Phe Val Lys Lys Cys Ala Ala Ser Gly Val
        275                 280                 285
Thr Glu Asn Gly Pro Glu Thr Thr Val Asn Asn Thr Pro Glu Thr Ala
    290                 295                 300
Ala Leu Leu Arg Lys Val Gly Asn Glu Gly Ile Val Leu Leu Lys Asn
305                 310                 315                 320
Glu Asn Asn Val Leu Pro Leu Ser Lys Lys Lys Lys Thr Leu Ile Val
                325                 330                 335
Gly Pro Asn Ala Lys Gln Ala Thr Tyr His Gly Gly Gly Ser Ala Ala
            340                 345                 350
Leu Arg Ala Tyr Tyr Ala Val Thr Pro Phe Asp Gly Leu Ser Lys Gln
        355                 360                 365
Leu Glu Thr Pro Pro Ser Tyr Thr Val Gly Ala Tyr Thr His Arg Phe
    370                 375                 380
Leu Pro Ile Leu Gly Glu Gln Cys Leu Thr Pro Asp Gly Ala Pro Gly
385                 390                 395                 400
Met Arg Trp Arg Val Phe Asn Glu Pro Pro Gly Thr Pro Asn Arg Gln
                405                 410                 415
His Ile Asp Glu Leu Phe Phe Thr Lys Thr Asp Met His Leu Val Asp
            420                 425                 430
Tyr Tyr His Pro Lys Ala Ala Asp Thr Trp Tyr Ala Asp Met Glu Gly
        435                 440                 445
Thr Tyr Thr Ala Asp Glu Asp Cys Thr Tyr Glu Leu Gly Leu Val Val
    450                 455                 460
Cys Gly Thr Ala Lys Ala Tyr Val Asp Asp Gln Leu Val Val Asp Asn
465                 470                 475                 480
Ala Thr Lys Gln Val Pro Gly Asp Ala Phe Phe Gly Ser Ala Thr Arg
                485                 490                 495
Glu Glu Thr Gly Arg Ile Asn Leu Val Lys Gly Asn Thr Tyr Lys Phe
            500                 505                 510
Lys Ile Glu Phe Gly Ser Ala Pro Thr Tyr Thr Leu Lys Gly Asp Thr
        515                 520                 525
Ile Val Pro Gly His Gly Ser Leu Arg Val Gly Gly Cys Lys Val Ile
    530                 535                 540
Asp Asp Gln Ala Glu Ile Glu Lys Ser Val Ala Leu Ala Lys Glu His
545                 550                 555                 560
Asp Gln Val Ile Ile Cys Ala Gly Leu Asn Ala Asp Trp Glu Thr Glu
                565                 570                 575
Gly Ala Asp Arg Ala Ser Met Lys Leu Pro Gly Val Leu Asp Gln Leu
            580                 585                 590
Ile Ala Asp Val Ala Ala Ala Asn Pro Asn Thr Val Val Val Met Gln
        595                 600                 605
Thr Gly Thr Pro Glu Glu Met Pro Trp Leu Asp Ala Thr Pro Ala Val
    610                 615                 620
Ile Gln Ala Trp Tyr Gly Gly Asn Glu Thr Gly Asn Ser Ile Ala Asp
625                 630                 635                 640
Val Val Phe Gly Asp Tyr Asn Pro Ser Gly Lys Leu Ser Leu Ser Phe
                645                 650                 655
Pro Lys Arg Leu Gln Asp Asn Pro Ala Phe Leu Asn Phe Arg Thr Glu
            660                 665                 670
Ala Gly Arg Thr Leu Tyr Gly Glu Asp Val Tyr Val Gly Tyr Arg Tyr
        675                 680                 685
```

```
Tyr Glu Phe Ala Asp Lys Asp Val Asn Phe Pro Phe Gly His Gly Leu
    690                 695                 700
Ser Tyr Thr Thr Phe Ala Phe Ser Asn Leu Ser Val Ser His Lys Asp
705                 710                 715                 720
Gly Lys Leu Ser Val Ser Leu Ser Val Lys Asn Thr Gly Ser Val Pro
                725                 730                 735
Gly Ala Gln Val Ala Gln Leu Tyr Val Lys Pro Leu Gln Ala Ala Lys
            740                 745                 750
Ile Asn Arg Pro Val Lys Glu Leu Lys Gly Phe Ala Lys Val Glu Leu
        755                 760                 765
Gln Pro Gly Glu Thr Lys Ala Val Thr Ile Glu Glu Gln Glu Lys Tyr
    770                 775                 780
Val Ala Ala Tyr Phe Asp Glu Glu Arg Asp Gln Trp Cys Val Glu Lys
785                 790                 795                 800
Gly Asp Tyr Glu Val Ile Val Ser Asp Ser Ser Ala Ala Lys Asp Gly
                805                 810                 815
Val Ala Leu Arg Gly Lys Phe Thr Val Gly Glu Thr Tyr Trp Trp Ser
            820                 825                 830
Gly Val
```

<210> 725
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Velvet complex subunit 2 49 aa
protein GRS98.2 GI:1881915

<400> 725

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

```
Pro Arg Arg Ala Arg Met Cys Gly Phe Gly Asp Lys Asp Arg Arg Pro
            180                 185                 190
Ile Thr Pro Pro Pro Cys Val Arg Leu Ile Ile Ile Asp Val Ala Thr
        195                 200                 205
Gly Lys Glu Ile Asp Cys Asn Asp Ile Asp His Ser Met Phe Val Leu
    210                 215                 220
Asn Val Asp Leu Trp Asn Glu Asp Gly Thr Arg Glu Val Asn Leu Val
225                 230                 235                 240
Arg Ser Ser Thr Ser Ser Ser Pro Ser Val Ser Ser Thr Val Thr Tyr
                245                 250                 255
Pro Tyr Gly Ser Ile Ser Val Gly Glu Ser Ser His Thr Tyr Gly Gln
            260                 265                 270
Ser Ala His Pro Pro Ser Arg Glu Ala Pro Tyr Ser Val Ser Gln Thr
        275                 280                 285
Ala Ser Tyr Ala Pro Glu Tyr Gln Thr Gln Pro Thr Tyr Ser Gln Gly
    290                 295                 300
Ser Ser Ala Tyr Pro Ser Asn Gly Thr Tyr Gly Pro Pro Gln Gln Tyr
305                 310                 315                 320
Phe Pro Gln His Gln Ala Tyr Arg Thr Glu Thr Gly Pro Pro Gly Ala
                325                 330                 335
Met Gln Thr Thr Val Gly Gly Phe Arg Gly Tyr Ala Gln Asp Gln Asn
            340                 345                 350
Ala Leu Thr Lys Met Ala Val Val Gly Gly Gln Pro Gln Gly Met Phe
        355                 360                 365
Thr Arg Asn Leu Ile Gly Ser Leu Ala Ala Ser Ala Phe Arg Leu Ala
    370                 375                 380
Asp Thr Ser Glu His Leu Gly Ile Trp Phe Val Leu Gln Asp Leu Ser
385                 390                 395                 400
Val Arg Thr Glu Gly Pro Phe Arg Leu Arg Phe Ser Phe Val Asn Val
                405                 410                 415
Gly Pro Leu Ala Gly Gln Asn Gly Ala Lys Val Asn Thr Gly Arg Ala
            420                 425                 430
Pro Ile Leu Ala Ser Cys Phe Ser Glu Val Phe Asn Val Tyr Ser Ala
        435                 440                 445
Lys Lys Phe Pro Gly Val Cys Glu Ser Thr Pro Leu Ser Lys Thr Phe
    450                 455                 460
Ala Ala Gln Gly Ile Lys Ile Pro Ile Arg Lys Asp Ala Asn Leu Lys
465                 470                 475                 480
Gly Gly Asp Gly Glu Asp Asp Tyr Gly Asp
                485                 490
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<210> 726
<211> 500
<212> PRT
<213> Artificial Sequence

<220>
<223> alpha-L-arabinofuranosidase [Trichoderma reesei] 5
aa protein CAA93243.1 GI:158814

<400> 726

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Met Leu Ser Asn Ala Arg Ile Ile Ala Ala Gly Cys Ile Ala Ala Gly
 1               5                  10                  15
```

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

```
Gln Gly Ser Ser Ile Arg Ser Trp Ser Tyr Pro Thr Arg Tyr Phe Arg
    450                 455                 460
His Tyr Asn Asn Thr Leu Tyr Ile Ala Ser Asn Gly Gly Val His Val
465                 470                 475                 480
Phe Asp Ala Thr Ala Ala Phe Asn Asp Asp Val Ser Phe Val Val Ser
                485                 490                 495
Gly Gly Phe Ala
            500
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<210> 727
<211> 797
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-xylosidase [Trichoderma reesei] 797 aa
protein
CAA93248.1 GI:2791278

<400> 727

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

```
            260                 265                 270
Leu Met Cys Ala Tyr Asn Ser Val Asn Gly Val Pro Ser Cys Ala Asn
        275                 280                 285
Ser Phe Phe Leu Gln Thr Leu Leu Arg Glu Ser Trp Gly Phe Pro Glu
    290                 295                 300
Trp Gly Tyr Val Ser Ser Asp Cys Asp Ala Val Tyr Asn Val Phe Asn
305                 310                 315                 320
Pro His Asp Tyr Ala Ser Asn Gln Ser Ser Ala Ala Ala Ser Ser Leu
                325                 330                 335
Arg Ala Gly Thr Asp Ile Asp Cys Gly Gln Thr Tyr Pro Trp His Leu
            340                 345                 350
Asn Glu Ser Phe Val Ala Gly Glu Val Ser Arg Gly Glu Ile Glu Arg
        355                 360                 365
Ser Val Thr Arg Leu Tyr Ala Asn Leu Val Arg Leu Gly Tyr Phe Asp
    370                 375                 380
Lys Lys Asn Gln Tyr Arg Ser Leu Gly Trp Lys Asp Val Val Lys Thr
385                 390                 395                 400
Asp Ala Trp Asn Ile Ser Tyr Glu Ala Ala Val Glu Gly Ile Val Leu
                405                 410                 415
Leu Lys Asn Asp Gly Thr Leu Pro Leu Ser Lys Lys Val Arg Ser Ile
            420                 425                 430
Ala Leu Ile Gly Pro Trp Ala Asn Ala Thr Thr Gln Met Gln Gly Asn
        435                 440                 445
Tyr Tyr Gly Pro Ala Pro Tyr Leu Ile Ser Pro Leu Glu Ala Ala Lys
    450                 455                 460
Lys Ala Gly Tyr His Val Asn Phe Glu Leu Gly Thr Glu Ile Ala Gly
465                 470                 475                 480
Asn Ser Thr Thr Gly Phe Ala Lys Ala Ile Ala Ala Ala Lys Lys Ser
                485                 490                 495
Asp Ala Ile Ile Tyr Leu Gly Gly Ile Asp Asn Thr Ile Glu Gln Glu
            500                 505                 510
Gly Ala Asp Arg Thr Asp Ile Ala Trp Pro Gly Asn Gln Leu Asp Leu
        515                 520                 525
Ile Lys Gln Leu Ser Glu Val Gly Lys Pro Leu Val Val Leu Gln Met
    530                 535                 540
Gly Gly Gly Gln Val Asp Ser Ser Ser Leu Lys Ser Asn Lys Lys Val
545                 550                 555                 560
Asn Ser Leu Val Trp Gly Gly Tyr Pro Gly Gln Ser Gly Gly Val Ala
                565                 570                 575
Leu Phe Asp Ile Leu Ser Gly Lys Arg Ala Pro Ala Gly Arg Leu Val
            580                 585                 590
Thr Thr Gln Tyr Pro Ala Glu Tyr Val His Gln Phe Pro Gln Asn Asp
        595                 600                 605
Met Asn Leu Arg Pro Asp Gly Lys Ser Asn Pro Gly Gln Thr Tyr Ile
    610                 615                 620
Trp Tyr Thr Gly Lys Pro Val Tyr Glu Phe Gly Ser Gly Leu Phe Tyr
625                 630                 635                 640
Thr Thr Phe Lys Glu Thr Leu Ala Ser His Pro Lys Ser Leu Lys Phe
                645                 650                 655
Asn Thr Ser Ser Ile Leu Ser Ala Pro His Pro Gly Tyr Thr Tyr Ser
            660                 665                 670
Glu Gln Ile Pro Val Phe Thr Phe Glu Ala Asn Ile Lys Asn Ser Gly
        675                 680                 685
Lys Thr Glu Ser Pro Tyr Thr Ala Met Leu Phe Val Arg Thr Ser Asn
```

```
    690                 695                 700
Ala Gly Pro Ala Pro Tyr Pro Asn Lys Trp Leu Val Gly Phe Asp Arg
705                 710                 715                 720
Leu Ala Asp Ile Lys Pro Gly His Ser Ser Lys Leu Ser Ile Pro Ile
                725                 730                 735
Pro Val Ser Ala Leu Ala Arg Val Asp Ser His Gly Asn Arg Ile Val
            740                 745                 750
Tyr Pro Gly Lys Tyr Glu Leu Ala Leu Asn Thr Asp Glu Ser Val Lys
        755                 760                 765
Leu Glu Phe Glu Leu Val Gly Glu Glu Val Thr Ile Glu Asn Trp Pro
    770                 775                 780
Leu Glu Glu Gln Gln Ile Lys Asp Ala Thr Pro Asp Ala
785                 790                 795


<210> 728
<211> 797
<212> PRT
<213> Artificial Sequence

<220>
<223> unnamed protein product [Trichoderma reesei] 797
      aa protein CAW52645.1 GI:219752323

<400> 728
Met Val Asn Asn Ala Ala Leu Leu Ala Ala Leu Ser Ala Leu Leu Pro
 1               5                  10                  15
Thr Ala Leu Ala Gln Asn Asn Gln Thr Tyr Ala Asn Tyr Ser Ala Gln
            20                  25                  30
Gly Gln Pro Asp Leu Tyr Pro Glu Thr Leu Ala Thr Leu Thr Leu Ser
        35                  40                  45
Phe Pro Asp Cys Glu His Gly Pro Leu Lys Asn Asn Leu Val Cys Asp
    50                  55                  60
Ser Ser Ala Gly Tyr Val Glu Arg Ala Gln Ala Leu Ile Ser Leu Phe
65                  70                  75                  80
Thr Leu Glu Glu Leu Ile Leu Asn Thr Gln Asn Ser Gly Pro Gly Val
                85                  90                  95
Pro Arg Leu Gly Leu Pro Asn Tyr Gln Val Trp Asn Glu Ala Leu His
            100                 105                 110
Gly Leu Asp Arg Ala Asn Phe Ala Thr Lys Gly Gly Gln Phe Glu Trp
        115                 120                 125
Ala Thr Ser Phe Pro Met Pro Ile Leu Thr Thr Ala Ala Leu Asn Arg
    130                 135                 140
Thr Leu Ile His Gln Ile Ala Asp Ile Ile Ser Thr Gln Ala Arg Ala
145                 150                 155                 160
Phe Ser Asn Ser Gly Arg Tyr Gly Leu Asp Val Tyr Ala Pro Asn Val
                165                 170                 175
Asn Gly Phe Arg Ser Pro Leu Trp Gly Arg Gly Gln Glu Thr Pro Gly
            180                 185                 190
Glu Asp Ala Phe Phe Leu Ser Ser Ala Tyr Thr Tyr Glu Tyr Ile Thr
        195                 200                 205
Gly Ile Gln Gly Gly Val Asp Pro Glu His Leu Lys Val Ala Ala Thr
    210                 215                 220
Val Lys His Phe Ala Gly Tyr Asp Leu Glu Asn Trp Asn Asn Gln Ser
```

```
225                 230                 235                 240
Arg Leu Gly Phe Asp Ala Ile Ile Thr Gln Gln Asp Leu Ser Glu Tyr
                245                 250                 255
Tyr Thr Pro Gln Phe Leu Ala Ala Ala Arg Tyr Ala Lys Ser Arg Ser
            260                 265                 270
Leu Met Cys Ala Tyr Asn Ser Val Asn Gly Val Pro Ser Cys Ala Asn
        275                 280                 285
Ser Phe Phe Leu Gln Thr Leu Leu Arg Glu Ser Trp Gly Phe Pro Glu
    290                 295                 300
Trp Gly Tyr Val Ser Ser Asp Cys Asp Ala Val Tyr Asn Val Phe Asn
305                 310                 315                 320
Pro His Asp Tyr Ala Ser Asn Gln Ser Ser Ala Ala Ala Ser Ser Leu
                325                 330                 335
Arg Ala Gly Thr Asp Ile Asp Cys Gly Gln Thr Tyr Pro Trp His Leu
            340                 345                 350
Asn Glu Ser Phe Val Ala Gly Glu Val Ser Arg Gly Glu Ile Glu Arg
        355                 360                 365
Ser Val Thr Arg Leu Tyr Ala Asn Leu Val Arg Leu Gly Tyr Phe Asp
    370                 375                 380
Lys Lys Asn Gln Tyr Arg Ser Leu Gly Trp Lys Asp Val Val Lys Thr
385                 390                 395                 400
Asp Ala Trp Asn Ile Ser Tyr Glu Ala Ala Val Glu Gly Ile Val Leu
                405                 410                 415
Leu Lys Asn Asp Gly Thr Leu Pro Leu Ser Lys Lys Val Arg Ser Ile
            420                 425                 430
Ala Leu Ile Gly Pro Trp Ala Asn Ala Thr Thr Gln Met Gln Gly Asn
        435                 440                 445
Tyr Tyr Gly Pro Ala Pro Tyr Leu Ile Ser Pro Leu Glu Ala Ala Lys
    450                 455                 460
Lys Ala Gly Tyr His Val Asn Phe Glu Leu Gly Thr Glu Ile Ala Gly
465                 470                 475                 480
Asn Ser Thr Thr Gly Phe Ala Lys Ala Ile Ala Ala Ala Lys Lys Ser
                485                 490                 495
Asp Ala Ile Ile Tyr Leu Gly Gly Ile Asp Asn Thr Ile Glu Gln Glu
            500                 505                 510
Gly Ala Asp Arg Thr Asp Ile Ala Trp Pro Gly Asn Gln Leu Asp Leu
        515                 520                 525
Ile Lys Gln Leu Ser Glu Val Gly Lys Pro Leu Val Val Leu Gln Met
    530                 535                 540
Gly Gly Gly Gln Val Asp Ser Ser Ser Leu Lys Ser Asn Lys Lys Val
545                 550                 555                 560
Asn Ser Leu Val Trp Gly Gly Tyr Pro Gly Gln Ser Gly Gly Val Ala
                565                 570                 575
Leu Phe Asp Ile Leu Ser Gly Lys Arg Ala Pro Ala Gly Arg Leu Val
            580                 585                 590
Thr Thr Gln Tyr Pro Ala Glu Tyr Val His Gln Phe Pro Gln Asn Asp
        595                 600                 605
Met Asn Leu Arg Pro Asp Gly Lys Ser Asn Pro Gly Gln Thr Tyr Ile
    610                 615                 620
Trp Tyr Thr Gly Lys Pro Val Tyr Glu Phe Gly Ser Gly Leu Phe Tyr
625                 630                 635                 640
Thr Thr Phe Lys Glu Thr Leu Ala Ser His Pro Lys Ser Leu Lys Phe
                645                 650                 655
Asn Thr Ser Ser Ile Leu Ser Ala Pro His Pro Gly Tyr Thr Tyr Ser
```

```
            660                 665                 670
Glu Gln Ile Pro Val Phe Thr Phe Glu Ala Asn Ile Lys Asn Ser Gly
        675                 680                 685
Lys Thr Glu Ser Pro Tyr Thr Ala Met Leu Phe Val Arg Thr Ser Asn
    690                 695                 700
Ala Gly Pro Ala Pro Tyr Pro Asn Lys Trp Leu Val Gly Phe Asp Arg
705                 710                 715                 720
Leu Ala Asp Ile Lys Pro Gly His Ser Ser Lys Leu Ser Ile Pro Ile
                725                 730                 735
Pro Val Ser Ala Leu Ala Arg Val Asp Ser His Gly Asn Arg Ile Val
            740                 745                 750
Tyr Pro Gly Lys Tyr Glu Leu Ala Leu Asn Thr Asp Glu Ser Val Lys
        755                 760                 765
Leu Glu Phe Glu Leu Val Gly Glu Glu Val Thr Ile Glu Asn Trp Pro
    770                 775                 780
Leu Glu Glu Gln Gln Ile Lys Asp Ala Thr Pro Asp Ala
785                 790                 795


<210> 729
<211> 797
<212> PRT
<213> Artificial Sequence

<220>
<223> unnamed protein product [Trichoderma reesei] 797
      aa protein CBC2392.1 GI:257341433

<400> 729
Met Val Asn Asn Ala Ala Leu Leu Ala Ala Leu Ser Ala Leu Leu Pro
 1               5                  10                  15
Thr Ala Leu Ala Gln Asn Asn Gln Thr Tyr Ala Asn Tyr Ser Ala Gln
            20                  25                  30
Gly Gln Pro Asp Leu Tyr Pro Glu Thr Leu Ala Thr Leu Thr Leu Ser
        35                  40                  45
Phe Pro Asp Cys Glu His Gly Pro Leu Lys Asn Asn Leu Val Cys Asp
    50                  55                  60
Ser Ser Ala Gly Tyr Val Glu Arg Ala Gln Ala Leu Ile Ser Leu Phe
65                  70                  75                  80
Thr Leu Glu Glu Leu Ile Leu Asn Thr Gln Asn Ser Gly Pro Gly Val
                85                  90                  95
Pro Arg Leu Gly Leu Pro Asn Tyr Gln Val Trp Asn Glu Ala Leu His
            100                 105                 110
Gly Leu Asp Arg Ala Asn Phe Ala Thr Lys Gly Gly Gln Phe Glu Trp
        115                 120                 125
Ala Thr Ser Phe Pro Met Pro Ile Leu Thr Thr Ala Ala Leu Asn Arg
    130                 135                 140
Thr Leu Ile His Gln Ile Ala Asp Ile Ile Ser Thr Gln Ala Arg Ala
145                 150                 155                 160
Phe Ser Asn Ser Gly Arg Tyr Gly Leu Asp Val Tyr Ala Pro Asn Val
                165                 170                 175
Asn Gly Phe Arg Ser Pro Leu Trp Gly Arg Gly Gln Glu Thr Pro Gly
            180                 185                 190
Glu Asp Ala Phe Phe Leu Ser Ser Ala Tyr Thr Tyr Glu Tyr Ile Thr
```

```
        195                 200                 205
Gly Ile Gln Gly Gly Val Asp Pro Glu His Leu Lys Val Ala Ala Thr
    210                 215                 220
Val Lys His Phe Ala Gly Tyr Asp Leu Glu Asn Trp Asn Asn Gln Ser
225                 230                 235                 240
Arg Leu Gly Phe Asp Ala Ile Ile Thr Gln Gln Asp Leu Ser Glu Tyr
                245                 250                 255
Tyr Thr Pro Gln Phe Leu Ala Ala Ala Arg Tyr Ala Lys Ser Arg Ser
            260                 265                 270
Leu Met Cys Ala Tyr Asn Ser Val Asn Gly Val Pro Ser Cys Ala Asn
        275                 280                 285
Ser Phe Phe Leu Gln Thr Leu Leu Arg Glu Ser Trp Gly Phe Pro Glu
    290                 295                 300
Trp Gly Tyr Val Ser Ser Asp Cys Asp Ala Val Tyr Asn Val Phe Asn
305                 310                 315                 320
Pro His Asp Tyr Ala Ser Asn Gln Ser Ser Ala Ala Ala Ser Ser Leu
                325                 330                 335
Arg Ala Gly Thr Asp Ile Asp Cys Gly Gln Thr Tyr Pro Trp His Leu
            340                 345                 350
Asn Glu Ser Phe Val Ala Gly Glu Val Ser Arg Gly Glu Ile Glu Arg
        355                 360                 365
Ser Val Thr Arg Leu Tyr Ala Asn Leu Val Arg Leu Gly Tyr Phe Asp
    370                 375                 380
Lys Lys Asn Gln Tyr Arg Ser Leu Gly Trp Lys Asp Val Val Lys Thr
385                 390                 395                 400
Asp Ala Trp Asn Ile Ser Tyr Glu Ala Ala Val Glu Gly Ile Val Leu
                405                 410                 415
Leu Lys Asn Asp Gly Thr Leu Pro Leu Ser Lys Lys Val Arg Ser Ile
            420                 425                 430
Ala Leu Ile Gly Pro Trp Ala Asn Ala Thr Thr Gln Met Gln Gly Asn
        435                 440                 445
Tyr Tyr Gly Pro Ala Pro Tyr Leu Ile Ser Pro Leu Glu Ala Ala Lys
    450                 455                 460
Lys Ala Gly Tyr His Val Asn Phe Glu Leu Gly Thr Glu Ile Ala Gly
465                 470                 475                 480
Asn Ser Thr Thr Gly Phe Ala Lys Ala Ile Ala Ala Ala Lys Lys Ser
                485                 490                 495
Asp Ala Ile Ile Tyr Leu Gly Gly Ile Asp Asn Thr Ile Glu Gln Glu
            500                 505                 510
Gly Ala Asp Arg Thr Asp Ile Ala Trp Pro Gly Asn Gln Leu Asp Leu
        515                 520                 525
Ile Lys Gln Leu Ser Glu Val Gly Lys Pro Leu Val Val Leu Gln Met
    530                 535                 540
Gly Gly Gly Gln Val Asp Ser Ser Ser Leu Lys Ser Asn Lys Lys Val
545                 550                 555                 560
Asn Ser Leu Val Trp Gly Gly Tyr Pro Gly Gln Ser Gly Gly Val Ala
                565                 570                 575
Leu Phe Asp Ile Leu Ser Gly Lys Arg Ala Pro Ala Gly Arg Leu Val
            580                 585                 590
Thr Thr Gln Tyr Pro Ala Glu Tyr Val His Gln Phe Pro Gln Asn Asp
        595                 600                 605
Met Asn Leu Arg Pro Asp Gly Lys Ser Asn Pro Gly Gln Thr Tyr Ile
    610                 615                 620
Trp Tyr Thr Gly Lys Pro Val Tyr Glu Phe Gly Ser Gly Leu Phe Tyr
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625 630 635 640
Thr Thr Phe Lys Glu Thr Leu Ala Ser His Pro Lys Ser Leu Lys Phe
645 650 655
Asn Thr Ser Ser Ile Leu Ser Ala Pro His Pro Gly Tyr Thr Tyr Ser
660 665 670
Glu Gln Ile Pro Val Phe Thr Phe Glu Ala Asn Ile Lys Asn Ser Gly
675 680 685
Lys Thr Glu Ser Pro Tyr Thr Ala Met Leu Phe Val Arg Thr Ser Asn
690 695 700
Ala Gly Pro Ala Pro Tyr Pro Asn Lys Trp Leu Val Gly Phe Asp Arg
705 710 715 720
Leu Ala Asp Ile Lys Pro Gly His Ser Ser Lys Leu Ser Ile Pro Ile
725 730 735
Pro Val Ser Ala Leu Ala Arg Val Asp Ser His Gly Asn Arg Ile Val
740 745 750
Tyr Pro Gly Lys Tyr Glu Leu Ala Leu Asn Thr Asp Glu Ser Val Lys
755 760 765
Leu Glu Phe Glu Leu Val Gly Glu Glu Val Thr Ile Glu Asn Trp Pro
770 775 780
Leu Glu Glu Gln Gln Ile Lys Asp Ala Thr Pro Asp Ala
785 790 795

<210> 730
<211> 766
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, The Structure Of Hypocrea Jecorina
Beta-xylosidase Xyl3a (bxl1) 766 aa protein 5A7M_A
GI:152244671

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 730
Xaa Asn Asn Gln Thr Tyr Ala Asn Tyr Ser Ala Gln Gly Gln Pro Asp
1 5 10 15
Leu Tyr Pro Glu Thr Leu Ala Thr Leu Thr Leu Ser Phe Pro Asp Cys
20 25 30
Glu His Gly Pro Leu Lys Asn Asn Leu Val Cys Asp Ser Ser Ala Gly
35 40 45
Tyr Val Glu Arg Ala Gln Ala Leu Ile Ser Leu Phe Thr Leu Glu Glu
50 55 60
Leu Ile Leu Asn Thr Gln Asn Ser Gly Pro Gly Val Pro Arg Leu Gly
65 70 75 80
Leu Pro Asn Tyr Gln Val Trp Asn Glu Ala Leu His Gly Leu Asp Arg
85 90 95
Ala Asn Phe Ala Thr Lys Gly Gly Gln Phe Glu Trp Ala Thr Ser Phe
100 105 110
Pro Met Pro Ile Leu Thr Thr Ala Ala Leu Asn Arg Thr Leu Ile His

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        115                 120                 125
Gln Ile Ala Asp Ile Ile Ser Thr Gln Ala Arg Ala Phe Ser Asn Ser
    130                 135                 140
Gly Arg Tyr Gly Leu Asp Val Tyr Ala Pro Asn Val Asn Gly Phe Arg
145                 150                 155                 160
Ser Pro Leu Trp Gly Arg Gly Gln Glu Thr Pro Gly Glu Asp Ala Phe
                165                 170                 175
Phe Leu Ser Ser Ala Tyr Thr Tyr Glu Tyr Ile Thr Gly Ile Gln Gly
            180                 185                 190
Gly Val Asp Pro Glu His Leu Lys Val Ala Ala Thr Val Lys His Phe
        195                 200                 205
Ala Gly Tyr Asp Leu Glu Asn Trp Asn Asn Gln Ser Arg Leu Gly Phe
    210                 215                 220
Asp Ala Ile Ile Thr Gln Gln Asp Leu Ser Glu Tyr Tyr Thr Pro Gln
225                 230                 235                 240
Phe Leu Ala Ala Ala Arg Tyr Ala Lys Ser Arg Ser Leu Met Cys Ala
                245                 250                 255
Tyr Asn Ser Val Asn Gly Val Pro Ser Cys Ala Asn Ser Phe Phe Leu
            260                 265                 270
Gln Thr Leu Leu Arg Glu Ser Trp Gly Phe Pro Glu Trp Gly Tyr Val
        275                 280                 285
Ser Ser Asp Cys Asp Ala Val Tyr Asn Val Phe Asn Pro His Asp Tyr
    290                 295                 300
Ala Ser Asn Gln Ser Ser Ala Ala Ala Ser Ser Leu Arg Ala Gly Thr
305                 310                 315                 320
Asp Ile Asp Cys Gly Gln Thr Tyr Pro Trp His Leu Asn Glu Ser Phe
                325                 330                 335
Val Ala Gly Glu Val Ser Arg Gly Glu Ile Glu Arg Ser Val Thr Arg
            340                 345                 350
Leu Tyr Ala Asn Leu Val Arg Leu Gly Tyr Phe Asp Lys Lys Asn Gln
        355                 360                 365
Tyr Arg Ser Leu Gly Trp Lys Asp Val Val Lys Thr Asp Ala Trp Asn
    370                 375                 380
Ile Ser Tyr Glu Ala Ala Val Glu Gly Ile Val Leu Leu Lys Asn Asp
385                 390                 395                 400
Gly Thr Leu Pro Leu Ser Lys Lys Val Arg Ser Ile Ala Leu Ile Gly
                405                 410                 415
Pro Trp Ala Asn Ala Thr Thr Gln Met Gln Gly Asn Tyr Tyr Gly Pro
            420                 425                 430
Ala Pro Tyr Leu Ile Ser Pro Leu Glu Ala Ala Lys Lys Ala Gly Tyr
        435                 440                 445
His Val Asn Phe Glu Leu Gly Thr Glu Ile Ala Gly Asn Ser Thr Thr
    450                 455                 460
Gly Phe Ala Lys Ala Ile Ala Ala Ala Lys Lys Ser Asp Ala Ile Ile
465                 470                 475                 480
Tyr Leu Gly Gly Ile Asp Asn Thr Ile Glu Gln Glu Gly Ala Asp Arg
                485                 490                 495
Thr Asp Ile Ala Trp Pro Gly Asn Gln Leu Asp Leu Ile Lys Gln Leu
            500                 505                 510
Ser Glu Val Gly Lys Pro Leu Val Val Leu Gln Met Gly Gly Gly Gln
        515                 520                 525
Val Asp Ser Ser Ser Leu Lys Ser Asn Lys Lys Val Asn Ser Leu Val
    530                 535                 540
Trp Gly Gly Tyr Pro Gly Gln Ser Gly Gly Val Ala Leu Phe Asp Ile
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545 550 555 560
Leu Ser Gly Lys Arg Ala Pro Ala Gly Arg Leu Val Thr Thr Gln Tyr
565 570 575
Pro Ala Glu Tyr Val His Gln Phe Pro Gln Asn Asp Met Asn Leu Arg
580 585 590
Pro Asp Gly Lys Ser Asn Pro Gly Gln Thr Tyr Ile Trp Tyr Thr Gly
595 600 605
Lys Pro Val Tyr Glu Phe Gly Ser Gly Leu Phe Tyr Thr Thr Phe Lys
610 615 620
Glu Thr Leu Ala Ser His Pro Lys Ser Leu Lys Phe Asn Thr Ser Ser
625 630 635 640
Ile Leu Ser Ala Pro His Pro Gly Tyr Thr Tyr Ser Glu Gln Ile Pro
645 650 655
Val Phe Thr Phe Glu Ala Asn Ile Lys Asn Ser Gly Lys Thr Glu Ser
660 665 670
Pro Tyr Thr Ala Met Leu Phe Val Arg Thr Ser Asn Ala Gly Pro Ala
675 680 685
Pro Tyr Pro Asn Lys Trp Leu Val Gly Phe Asp Arg Leu Ala Asp Ile
690 695 700
Lys Pro Gly His Ser Ser Lys Leu Ser Ile Pro Ile Pro Val Ser Ala
705 710 715 720
Leu Ala Arg Val Asp Ser His Gly Asn Arg Ile Val Tyr Pro Gly Lys
725 730 735
Tyr Glu Leu Ala Leu Asn Thr Asp Glu Ser Val Lys Leu Glu Phe Glu
740 745 750
Leu Val Gly Glu Glu Val Thr Ile Glu Asn Trp Pro Leu Glu
755 760 765

<210> 731
<211> 766
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, The Structure Of Hypocrea Jecorina
Beta-xylosidase Xyl3a (bxl1) 766 aa protein 5A7M_B
GI:152244672

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 731
Xaa Asn Asn Gln Thr Tyr Ala Asn Tyr Ser Ala Gln Gly Gln Pro Asp
1 5 10 15
Leu Tyr Pro Glu Thr Leu Ala Thr Leu Thr Leu Ser Phe Pro Asp Cys
20 25 30
Glu His Gly Pro Leu Lys Asn Asn Leu Val Cys Asp Ser Ser Ala Gly
35 40 45
Tyr Val Glu Arg Ala Gln Ala Leu Ile Ser Leu Phe Thr Leu Glu Glu
50 55 60
Leu Ile Leu Asn Thr Gln Asn Ser Gly Pro Gly Val Pro Arg Leu Gly

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65                  70                  75                  80
Leu Pro Asn Tyr Gln Val Trp Asn Glu Ala Leu His Gly Leu Asp Arg
                85                  90                  95
Ala Asn Phe Ala Thr Lys Gly Gly Gln Phe Glu Trp Ala Thr Ser Phe
            100                 105                 110
Pro Met Pro Ile Leu Thr Thr Ala Ala Leu Asn Arg Thr Leu Ile His
        115                 120                 125
Gln Ile Ala Asp Ile Ile Ser Thr Gln Ala Arg Ala Phe Ser Asn Ser
    130                 135                 140
Gly Arg Tyr Gly Leu Asp Val Tyr Ala Pro Asn Val Asn Gly Phe Arg
145                 150                 155                 160
Ser Pro Leu Trp Gly Arg Gly Gln Glu Thr Pro Gly Glu Asp Ala Phe
                165                 170                 175
Phe Leu Ser Ser Ala Tyr Thr Tyr Glu Tyr Ile Thr Gly Ile Gln Gly
            180                 185                 190
Gly Val Asp Pro Glu His Leu Lys Val Ala Ala Thr Val Lys His Phe
        195                 200                 205
Ala Gly Tyr Asp Leu Glu Asn Trp Asn Asn Gln Ser Arg Leu Gly Phe
    210                 215                 220
Asp Ala Ile Ile Thr Gln Gln Asp Leu Ser Glu Tyr Tyr Thr Pro Gln
225                 230                 235                 240
Phe Leu Ala Ala Ala Arg Tyr Ala Lys Ser Arg Ser Leu Met Cys Ala
                245                 250                 255
Tyr Asn Ser Val Asn Gly Val Pro Ser Cys Ala Asn Ser Phe Phe Leu
            260                 265                 270
Gln Thr Leu Leu Arg Glu Ser Trp Gly Phe Pro Glu Trp Gly Tyr Val
        275                 280                 285
Ser Ser Asp Cys Asp Ala Val Tyr Asn Val Phe Asn Pro His Asp Tyr
    290                 295                 300
Ala Ser Asn Gln Ser Ser Ala Ala Ala Ser Ser Leu Arg Ala Gly Thr
305                 310                 315                 320
Asp Ile Asp Cys Gly Gln Thr Tyr Pro Trp His Leu Asn Glu Ser Phe
                325                 330                 335
Val Ala Gly Glu Val Ser Arg Gly Glu Ile Glu Arg Ser Val Thr Arg
            340                 345                 350
Leu Tyr Ala Asn Leu Val Arg Leu Gly Tyr Phe Asp Lys Lys Asn Gln
        355                 360                 365
Tyr Arg Ser Leu Gly Trp Lys Asp Val Val Lys Thr Asp Ala Trp Asn
    370                 375                 380
Ile Ser Tyr Glu Ala Ala Val Glu Gly Ile Val Leu Leu Lys Asn Asp
385                 390                 395                 400
Gly Thr Leu Pro Leu Ser Lys Lys Val Arg Ser Ile Ala Leu Ile Gly
                405                 410                 415
Pro Trp Ala Asn Ala Thr Thr Gln Met Gln Gly Asn Tyr Tyr Gly Pro
            420                 425                 430
Ala Pro Tyr Leu Ile Ser Pro Leu Glu Ala Ala Lys Lys Ala Gly Tyr
        435                 440                 445
His Val Asn Phe Glu Leu Gly Thr Glu Ile Ala Gly Asn Ser Thr Thr
    450                 455                 460
Gly Phe Ala Lys Ala Ile Ala Ala Ala Lys Lys Ser Asp Ala Ile Ile
465                 470                 475                 480
Tyr Leu Gly Gly Ile Asp Asn Thr Ile Glu Gln Glu Gly Ala Asp Arg
                485                 490                 495
Thr Asp Ile Ala Trp Pro Gly Asn Gln Leu Asp Leu Ile Lys Gln Leu
```

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            500                 505                 510
Ser Glu Val Gly Lys Pro Leu Val Val Leu Gln Met Gly Gly Gly Gln
        515                 520                 525
Val Asp Ser Ser Ser Leu Lys Ser Asn Lys Lys Val Asn Ser Leu Val
    530                 535                 540
Trp Gly Gly Tyr Pro Gly Gln Ser Gly Gly Val Ala Leu Phe Asp Ile
545                 550                 555                 560
Leu Ser Gly Lys Arg Ala Pro Ala Gly Arg Leu Val Thr Thr Gln Tyr
                565                 570                 575
Pro Ala Glu Tyr Val His Gln Phe Pro Gln Asn Asp Met Asn Leu Arg
            580                 585                 590
Pro Asp Gly Lys Ser Asn Pro Gly Gln Thr Tyr Ile Trp Tyr Thr Gly
        595                 600                 605
Lys Pro Val Tyr Glu Phe Gly Ser Gly Leu Phe Tyr Thr Thr Phe Lys
    610                 615                 620
Glu Thr Leu Ala Ser His Pro Lys Ser Leu Lys Phe Asn Thr Ser Ser
625                 630                 635                 640
Ile Leu Ser Ala Pro His Pro Gly Tyr Thr Tyr Ser Glu Gln Ile Pro
                645                 650                 655
Val Phe Thr Phe Glu Ala Asn Ile Lys Asn Ser Gly Lys Thr Glu Ser
            660                 665                 670
Pro Tyr Thr Ala Met Leu Phe Val Arg Thr Ser Asn Ala Gly Pro Ala
        675                 680                 685
Pro Tyr Pro Asn Lys Trp Leu Val Gly Phe Asp Arg Leu Ala Asp Ile
    690                 695                 700
Lys Pro Gly His Ser Ser Lys Leu Ser Ile Pro Ile Pro Val Ser Ala
705                 710                 715                 720
Leu Ala Arg Val Asp Ser His Gly Asn Arg Ile Val Tyr Pro Gly Lys
                725                 730                 735
Tyr Glu Leu Ala Leu Asn Thr Asp Glu Ser Val Lys Leu Glu Phe Glu
            740                 745                 750
Leu Val Gly Glu Glu Val Thr Ile Glu Asn Trp Pro Leu Glu
        755                 760                 765


<210> 732
<211> 767
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, The Structure Of Hypocrea Jecorina
      Beta-xylosidase Xyl3a (Bxl1) In Complex With
      4-thioxylobiose 767 aa protein 5AE6_A GI:169428461

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 732
Xaa Asn Asn Gln Thr Tyr Ala Asn Tyr Ser Ala Gln Gly Gln Pro Asp
 1               5                  10                  15
Leu Tyr Pro Glu Thr Leu Ala Thr Leu Thr Leu Ser Phe Pro Asp Cys
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            20                  25                  30
Glu His Gly Pro Leu Lys Asn Asn Leu Val Cys Asp Ser Ser Ala Gly
        35                  40                  45
Tyr Val Glu Arg Ala Gln Ala Leu Ile Ser Leu Phe Thr Leu Glu Glu
    50                  55                  60
Leu Ile Leu Asn Thr Gln Asn Ser Gly Pro Gly Val Pro Arg Leu Gly
65                  70                  75                  80
Leu Pro Asn Tyr Gln Val Trp Asn Glu Ala Leu His Gly Leu Asp Arg
                85                  90                  95
Ala Asn Phe Ala Thr Lys Gly Gly Gln Phe Glu Trp Ala Thr Ser Phe
            100                 105                 110
Pro Met Pro Ile Leu Thr Thr Ala Ala Leu Asn Arg Thr Leu Ile His
        115                 120                 125
Gln Ile Ala Asp Ile Ile Ser Thr Gln Ala Arg Ala Phe Ser Asn Ser
    130                 135                 140
Gly Arg Tyr Gly Leu Asp Val Tyr Ala Pro Asn Val Asn Gly Phe Arg
145                 150                 155                 160
Ser Pro Leu Trp Gly Arg Gly Gln Glu Thr Pro Gly Glu Asp Ala Phe
                165                 170                 175
Phe Leu Ser Ser Ala Tyr Thr Tyr Glu Tyr Ile Thr Gly Ile Gln Gly
            180                 185                 190
Gly Val Asp Pro Glu His Leu Lys Val Ala Ala Thr Val Lys His Phe
        195                 200                 205
Ala Gly Tyr Asp Leu Glu Asn Trp Asn Asn Gln Ser Arg Leu Gly Phe
    210                 215                 220
Asp Ala Ile Ile Thr Gln Gln Asp Leu Ser Glu Tyr Tyr Thr Pro Gln
225                 230                 235                 240
Phe Leu Ala Ala Ala Arg Tyr Ala Lys Ser Arg Ser Leu Met Cys Ala
                245                 250                 255
Tyr Asn Ser Val Asn Gly Val Pro Ser Cys Ala Asn Ser Phe Phe Leu
            260                 265                 270
Gln Thr Leu Leu Arg Glu Ser Trp Gly Phe Pro Glu Trp Gly Tyr Val
        275                 280                 285
Ser Ser Asp Cys Asp Ala Val Tyr Asn Val Phe Asn Pro His Asp Tyr
    290                 295                 300
Ala Ser Asn Gln Ser Ser Ala Ala Ala Ser Ser Leu Arg Ala Gly Thr
305                 310                 315                 320
Asp Ile Asp Cys Gly Gln Thr Tyr Pro Trp His Leu Asn Glu Ser Phe
                325                 330                 335
Val Ala Gly Glu Val Ser Arg Gly Glu Ile Glu Arg Ser Val Thr Arg
            340                 345                 350
Leu Tyr Ala Asn Leu Val Arg Leu Gly Tyr Phe Asp Lys Lys Asn Gln
        355                 360                 365
Tyr Arg Ser Leu Gly Trp Lys Asp Val Val Lys Thr Asp Ala Trp Asn
    370                 375                 380
Ile Ser Tyr Glu Ala Ala Val Glu Gly Ile Val Leu Leu Lys Asn Asp
385                 390                 395                 400
Gly Thr Leu Pro Leu Ser Lys Lys Val Arg Ser Ile Ala Leu Ile Gly
                405                 410                 415
Pro Trp Ala Asn Ala Thr Thr Gln Met Gln Gly Asn Tyr Tyr Gly Pro
            420                 425                 430
Ala Pro Tyr Leu Ile Ser Pro Leu Glu Ala Ala Lys Lys Ala Gly Tyr
        435                 440                 445
His Val Asn Phe Glu Leu Gly Thr Glu Ile Ala Gly Asn Ser Thr Thr
```

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


<210> 733
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, The Structure Of Hypocrea Jecorina
      Beta-xylosidase Xyl3a (Bxl1) In Complex With
      4-thioxylobiose 767 aa protein 5AE6_B GI:169428462

<220>
<221> VARIANT
<222> 1
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<223> Xaa = Any Amino Acid

<400> 733
Xaa Asn Asn Gln Thr Tyr Ala Asn Tyr Ser Ala Gln Gly Gln Pro Asp
 1               5                  10                  15
Leu Tyr Pro Glu Thr Leu Ala Thr Leu Thr Leu Ser Phe Pro Asp Cys
            20                  25                  30
Glu His Gly Pro Leu Lys Asn Asn Leu Val Cys Asp Ser Ser Ala Gly
        35                  40                  45
Tyr Val Glu Arg Ala Gln Ala Leu Ile Ser Leu Phe Thr Leu Glu Glu
    50                  55                  60
Leu Ile Leu Asn Thr Gln Asn Ser Gly Pro Gly Val Pro Arg Leu Gly
65                  70                  75                  80
Leu Pro Asn Tyr Gln Val Trp Asn Glu Ala Ala Leu Asn Arg Thr Leu
                85                  90                  95
Ile His Gln Ile Ala Asp Ile Ile Ser Thr Gln Ala Arg Ala Phe Ser
            100                 105                 110
Asn Ser Gly Arg Tyr Gly Leu Asp Val Tyr Ala Pro Asn Val Asn Gly
        115                 120                 125
Phe Arg Ser Pro Leu Trp Gly Arg Gly Gln Glu Thr Pro Gly Glu Asp
    130                 135                 140
Ala Phe Phe Leu Ser Ser Ala Tyr Thr Tyr Glu Tyr Ile Thr Gly Ile
145                 150                 155                 160
Gln Gly Gly Val Asp Pro Glu His Leu Lys Val Ala Ala Thr Val Lys
                165                 170                 175
His Phe Ala Gly Tyr Asp Leu Glu Asn Trp Asn Asn Gln Ser Arg Leu
            180                 185                 190
Gly Phe Asp Ala Ile Ile Thr Gln Gln Asp Leu Ser Glu Tyr Tyr Thr
        195                 200                 205
Pro Gln Phe Leu Ala Ala Ala Arg Tyr Ala Lys Ser Arg Ser Leu Met
    210                 215                 220
Cys Ala Tyr Asn Ser Val Asn Gly Val Pro Ser Cys Ala Asn Ser Phe
225                 230                 235                 240
Phe Leu Gln Thr Leu Leu Arg Glu Ser Trp Gly Phe Pro Glu Trp Gly
                245                 250                 255
Tyr Val Ser Ser Asp Cys Asp Ala Val Tyr Asn Val Phe Asn Pro His
            260                 265                 270
Asp Tyr Ala Ser Asn Gln Ser Ser Ala Ala Ala Ser Ser Leu Arg Ala
        275                 280                 285
Gly Thr Asp Ile Asp Cys Gly Gln Thr Tyr Pro Trp His Leu Asn Glu
    290                 295                 300
Ser Phe Val Ala Gly Glu Val Ser Arg Gly Glu Ile Glu Arg Ser Val
305                 310                 315                 320
Thr Arg Leu Tyr Ala Asn Leu Val Arg Leu Gly Tyr Phe Asp Lys Lys
                325                 330                 335
Asn Gln Tyr Arg Ser Leu Gly Trp Lys Asp Val Val Lys Thr Asp Ala
            340                 345                 350
Trp Asn Ile Ser Tyr Glu Ala Ala Val Glu Gly Ile Val Leu Leu Lys
        355                 360                 365
Asn Asp Gly Thr Leu Pro Leu Ser Lys Lys Val Arg Ser Ile Ala Leu
    370                 375                 380
Ile Gly Pro Trp Ala Asn Ala Thr Thr Gln Met Gln Gly Asn Tyr Tyr
385                 390                 395                 400
Gly Pro Ala Pro Tyr Leu Ile Ser Pro Leu Glu Ala Ala Lys Lys Ala

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                405                 410                 415
Gly Tyr His Val Asn Phe Glu Leu Gly Thr Glu Ile Ala Gly Asn Ser
            420                 425                 430
Thr Thr Gly Phe Ala Lys Ala Ile Ala Ala Ala Lys Lys Ser Asp Ala
        435                 440                 445
Ile Ile Tyr Leu Gly Gly Ile Asp Asn Thr Ile Glu Gln Glu Gly Ala
    450                 455                 460
Asp Arg Thr Asp Ile Ala Trp Pro Gly Asn Gln Leu Asp Leu Ile Lys
465                 470                 475                 480
Gln Leu Ser Glu Val Gly Lys Pro Leu Val Val Leu Gln Met Gly Gly
                485                 490                 495
Gly Gln Val Asp Ser Ser Ser Leu Lys Ser Asn Lys Lys Val Asn Ser
            500                 505                 510
Leu Val Trp Gly Gly Tyr Pro Gly Gln Ser Gly Gly Val Ala Leu Phe
        515                 520                 525
Asp Ile Leu Ser Gly Lys Arg Ala Pro Ala Gly Arg Leu Val Thr Thr
    530                 535                 540
Gln Tyr Pro Ala Glu Tyr Val His Gln Phe Pro Gln Asn Asp Met Asn
545                 550                 555                 560
Leu Arg Pro Asp Gly Lys Ser Asn Pro Gly Gln Thr Tyr Ile Trp Tyr
                565                 570                 575
Thr Gly Lys Pro Val Tyr Glu Phe Gly Ser Gly Leu Phe Tyr Thr Thr
            580                 585                 590
Phe Lys Glu Thr Leu Ala Ser His Pro Lys Ser Leu Lys Phe Asn Thr
        595                 600                 605
Ser Ser Ile Leu Ser Ala Pro His Pro Gly Tyr Thr Tyr Ser Glu Gln
    610                 615                 620
Ile Pro Val Phe Thr Phe Glu Ala Asn Ile Lys Asn Ser Gly Lys Thr
625                 630                 635                 640
Glu Ser Pro Tyr Thr Ala Met Leu Phe Val Arg Thr Ser Asn Ala Gly
                645                 650                 655
Pro Ala Pro Tyr Pro Asn Lys Trp Leu Val Gly Phe Asp Arg Leu Ala
            660                 665                 670
Asp Ile Lys Pro Gly His Ser Ser Lys Leu Ser Ile Pro Ile Pro Val
        675                 680                 685
Ser Ala Leu Ala Arg Val Asp Ser His Gly Asn Arg Ile Val Tyr Pro
    690                 695                 700
Gly Lys Tyr Glu Leu Ala Leu Asn Thr Asp Glu Ser Val Lys Leu Glu
705                 710                 715                 720
Phe Glu Leu Val Gly Glu Glu Val Thr Ile Glu Asn Trp Pro Leu Glu
                725                 730                 735
Glu
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<210> 734
<211> 553
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 43 [Trichoderma reesei QM6a] 553 aa protein EGR49145.1 GI:3451895

<400> 734
Met Pro Leu Ile Arg Asn Pro Ile Leu Pro Gly Phe Asn Ala Asp Pro
 1               5                  10                  15
Ser Ile Val Arg Val Gly Ser Asp Tyr Tyr Ile Ala Thr Ser Thr Phe
            20                  25                  30
Glu Trp Tyr Pro Gly Val Gln Ile His His Ser Thr Asp Leu Ala Asn
        35                  40                  45
Trp Glu Leu Ala Val Arg Pro Leu Ser Arg Arg Ser Gln Leu Asp Leu
    50                  55                  60
Arg Gly Glu Pro Asp Ser Cys Gly Val Trp Ala Pro Cys Leu Thr His
65                  70                  75                  80
Asp Gly Asp Lys Phe Trp Leu Val Tyr Thr Asp Val Lys Arg Lys Asp
                85                  90                  95
Gly Ser Phe Lys Asp Thr His Asn Tyr Ile Val Thr Ala Pro Arg Ile
            100                 105                 110
Glu Gly Pro Trp Ser Asp Pro Val Tyr Ala Asn Ser Ser Gly Phe Asp
        115                 120                 125
Pro Ser Leu Phe His Asp Asp Asp Gly Arg Lys Trp Leu Val Asn Met
    130                 135                 140
Val Gln Asp His Arg Ala Arg Pro Arg Thr Phe Ala Gly Ile Ala Leu
145                 150                 155                 160
Gln Glu Phe Asp Pro Ala Gln Gly Lys Leu Val Gly Thr Arg Lys Val
                165                 170                 175
Val Phe His Gly Ser Glu Leu Gly Leu Val Glu Gly Pro His Leu Tyr
            180                 185                 190
Lys Arg Asn Gly Trp Tyr Tyr Leu Leu Thr Ala Glu Gly Gly Thr Gly
        195                 200                 205
Tyr Thr His Ala Ala Thr Leu Ala Arg Ser Arg Ser Ile Trp Gly Pro
    210                 215                 220
Tyr Glu Leu His Pro Gln Gln His Ile Leu Thr Ser Lys Asp His Pro
225                 230                 235                 240
Phe Ala Ala Leu Gln Arg Ala Gly His Ala Asp Ile Val Glu Thr Ala
                245                 250                 255
Asp Gly Lys Thr Tyr Leu Val His Leu Ala Gly Arg Pro Ile Gly Gln
            260                 265                 270
Lys Arg Arg Cys Val Leu Gly Arg Glu Thr Ala Leu Gln Glu Ala Tyr
        275                 280                 285
Trp Gly Glu Asp Asp Trp Leu Tyr Val Lys Asn Gly Pro Val Pro Ser
    290                 295                 300
Leu Asp Val Glu Val Pro Gly Val Arg Asp Glu Glu Ala Tyr Trp Lys
305                 310                 315                 320
Glu Lys Arg Tyr Glu Phe His Asp Gly Leu His Lys Asp Phe Gln Trp
                325                 330                 335
Leu Arg Thr Pro Glu Pro Glu Arg Leu Phe Ala Ile Glu Asp Gly Lys
            340                 345                 350
Leu Val Leu Thr Gly Arg Glu Ser Ile Gly Ser Trp Phe Glu Gln Ser
        355                 360                 365
Leu Val Ala Arg Arg Gln Thr His Phe Ser Phe Asp Ala Glu Thr Val
    370                 375                 380
Ile Asp Phe Ser Pro Glu Asp Glu Arg Gln Phe Ala Gly Leu Thr Leu
385                 390                 395                 400
Tyr Tyr Ser Arg Tyr Asn Phe Phe Tyr Leu Ala Val Ser Ala His Ser
                405                 410                 415
Asp Gly Arg Arg Glu Val Gln Ile Leu Arg Ser Glu Ala Ser Trp Pro

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            420                 425                 430
Asn Gly Lys Leu Glu Asp Val Gly Ala Asn Ala Cys Tyr Val Arg Ile
        435                 440                 445
Pro Gln Gln Gly Arg Val Lys Leu Ala Ala Thr Ile Arg Gly Glu Arg
    450                 455                 460
Leu Gln Phe Tyr Tyr Ala Leu Val Ala Glu Gly Gly Glu Glu Gln Glu
465                 470                 475                 480
Glu Leu Gln Arg Ile Gly Pro Val Leu Asp Ala Ser Ile Val Ser Asp
                485                 490                 495
Glu Cys Gly Gly His Gln Ala His Gly Ser Phe Thr Gly Ser Phe Val
            500                 505                 510
Gly Val Ala Cys Ser Asp Val Asn Gly Thr Glu Lys Arg Ala Val Phe
        515                 520                 525
Asp Tyr Phe Val Tyr Arg Pro Ala His Asp Ser Thr Asp Arg Tyr Ser
    530                 535                 540
Val Ser Met Glu Gly Ile Gln Arg Val
545                 550


<210> 735
<211> 797
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 3 [Trichoderma reesei
      QM6a] 797 aa protein EGR4972.1 GI:34519464

<400> 735
Met Val Asn Asn Ala Ala Leu Leu Ala Ala Leu Ser Ala Leu Leu Pro
 1               5                  10                  15
Thr Ala Leu Ala Gln Asn Asn Gln Thr Tyr Ala Asn Tyr Ser Ala Gln
            20                  25                  30
Gly Gln Pro Asp Leu Tyr Pro Glu Thr Leu Ala Thr Leu Thr Leu Ser
        35                  40                  45
Phe Pro Asp Cys Glu His Gly Pro Leu Lys Asn Asn Leu Val Cys Asp
    50                  55                  60
Ser Ser Ala Gly Tyr Val Glu Arg Ala Gln Ala Leu Ile Ser Leu Phe
65                  70                  75                  80
Thr Leu Glu Glu Leu Ile Leu Asn Thr Gln Asn Ser Gly Pro Gly Val
                85                  90                  95
Pro Arg Leu Gly Leu Pro Asn Tyr Gln Val Trp Asn Glu Ala Leu His
            100                 105                 110
Gly Leu Asp Arg Ala Asn Phe Ala Thr Lys Gly Gly Gln Phe Glu Trp
        115                 120                 125
Ala Thr Ser Phe Pro Met Pro Ile Leu Thr Thr Ala Ala Leu Asn Arg
    130                 135                 140
Thr Leu Ile His Gln Ile Ala Asp Ile Ile Ser Thr Gln Ala Arg Ala
145                 150                 155                 160
Phe Ser Asn Ser Gly Arg Tyr Gly Leu Asp Val Tyr Ala Pro Asn Val
                165                 170                 175
Asn Gly Phe Arg Ser Pro Leu Trp Gly Arg Gly Gln Glu Thr Pro Gly
            180                 185                 190
Glu Asp Ala Phe Phe Leu Ser Ser Ala Tyr Thr Tyr Glu Tyr Ile Thr
```

```
        195                 200                 205
Gly Ile Gln Gly Gly Val Asp Pro Glu His Leu Lys Val Ala Ala Thr
    210                 215                 220
Val Lys His Phe Ala Gly Tyr Asp Leu Glu Asn Trp Asn Asn Gln Ser
225                 230                 235                 240
Arg Leu Gly Phe Asp Ala Ile Ile Thr Gln Gln Asp Leu Ser Glu Tyr
                245                 250                 255
Tyr Thr Pro Gln Phe Leu Ala Ala Ala Arg Tyr Ala Lys Ser Arg Ser
            260                 265                 270
Leu Met Cys Ala Tyr Asn Ser Val Asn Gly Val Pro Ser Cys Ala Asn
        275                 280                 285
Ser Phe Phe Leu Gln Thr Leu Leu Arg Glu Ser Trp Gly Phe Pro Glu
    290                 295                 300
Trp Gly Tyr Val Ser Ser Asp Cys Asp Ala Val Tyr Asn Val Phe Asn
305                 310                 315                 320
Pro His Asp Tyr Ala Ser Asn Gln Ser Ser Ala Ala Ala Ser Ser Leu
                325                 330                 335
Arg Ala Gly Thr Asp Ile Asp Cys Gly Gln Thr Tyr Pro Trp His Leu
            340                 345                 350
Asn Glu Ser Phe Val Ala Gly Glu Val Ser Arg Gly Glu Ile Glu Arg
        355                 360                 365
Ser Val Thr Arg Leu Tyr Ala Asn Leu Val Arg Leu Gly Tyr Phe Asp
    370                 375                 380
Lys Lys Asn Gln Tyr Arg Ser Leu Gly Trp Lys Asp Val Val Lys Thr
385                 390                 395                 400
Asp Ala Trp Asn Ile Ser Tyr Glu Ala Ala Val Glu Gly Ile Val Leu
                405                 410                 415
Leu Lys Asn Asp Gly Thr Leu Pro Leu Ser Lys Lys Val Arg Ser Ile
            420                 425                 430
Ala Leu Ile Gly Pro Trp Ala Asn Ala Thr Thr Gln Met Gln Gly Asn
        435                 440                 445
Tyr Tyr Gly Pro Ala Pro Tyr Leu Ile Ser Pro Leu Glu Ala Ala Lys
    450                 455                 460
Lys Ala Gly Tyr His Val Asn Phe Glu Leu Gly Thr Glu Ile Ala Gly
465                 470                 475                 480
Asn Ser Thr Thr Gly Phe Ala Lys Ala Ile Ala Ala Ala Lys Lys Ser
                485                 490                 495
Asp Ala Ile Ile Tyr Leu Gly Gly Ile Asp Asn Thr Ile Glu Gln Glu
            500                 505                 510
Gly Ala Asp Arg Thr Asp Ile Ala Trp Pro Gly Asn Gln Leu Asp Leu
        515                 520                 525
Ile Lys Gln Leu Ser Glu Val Gly Lys Pro Leu Val Val Leu Gln Met
    530                 535                 540
Gly Gly Gly Gln Val Asp Ser Ser Ser Leu Lys Ser Asn Lys Lys Val
545                 550                 555                 560
Asn Ser Leu Val Trp Gly Gly Tyr Pro Gly Gln Ser Gly Gly Val Ala
                565                 570                 575
Leu Phe Asp Ile Leu Ser Gly Lys Arg Ala Pro Ala Gly Arg Leu Val
            580                 585                 590
Thr Thr Gln Tyr Pro Ala Glu Tyr Val His Gln Phe Pro Gln Asn Asp
        595                 600                 605
Met Asn Leu Arg Pro Asp Gly Lys Ser Asn Pro Gly Gln Thr Tyr Ile
    610                 615                 620
Trp Tyr Thr Gly Lys Pro Val Tyr Glu Phe Gly Ser Gly Leu Phe Tyr
```

625 630 635 640
Thr Thr Phe Lys Glu Thr Leu Ala Ser His Pro Lys Ser Leu Lys Phe
645 650 655
Asn Thr Ser Ser Ile Leu Ser Ala Pro His Pro Gly Tyr Thr Tyr Ser
660 665 670
Glu Gln Ile Pro Val Phe Thr Phe Glu Ala Asn Ile Lys Asn Ser Gly
675 680 685
Lys Thr Glu Ser Pro Tyr Thr Ala Met Leu Phe Val Arg Thr Ser Asn
690 695 700
Ala Gly Pro Ala Pro Tyr Pro Asn Lys Trp Leu Val Gly Phe Asp Arg
705 710 715 720
Leu Ala Asp Ile Lys Pro Gly His Ser Ser Lys Leu Ser Ile Pro Ile
725 730 735
Pro Val Ser Ala Leu Ala Arg Val Asp Ser His Gly Asn Arg Ile Val
740 745 750
Tyr Pro Gly Lys Tyr Glu Leu Ala Leu Asn Thr Asp Glu Ser Val Lys
755 760 765
Leu Glu Phe Glu Leu Val Gly Glu Glu Val Thr Ile Glu Asn Trp Pro
770 775 780
Leu Glu Glu Gln Gln Ile Lys Asp Ala Thr Pro Asp Ala
785 790 795

<210> 736
<211> 796
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 3 [Trichoderma reesei QM6a] 796 aa protein EGR586.1 GI:34519849

<400> 736
Met Arg Val Asn Val Pro Leu His Ala Leu Gln Ile Ala Ala Arg Ser
1 5 10 15
Val Ala Ala Ala Ile Cys Lys Ser Ser Ser Ala Ser Gly Arg Ser Leu
20 25 30
Arg Gly Gly Lys Ile Asp Gln Ala Ser Arg Ile Asn Ile Tyr Ser Ile
35 40 45
Ser Asn Pro Ser Pro Asn Pro Pro Leu Thr Pro Ser Phe Pro Asp Cys
50 55 60
Thr Arg Asp Pro Leu Cys Ser Asn Asp Val Cys Asp Thr Thr Lys Ser
65 70 75 80
Ile Ala Glu Arg Ala Ala Ala Ile Val Lys Pro Met Thr Leu Asn Glu
85 90 95
Lys Val Ala Asn Val Gly Ser Ser Ala Ser Gly Ser Ala Arg Leu Gly
100 105 110
Leu Pro Ala Tyr Gln Trp Gln Asn Glu Ala Leu His Gly Val Ala Gly
115 120 125
Ser Thr Gly Val Gln Phe Gln Ser Pro Leu Gly Ala Asn Phe Ser Ala
130 135 140
Ala Thr Ser Phe Pro Met Pro Ile Leu Leu Ser Ala Ala Phe Asp Asp
145 150 155 160
Ala Leu Val Lys Ser Val Ala Thr Ala Ile Ser Thr Glu Ala Arg Ala

```
                165                 170                 175
Phe Ala Asn Tyr Gly Phe Ala Gly Leu Asp Phe Trp Thr Pro Asn Ile
            180                 185                 190
Asn Pro Phe Arg Asp Pro Arg Trp Gly Arg Gly Met Glu Thr Pro Gly
        195                 200                 205
Glu Asp Ala Phe Arg Ile Gln Gly Tyr Val Leu Ala Leu Val Asp Gly
    210                 215                 220
Leu Gln Gly Gly Ile Asp Pro Asp Phe Tyr Arg Thr Leu Ser Thr Cys
225                 230                 235                 240
Lys His Phe Ala Ala Tyr Asp Ile Glu Asn Gly Arg Thr Ala Asn Asn
                245                 250                 255
Leu Ser Pro Thr Gln Gln Asp Met Ala Asp Tyr Tyr Leu Pro Met Phe
            260                 265                 270
Glu Thr Cys Val Arg Asp Ala Lys Val Ala Ser Ile Met Cys Ala Tyr
        275                 280                 285
Asn Ala Val Asp Gly Val Pro Ala Cys Ala Asp Ser Tyr Leu Leu Gln
    290                 295                 300
Asp Val Leu Arg Asp Thr Tyr Gly Phe Thr Glu Asp Phe Asn Tyr Val
305                 310                 315                 320
Val Ser Asp Cys Asp Ala Val Glu Asn Val Phe Asp Pro His His Tyr
                325                 330                 335
Ala Ala Asn Leu Thr Gln Ala Ala Ala Met Ser Ile Asn Ala Gly Thr
            340                 345                 350
Asp Leu Asp Cys Gly Ser Ser Tyr Asn Val Leu Asn Ala Ser Val Gln
        355                 360                 365
Ala Gly Leu Thr Thr Glu Ala Thr Leu Asp Lys Ser Leu Ile Arg Leu
    370                 375                 380
Tyr Ser Ala Leu Val Lys Val Gly Tyr Phe Asp Gln Pro Ala Glu Tyr
385                 390                 395                 400
Asn Ser Leu Gly Trp Gly Asn Val Asn Thr Thr Gln Ser Gln Ala Leu
                405                 410                 415
Ala His Asp Ala Ala Thr Glu Gly Met Thr Leu Leu Lys Asn Asp Gly
            420                 425                 430
Thr Leu Pro Leu Ser Arg Thr Leu Ser Asn Val Ala Val Ile Gly Pro
        435                 440                 445
Trp Ala Asn Val Thr Thr Gln Met Gln Gly Asn Tyr Ala Gly Thr Ala
    450                 455                 460
Pro Leu Leu Val Asn Pro Leu Ser Val Phe Gln Gln Lys Trp Arg Asn
465                 470                 475                 480
Val Lys Tyr Ala Gln Gly Thr Ala Ile Asn Ser Gln Asp Thr Ser Gly
                485                 490                 495
Phe Asn Ala Ala Leu Ser Ala Ala Ser Ser Ser Asp Val Ile Val Tyr
            500                 505                 510
Leu Gly Gly Ile Asp Ile Ser Val Glu Asn Glu Gly Phe Asp Arg Ser
        515                 520                 525
Ser Ile Thr Trp Pro Gly Asn Gln Leu Asn Leu Ile Ser Gln Leu Ala
    530                 535                 540
Asn Leu Gly Lys Pro Leu Val Ile Val Gln Phe Gly Gly Gly Gln Ile
545                 550                 555                 560
Asp Asp Ser Ala Leu Leu Ser Asn Ser Lys Val Asn Ser Ile Leu Trp
                565                 570                 575
Ala Gly Tyr Pro Gly Gln Asp Gly Gly Asn Ala Ile Phe Asp Val Leu
            580                 585                 590
Thr Gly Ala Asn Pro Pro Ala Gly Arg Leu Pro Val Thr Gln Tyr Pro
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        595                 600                 605
Ala Asn Tyr Val Asn Asn Asn Asn Ile Gln Asp Met Asn Leu Arg Pro
    610                 615                 620
Ser Asn Gly Ile Pro Gly Arg Thr Tyr Ala Trp Tyr Thr Gly Thr Pro
625                 630                 635                 640
Val Leu Pro Phe Gly Tyr Gly Leu His Tyr Thr Asn Phe Ser Leu Ser
                645                 650                 655
Phe Gln Ser Thr Lys Thr Ala Gly Ser Asp Ile Ala Thr Leu Val Asn
            660                 665                 670
Asn Ala Gly Ser Asn Lys Asp Leu Ala Thr Phe Ala Thr Ile Val Val
        675                 680                 685
Asn Val Lys Asn Thr Gly Gly Lys Ala Asn Leu Ala Ser Asp Tyr Val
    690                 695                 700
Gly Leu Leu Phe Leu Lys Ser Thr Asn Ala Gly Pro Ala Pro His Pro
705                 710                 715                 720
Asn Lys Gln Leu Ala Ala Tyr Gly Arg Val Arg Asn Val Gly Val Gly
                725                 730                 735
Ala Thr Gln Gln Leu Thr Leu Thr Val Asn Leu Gly Ser Leu Ala Arg
            740                 745                 750
Ala Asp Thr Asn Gly Asp Arg Trp Ile Tyr Pro Gly Ala Tyr Thr Leu
        755                 760                 765
Ile Leu Asp Val Asn Gly Pro Leu Thr Phe Asn Phe Thr Leu Thr Gly
    770                 775                 780
Thr Ala Thr Lys Ile Ser Thr Leu Pro Ser Arg Ser
785                 790                 795


<210> 737
<211> 796
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 3 [Trichoderma reesei
      QM6a] 796 aa protein XP_6963621.1 GI:58913197

<400> 737
Met Arg Val Asn Val Pro Leu His Ala Leu Gln Ile Ala Ala Arg Ser
 1               5                  10                  15
Val Ala Ala Ala Ile Cys Lys Ser Ser Ser Ala Ser Gly Arg Ser Leu
            20                  25                  30
Arg Gly Gly Lys Ile Asp Gln Ala Ser Arg Ile Asn Ile Tyr Ser Ile
        35                  40                  45
Ser Asn Pro Ser Pro Asn Pro Pro Leu Thr Pro Ser Phe Pro Asp Cys
    50                  55                  60
Thr Arg Asp Pro Leu Cys Ser Asn Asp Val Cys Asp Thr Thr Lys Ser
65                  70                  75                  80
Ile Ala Glu Arg Ala Ala Ala Ile Val Lys Pro Met Thr Leu Asn Glu
                85                  90                  95
Lys Val Ala Asn Val Gly Ser Ser Ala Ser Gly Ser Ala Arg Leu Gly
            100                 105                 110
Leu Pro Ala Tyr Gln Trp Gln Asn Glu Ala Leu His Gly Val Ala Gly
        115                 120                 125
Ser Thr Gly Val Gln Phe Gln Ser Pro Leu Gly Ala Asn Phe Ser Ala
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```
    130                 135                 140
Ala Thr Ser Phe Pro Met Pro Ile Leu Leu Ser Ala Ala Phe Asp Asp
145                 150                 155                 160
Ala Leu Val Lys Ser Val Ala Thr Ala Ile Ser Thr Glu Ala Arg Ala
                165                 170                 175
Phe Ala Asn Tyr Gly Phe Ala Gly Leu Asp Phe Trp Thr Pro Asn Ile
            180                 185                 190
Asn Pro Phe Arg Asp Pro Arg Trp Gly Arg Gly Met Glu Thr Pro Gly
        195                 200                 205
Glu Asp Ala Phe Arg Ile Gln Gly Tyr Val Leu Ala Leu Val Asp Gly
    210                 215                 220
Leu Gln Gly Gly Ile Asp Pro Asp Phe Tyr Arg Thr Leu Ser Thr Cys
225                 230                 235                 240
Lys His Phe Ala Ala Tyr Asp Ile Glu Asn Gly Arg Thr Ala Asn Asn
                245                 250                 255
Leu Ser Pro Thr Gln Gln Asp Met Ala Asp Tyr Tyr Leu Pro Met Phe
            260                 265                 270
Glu Thr Cys Val Arg Asp Ala Lys Val Ala Ser Ile Met Cys Ala Tyr
        275                 280                 285
Asn Ala Val Asp Gly Val Pro Ala Cys Ala Asp Ser Tyr Leu Leu Gln
    290                 295                 300
Asp Val Leu Arg Asp Thr Tyr Gly Phe Thr Glu Asp Phe Asn Tyr Val
305                 310                 315                 320
Val Ser Asp Cys Asp Ala Val Glu Asn Val Phe Asp Pro His His Tyr
                325                 330                 335
Ala Ala Asn Leu Thr Gln Ala Ala Ala Met Ser Ile Asn Ala Gly Thr
            340                 345                 350
Asp Leu Asp Cys Gly Ser Ser Tyr Asn Val Leu Asn Ala Ser Val Gln
        355                 360                 365
Ala Gly Leu Thr Thr Glu Ala Thr Leu Asp Lys Ser Leu Ile Arg Leu
    370                 375                 380
Tyr Ser Ala Leu Val Lys Val Gly Tyr Phe Asp Gln Pro Ala Glu Tyr
385                 390                 395                 400
Asn Ser Leu Gly Trp Gly Asn Val Asn Thr Thr Gln Ser Gln Ala Leu
                405                 410                 415
Ala His Asp Ala Ala Thr Glu Gly Met Thr Leu Leu Lys Asn Asp Gly
            420                 425                 430
Thr Leu Pro Leu Ser Arg Thr Leu Ser Asn Val Ala Val Ile Gly Pro
        435                 440                 445
Trp Ala Asn Val Thr Thr Gln Met Gln Gly Asn Tyr Ala Gly Thr Ala
    450                 455                 460
Pro Leu Leu Val Asn Pro Leu Ser Val Phe Gln Gln Lys Trp Arg Asn
465                 470                 475                 480
Val Lys Tyr Ala Gln Gly Thr Ala Ile Asn Ser Gln Asp Thr Ser Gly
                485                 490                 495
Phe Asn Ala Ala Leu Ser Ala Ala Ser Ser Ser Asp Val Ile Val Tyr
            500                 505                 510
Leu Gly Gly Ile Asp Ile Ser Val Glu Asn Glu Gly Phe Asp Arg Ser
        515                 520                 525
Ser Ile Thr Trp Pro Gly Asn Gln Leu Asn Leu Ile Ser Gln Leu Ala
    530                 535                 540
Asn Leu Gly Lys Pro Leu Val Ile Val Gln Phe Gly Gly Gly Gln Ile
545                 550                 555                 560
Asp Asp Ser Ala Leu Leu Ser Asn Ser Lys Val Asn Ser Ile Leu Trp
```

```
                565                 570                 575
Ala Gly Tyr Pro Gly Gln Asp Gly Gly Asn Ala Ile Phe Asp Val Leu
            580                 585                 590
Thr Gly Ala Asn Pro Pro Ala Gly Arg Leu Pro Val Thr Gln Tyr Pro
        595                 600                 605
Ala Asn Tyr Val Asn Asn Asn Asn Ile Gln Asp Met Asn Leu Arg Pro
    610                 615                 620
Ser Asn Gly Ile Pro Gly Arg Thr Tyr Ala Trp Tyr Thr Gly Thr Pro
625                 630                 635                 640
Val Leu Pro Phe Gly Tyr Gly Leu His Tyr Thr Asn Phe Ser Leu Ser
                645                 650                 655
Phe Gln Ser Thr Lys Thr Ala Gly Ser Asp Ile Ala Thr Leu Val Asn
            660                 665                 670
Asn Ala Gly Ser Asn Lys Asp Leu Ala Thr Phe Ala Thr Ile Val Val
        675                 680                 685
Asn Val Lys Asn Thr Gly Gly Lys Ala Asn Leu Ala Ser Asp Tyr Val
    690                 695                 700
Gly Leu Leu Phe Leu Lys Ser Thr Asn Ala Gly Pro Ala Pro His Pro
705                 710                 715                 720
Asn Lys Gln Leu Ala Ala Tyr Gly Arg Val Arg Asn Val Gly Val Gly
                725                 730                 735
Ala Thr Gln Gln Leu Thr Leu Thr Val Asn Leu Gly Ser Leu Ala Arg
            740                 745                 750
Ala Asp Thr Asn Gly Asp Arg Trp Ile Tyr Pro Gly Ala Tyr Thr Leu
        755                 760                 765
Ile Leu Asp Val Asn Gly Pro Leu Thr Phe Asn Phe Thr Leu Thr Gly
    770                 775                 780
Thr Ala Thr Lys Ile Ser Thr Leu Pro Ser Arg Ser
785                 790                 795


<210> 738
<211> 797
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 3 [Trichoderma reesei
      QM6a] 797 aa protein XP_696475.1 GI:5891415

<400> 738
Met Val Asn Asn Ala Ala Leu Leu Ala Ala Leu Ser Ala Leu Leu Pro
 1               5                  10                  15
Thr Ala Leu Ala Gln Asn Asn Gln Thr Tyr Ala Asn Tyr Ser Ala Gln
            20                  25                  30
Gly Gln Pro Asp Leu Tyr Pro Glu Thr Leu Ala Thr Leu Thr Leu Ser
        35                  40                  45
Phe Pro Asp Cys Glu His Gly Pro Leu Lys Asn Asn Leu Val Cys Asp
    50                  55                  60
Ser Ser Ala Gly Tyr Val Glu Arg Ala Gln Ala Leu Ile Ser Leu Phe
65                  70                  75                  80
Thr Leu Glu Glu Leu Ile Leu Asn Thr Gln Asn Ser Gly Pro Gly Val
                85                  90                  95
Pro Arg Leu Gly Leu Pro Asn Tyr Gln Val Trp Asn Glu Ala Leu His
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```
            100                 105                 110
Gly Leu Asp Arg Ala Asn Phe Ala Thr Lys Gly Gly Gln Phe Glu Trp
        115                 120                 125
Ala Thr Ser Phe Pro Met Pro Ile Leu Thr Thr Ala Ala Leu Asn Arg
    130                 135                 140
Thr Leu Ile His Gln Ile Ala Asp Ile Ile Ser Thr Gln Ala Arg Ala
145                 150                 155                 160
Phe Ser Asn Ser Gly Arg Tyr Gly Leu Asp Val Tyr Ala Pro Asn Val
                165                 170                 175
Asn Gly Phe Arg Ser Pro Leu Trp Gly Arg Gly Gln Glu Thr Pro Gly
            180                 185                 190
Glu Asp Ala Phe Phe Leu Ser Ser Ala Tyr Thr Tyr Glu Tyr Ile Thr
        195                 200                 205
Gly Ile Gln Gly Gly Val Asp Pro Glu His Leu Lys Val Ala Ala Thr
    210                 215                 220
Val Lys His Phe Ala Gly Tyr Asp Leu Glu Asn Trp Asn Asn Gln Ser
225                 230                 235                 240
Arg Leu Gly Phe Asp Ala Ile Ile Thr Gln Gln Asp Leu Ser Glu Tyr
                245                 250                 255
Tyr Thr Pro Gln Phe Leu Ala Ala Ala Arg Tyr Ala Lys Ser Arg Ser
            260                 265                 270
Leu Met Cys Ala Tyr Asn Ser Val Asn Gly Val Pro Ser Cys Ala Asn
        275                 280                 285
Ser Phe Phe Leu Gln Thr Leu Leu Arg Glu Ser Trp Gly Phe Pro Glu
    290                 295                 300
Trp Gly Tyr Val Ser Ser Asp Cys Asp Ala Val Tyr Asn Val Phe Asn
305                 310                 315                 320
Pro His Asp Tyr Ala Ser Asn Gln Ser Ser Ala Ala Ala Ser Ser Leu
                325                 330                 335
Arg Ala Gly Thr Asp Ile Asp Cys Gly Gln Thr Tyr Pro Trp His Leu
            340                 345                 350
Asn Glu Ser Phe Val Ala Gly Glu Val Ser Arg Gly Glu Ile Glu Arg
        355                 360                 365
Ser Val Thr Arg Leu Tyr Ala Asn Leu Val Arg Leu Gly Tyr Phe Asp
    370                 375                 380
Lys Lys Asn Gln Tyr Arg Ser Leu Gly Trp Lys Asp Val Val Lys Thr
385                 390                 395                 400
Asp Ala Trp Asn Ile Ser Tyr Glu Ala Ala Val Glu Gly Ile Val Leu
                405                 410                 415
Leu Lys Asn Asp Gly Thr Leu Pro Leu Ser Lys Lys Val Arg Ser Ile
            420                 425                 430
Ala Leu Ile Gly Pro Trp Ala Asn Ala Thr Thr Gln Met Gln Gly Asn
        435                 440                 445
Tyr Tyr Gly Pro Ala Pro Tyr Leu Ile Ser Pro Leu Glu Ala Ala Lys
    450                 455                 460
Lys Ala Gly Tyr His Val Asn Phe Glu Leu Gly Thr Glu Ile Ala Gly
465                 470                 475                 480
Asn Ser Thr Thr Gly Phe Ala Lys Ala Ile Ala Ala Ala Lys Lys Ser
                485                 490                 495
Asp Ala Ile Ile Tyr Leu Gly Gly Ile Asp Asn Thr Ile Glu Gln Glu
            500                 505                 510
Gly Ala Asp Arg Thr Asp Ile Ala Trp Pro Gly Asn Gln Leu Asp Leu
        515                 520                 525
Ile Lys Gln Leu Ser Glu Val Gly Lys Pro Leu Val Val Leu Gln Met
```

```
    530                 535                 540
Gly Gly Gly Gln Val Asp Ser Ser Ser Leu Lys Ser Asn Lys Lys Val
545                 550                 555                 560
Asn Ser Leu Val Trp Gly Gly Tyr Pro Gly Gln Ser Gly Gly Val Ala
                565                 570                 575
Leu Phe Asp Ile Leu Ser Gly Lys Arg Ala Pro Ala Gly Arg Leu Val
            580                 585                 590
Thr Thr Gln Tyr Pro Ala Glu Tyr Val His Gln Phe Pro Gln Asn Asp
        595                 600                 605
Met Asn Leu Arg Pro Asp Gly Lys Ser Asn Pro Gly Gln Thr Tyr Ile
    610                 615                 620
Trp Tyr Thr Gly Lys Pro Val Tyr Glu Phe Gly Ser Gly Leu Phe Tyr
625                 630                 635                 640
Thr Thr Phe Lys Glu Thr Leu Ala Ser His Pro Lys Ser Leu Lys Phe
                645                 650                 655
Asn Thr Ser Ser Ile Leu Ser Ala Pro His Pro Gly Tyr Thr Tyr Ser
            660                 665                 670
Glu Gln Ile Pro Val Phe Thr Phe Glu Ala Asn Ile Lys Asn Ser Gly
        675                 680                 685
Lys Thr Glu Ser Pro Tyr Thr Ala Met Leu Phe Val Arg Thr Ser Asn
    690                 695                 700
Ala Gly Pro Ala Pro Tyr Pro Asn Lys Trp Leu Val Gly Phe Asp Arg
705                 710                 715                 720
Leu Ala Asp Ile Lys Pro Gly His Ser Ser Lys Leu Ser Ile Pro Ile
                725                 730                 735
Pro Val Ser Ala Leu Ala Arg Val Asp Ser His Gly Asn Arg Ile Val
            740                 745                 750
Tyr Pro Gly Lys Tyr Glu Leu Ala Leu Asn Thr Asp Glu Ser Val Lys
        755                 760                 765
Leu Glu Phe Glu Leu Val Gly Glu Glu Val Thr Ile Glu Asn Trp Pro
    770                 775                 780
Leu Glu Glu Gln Gln Ile Lys Asp Ala Thr Pro Asp Ala
785                 790                 795


<210> 739
<211> 553
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 43 [Trichoderma reesei
      QM6a] 553 aa protein XP_6964816.1 GI:58915587

<400> 739
Met Pro Leu Ile Arg Asn Pro Ile Leu Pro Gly Phe Asn Ala Asp Pro
 1               5                  10                  15
Ser Ile Val Arg Val Gly Ser Asp Tyr Tyr Ile Ala Thr Ser Thr Phe
            20                  25                  30
Glu Trp Tyr Pro Gly Val Gln Ile His His Ser Thr Asp Leu Ala Asn
        35                  40                  45
Trp Glu Leu Ala Val Arg Pro Leu Ser Arg Arg Ser Gln Leu Asp Leu
    50                  55                  60
Arg Gly Glu Pro Asp Ser Cys Gly Val Trp Ala Pro Cys Leu Thr His
```

```
65                  70                  75                  80
Asp Gly Asp Lys Phe Trp Leu Val Tyr Thr Asp Val Lys Arg Lys Asp
                85                  90                  95
Gly Ser Phe Lys Asp Thr His Asn Tyr Ile Val Thr Ala Pro Arg Ile
            100                 105                 110
Glu Gly Pro Trp Ser Asp Pro Val Tyr Ala Asn Ser Ser Gly Phe Asp
        115                 120                 125
Pro Ser Leu Phe His Asp Asp Asp Gly Arg Lys Trp Leu Val Asn Met
    130                 135                 140
Val Gln Asp His Arg Ala Arg Pro Arg Thr Phe Ala Gly Ile Ala Leu
145                 150                 155                 160
Gln Glu Phe Asp Pro Ala Gln Gly Lys Leu Val Gly Thr Arg Lys Val
                165                 170                 175
Val Phe His Gly Ser Glu Leu Gly Leu Val Glu Gly Pro His Leu Tyr
            180                 185                 190
Lys Arg Asn Gly Trp Tyr Tyr Leu Leu Thr Ala Glu Gly Gly Thr Gly
        195                 200                 205
Tyr Thr His Ala Ala Thr Leu Ala Arg Ser Arg Ser Ile Trp Gly Pro
    210                 215                 220
Tyr Glu Leu His Pro Gln Gln His Ile Leu Thr Ser Lys Asp His Pro
225                 230                 235                 240
Phe Ala Ala Leu Gln Arg Ala Gly His Ala Asp Ile Val Glu Thr Ala
                245                 250                 255
Asp Gly Lys Thr Tyr Leu Val His Leu Ala Gly Arg Pro Ile Gly Gln
            260                 265                 270
Lys Arg Arg Cys Val Leu Gly Arg Glu Thr Ala Leu Gln Glu Ala Tyr
        275                 280                 285
Trp Gly Glu Asp Asp Trp Leu Tyr Val Lys Asn Gly Pro Val Pro Ser
    290                 295                 300
Leu Asp Val Glu Val Pro Gly Val Arg Asp Glu Glu Ala Tyr Trp Lys
305                 310                 315                 320
Glu Lys Arg Tyr Glu Phe His Asp Gly Leu His Lys Asp Phe Gln Trp
                325                 330                 335
Leu Arg Thr Pro Glu Pro Glu Arg Leu Phe Ala Ile Glu Asp Gly Lys
            340                 345                 350
Leu Val Leu Thr Gly Arg Glu Ser Ile Gly Ser Trp Phe Glu Gln Ser
        355                 360                 365
Leu Val Ala Arg Arg Gln Thr His Phe Ser Phe Asp Ala Glu Thr Val
    370                 375                 380
Ile Asp Phe Ser Pro Glu Asp Glu Arg Gln Phe Ala Gly Leu Thr Leu
385                 390                 395                 400
Tyr Tyr Ser Arg Tyr Asn Phe Phe Tyr Leu Ala Val Ser Ala His Ser
                405                 410                 415
Asp Gly Arg Arg Glu Val Gln Ile Leu Arg Ser Glu Ala Ser Trp Pro
            420                 425                 430
Asn Gly Lys Leu Glu Asp Val Gly Ala Asn Ala Cys Tyr Val Arg Ile
        435                 440                 445
Pro Gln Gln Gly Arg Val Lys Leu Ala Ala Thr Ile Arg Gly Glu Arg
    450                 455                 460
Leu Gln Phe Tyr Tyr Ala Leu Val Ala Glu Gly Gly Glu Glu Gln Glu
465                 470                 475                 480
Glu Leu Gln Arg Ile Gly Pro Val Leu Asp Ala Ser Ile Val Ser Asp
                485                 490                 495
Glu Cys Gly Gly His Gln Ala His Gly Ser Phe Thr Gly Ser Phe Val
```

```
            500                 505                 510
Gly Val Ala Cys Ser Asp Val Asn Gly Thr Glu Lys Arg Ala Val Phe
        515                 520                 525
Asp Tyr Phe Val Tyr Arg Pro Ala His Asp Ser Thr Asp Arg Tyr Ser
    530                 535                 540
Val Ser Met Glu Gly Ile Gln Arg Val
545                 550


<210> 740
<211> 553
<212> PRT
<213> Artificial Sequence

<220>
<223> family 43 glycoside hydrolase [Trichoderma reesei
      RUT C-3] 553 aa protein ETS2497.1 GI:572279375

<400> 740
Met Pro Leu Ile Arg Asn Pro Ile Leu Pro Gly Phe Asn Ala Asp Pro
 1               5                  10                  15
Ser Ile Val Arg Val Gly Ser Asp Tyr Tyr Ile Ala Thr Ser Thr Phe
            20                  25                  30
Glu Trp Tyr Pro Gly Val Gln Ile His His Ser Thr Asp Leu Ala Asn
        35                  40                  45
Trp Glu Leu Ala Val Arg Pro Leu Ser Arg Arg Ser Gln Leu Asp Leu
    50                  55                  60
Arg Gly Glu Pro Asp Ser Cys Gly Val Trp Ala Pro Cys Leu Thr His
65                  70                  75                  80
Asp Gly Asp Lys Phe Trp Leu Val Tyr Thr Asp Val Lys Arg Lys Asp
                85                  90                  95
Gly Ser Phe Lys Asp Thr His Asn Tyr Ile Val Thr Ala Pro Arg Ile
            100                 105                 110
Glu Gly Pro Trp Ser Asp Pro Val Tyr Ala Asn Ser Ser Gly Phe Asp
        115                 120                 125
Pro Ser Leu Phe His Asp Asp Asp Gly Arg Lys Trp Leu Val Asn Met
    130                 135                 140
Val Gln Asp His Arg Ala Arg Pro Arg Thr Phe Ala Gly Ile Ala Leu
145                 150                 155                 160
Gln Glu Phe Asp Pro Ala Gln Gly Lys Leu Val Gly Thr Arg Lys Val
                165                 170                 175
Val Phe His Gly Ser Glu Leu Gly Leu Val Glu Gly Pro His Leu Tyr
            180                 185                 190
Lys Arg Asn Gly Trp Tyr Tyr Leu Leu Thr Ala Glu Gly Gly Thr Gly
        195                 200                 205
Tyr Thr His Ala Ala Thr Leu Ala Arg Ser Arg Ser Ile Trp Gly Pro
    210                 215                 220
Tyr Glu Leu His Pro Gln Gln His Ile Leu Thr Ser Lys Asp His Pro
225                 230                 235                 240
Phe Ala Ala Leu Gln Arg Ala Gly His Ala Asp Ile Val Glu Thr Ala
                245                 250                 255
Asp Gly Lys Thr Tyr Leu Val His Leu Ala Gly Arg Pro Ile Gly Gln
            260                 265                 270
Lys Arg Arg Cys Val Leu Gly Arg Glu Thr Ala Leu Gln Glu Ala Tyr
```

```
        275                 280                 285
Trp Gly Glu Asp Asp Trp Leu Tyr Val Lys Asn Gly Pro Val Pro Ser
    290                 295                 300
Leu Asp Val Glu Val Pro Gly Val Arg Asp Glu Glu Ala Tyr Trp Lys
305                 310                 315                 320
Glu Lys Arg Tyr Glu Phe His Asp Gly Leu His Lys Asp Phe Gln Trp
                325                 330                 335
Leu Arg Thr Pro Glu Pro Glu Arg Leu Phe Ala Ile Glu Asp Gly Lys
            340                 345                 350
Leu Val Leu Thr Gly Arg Glu Ser Ile Gly Ser Trp Phe Glu Gln Ser
        355                 360                 365
Leu Val Ala Arg Arg Gln Thr His Phe Ser Phe Asp Ala Glu Thr Val
    370                 375                 380
Ile Asp Phe Ser Pro Glu Asp Glu Arg Gln Phe Ala Gly Leu Thr Leu
385                 390                 395                 400
Tyr Tyr Ser Arg Tyr Asn Phe Phe Tyr Leu Ala Val Ser Ala His Ser
                405                 410                 415
Asp Gly Arg Arg Glu Val Gln Ile Leu Arg Ser Glu Ala Ser Trp Pro
            420                 425                 430
Asn Gly Lys Leu Glu Asp Val Gly Ala Asn Ala Cys Tyr Val Arg Ile
        435                 440                 445
Pro Gln Gln Gly Arg Val Lys Leu Ala Ala Thr Ile Arg Gly Glu Arg
    450                 455                 460
Leu Gln Phe Tyr Tyr Ala Leu Val Ala Glu Gly Gly Glu Glu Gln Glu
465                 470                 475                 480
Glu Leu Gln Arg Ile Gly Pro Val Leu Asp Ala Ser Ile Val Ser Asp
                485                 490                 495
Glu Cys Gly Gly His Gln Ala His Gly Ser Phe Thr Gly Ser Phe Val
            500                 505                 510
Gly Val Ala Cys Ser Asp Val Asn Gly Thr Glu Lys Arg Ala Val Phe
        515                 520                 525
Asp Tyr Phe Val Tyr Arg Pro Ala His Asp Ser Thr Asp Arg Tyr Ser
    530                 535                 540
Val Ser Met Glu Gly Ile Gln Arg Val
545                 550


<210> 741
<211> 797
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-xylosidase [Trichoderma reesei RUT C-3] 797
      aa protein ETS3193.1 GI:5722896

<400> 741
Met Val Asn Asn Ala Ala Leu Leu Ala Ala Leu Ser Ala Leu Leu Pro
 1               5                  10                  15
Thr Ala Leu Ala Gln Asn Asn Gln Thr Tyr Ala Asn Tyr Ser Ala Gln
            20                  25                  30
Gly Gln Pro Asp Leu Tyr Pro Glu Thr Leu Ala Thr Leu Thr Leu Ser
        35                  40                  45
Phe Pro Asp Cys Glu His Gly Pro Leu Lys Asn Asn Leu Val Cys Asp
```

```
    50                  55                  60
Ser Ser Ala Gly Tyr Val Glu Arg Ala Gln Ala Leu Ile Ser Leu Phe
65                  70                  75                  80
Thr Leu Glu Glu Leu Ile Leu Asn Thr Gln Asn Ser Gly Pro Gly Val
                85                  90                  95
Pro Arg Leu Gly Leu Pro Asn Tyr Gln Val Trp Asn Glu Ala Leu His
            100                 105                 110
Gly Leu Asp Arg Ala Asn Phe Ala Thr Lys Gly Gly Gln Phe Glu Trp
        115                 120                 125
Ala Thr Ser Phe Pro Met Pro Ile Leu Thr Thr Ala Ala Leu Asn Arg
    130                 135                 140
Thr Leu Ile His Gln Ile Ala Asp Ile Ile Ser Thr Gln Ala Arg Ala
145                 150                 155                 160
Phe Ser Asn Ser Gly Arg Tyr Gly Leu Asp Val Tyr Ala Pro Asn Val
                165                 170                 175
Asn Gly Phe Arg Ser Pro Leu Trp Gly Arg Gly Gln Glu Thr Pro Gly
            180                 185                 190
Glu Asp Ala Phe Phe Leu Ser Ser Ala Tyr Thr Tyr Glu Tyr Ile Thr
        195                 200                 205
Gly Ile Gln Gly Gly Val Asp Pro Glu His Leu Lys Val Ala Ala Thr
    210                 215                 220
Val Lys His Phe Ala Gly Tyr Asp Leu Glu Asn Trp Asn Asn Gln Ser
225                 230                 235                 240
Arg Leu Gly Phe Asp Ala Ile Ile Thr Gln Gln Asp Leu Ser Glu Tyr
                245                 250                 255
Tyr Thr Pro Gln Phe Leu Ala Ala Ala Arg Tyr Ala Lys Ser Arg Ser
            260                 265                 270
Leu Met Cys Ala Tyr Asn Ser Val Asn Gly Val Pro Ser Cys Ala Asn
        275                 280                 285
Ser Phe Phe Leu Gln Thr Leu Leu Arg Glu Ser Trp Gly Phe Pro Glu
    290                 295                 300
Trp Gly Tyr Val Ser Ser Asp Cys Asp Ala Val Tyr Asn Val Phe Asn
305                 310                 315                 320
Pro His Asp Tyr Ala Ser Asn Gln Ser Ser Ala Ala Ala Ser Ser Leu
                325                 330                 335
Arg Ala Gly Thr Asp Ile Asp Cys Gly Gln Thr Tyr Pro Trp His Leu
            340                 345                 350
Asn Glu Ser Phe Val Ala Gly Glu Val Ser Arg Gly Glu Ile Glu Arg
        355                 360                 365
Ser Val Thr Arg Leu Tyr Ala Asn Leu Val Arg Leu Gly Tyr Phe Asp
    370                 375                 380
Lys Lys Asn Gln Tyr Arg Ser Leu Gly Trp Lys Asp Val Val Lys Thr
385                 390                 395                 400
Asp Ala Trp Asn Ile Ser Tyr Glu Ala Ala Val Glu Gly Ile Val Leu
                405                 410                 415
Leu Lys Asn Asp Gly Thr Leu Pro Leu Ser Lys Lys Val Arg Ser Ile
            420                 425                 430
Ala Leu Ile Gly Pro Trp Ala Asn Ala Thr Thr Gln Met Gln Gly Asn
        435                 440                 445
Tyr Tyr Gly Pro Ala Pro Tyr Leu Ile Ser Pro Leu Glu Ala Ala Lys
    450                 455                 460
Lys Ala Gly Tyr His Val Asn Phe Glu Leu Gly Thr Glu Ile Ala Gly
465                 470                 475                 480
Asn Ser Thr Thr Gly Phe Ala Lys Ala Ile Ala Ala Ala Lys Lys Ser
```

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


<210> 742
<211> 860
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase [Trichoderma reesei RUT C-3] 8
      aa protein ETS3636.1 GI:57228576

<400> 742
Met Ala Leu Phe His Leu Ala Gln Ala Arg Thr Cys Leu Pro Pro Tyr
 1               5                  10                  15
Gln Ala Gln Thr Thr Tyr Gln Gly Cys Tyr His Asp Pro Asn Ser Pro
```

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

```
    450                 455                 460
Asn Ser Leu Gly Trp Gly Asn Val Asn Thr Thr Gln Ser Gln Ala Leu
465                 470                 475                 480
Ala His Asp Ala Ala Thr Glu Gly Met Thr Leu Leu Lys Asn Asp Gly
                485                 490                 495
Thr Leu Pro Leu Ser Arg Thr Leu Ser Asn Val Ala Val Ile Gly Pro
            500                 505                 510
Trp Ala Asn Val Thr Thr Gln Met Gln Gly Asn Tyr Ala Gly Thr Ala
        515                 520                 525
Pro Leu Leu Val Asn Pro Leu Ser Val Phe Gln Gln Lys Trp Arg Asn
    530                 535                 540
Val Lys Tyr Ala Gln Gly Thr Ala Ile Asn Ser Gln Asp Thr Ser Gly
545                 550                 555                 560
Phe Asn Ala Ala Leu Ser Ala Ala Ser Ser Ser Asp Val Ile Val Tyr
                565                 570                 575
Leu Gly Gly Ile Asp Ile Ser Val Glu Asn Glu Gly Phe Asp Arg Ser
            580                 585                 590
Ser Ile Thr Trp Pro Gly Asn Gln Leu Asn Leu Ile Ser Gln Leu Ala
        595                 600                 605
Asn Leu Gly Lys Pro Leu Val Ile Val Gln Phe Gly Gly Gly Gln Ile
    610                 615                 620
Asp Asp Ser Ala Leu Leu Ser Asn Ser Lys Val Asn Ser Ile Leu Trp
625                 630                 635                 640
Ala Gly Tyr Pro Gly Gln Asp Gly Gly Asn Ala Ile Phe Asp Val Leu
                645                 650                 655
Thr Gly Ala Asn Pro Pro Ala Gly Arg Leu Pro Val Thr Gln Tyr Pro
            660                 665                 670
Ala Asn Tyr Val Asn Asn Asn Asn Ile Gln Asp Met Asn Leu Arg Pro
        675                 680                 685
Ser Asn Gly Ile Pro Gly Arg Thr Tyr Ala Trp Tyr Thr Gly Thr Pro
    690                 695                 700
Val Leu Pro Phe Gly Tyr Gly Leu His Tyr Thr Asn Phe Ser Leu Ser
705                 710                 715                 720
Phe Gln Ser Thr Lys Thr Ala Gly Ser Asp Ile Ala Thr Leu Val Asn
                725                 730                 735
Asn Ala Gly Ser Asn Lys Asp Leu Ala Thr Phe Ala Thr Ile Val Val
            740                 745                 750
Asn Val Lys Asn Thr Gly Gly Lys Ala Asn Leu Ala Ser Asp Tyr Val
        755                 760                 765
Gly Leu Leu Phe Leu Lys Ser Thr Asn Ala Gly Pro Ala Pro His Pro
    770                 775                 780
Asn Lys Gln Leu Ala Ala Tyr Gly Arg Val Arg Asn Val Gly Val Gly
785                 790                 795                 800
Ala Thr Gln Gln Leu Thr Leu Thr Val Asn Leu Gly Ser Leu Ala Arg
                805                 810                 815
Ala Asp Thr Asn Gly Asp Arg Trp Ile Tyr Pro Gly Ala Tyr Thr Leu
            820                 825                 830
Ile Leu Asp Val Asn Gly Pro Leu Thr Phe Asn Phe Thr Leu Thr Gly
        835                 840                 845
Thr Ala Thr Lys Ile Ser Thr Leu Pro Ser Arg Ser
    850                 855                 860
```

<210> 743

<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, The Three-Dimensional Crystal Structure
Of The Catalytic Core Of Cellobiohydrolase I From
Trichoderma Reesei 434 aa protein 1CEL_B GI:89287

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 743
Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe Val
                85                  90                  95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
            100                 105                 110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
        115                 120                 125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
    130                 135                 140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145                 150                 155                 160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                165                 170                 175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
            180                 185                 190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
        195                 200                 205
Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
    210                 215                 220
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly
225                 230                 235                 240
Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys
                245                 250                 255
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
            260                 265                 270
Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
        275                 280                 285
Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr
    290                 295                 300
Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser

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

<210> 744
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, The Three- Dimensional Crystal Structure
Of The Catalytic Core Of Cellobiohydrolase I From
Trichoderma Reesei 434 aa protein 1CEL_A GI:89286

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 744
Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
1 5 10 15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
20 25 30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
35 40 45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
50 55 60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65 70 75 80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe Val
85 90 95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
100 105 110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
115 120 125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
130 135 140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr

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

<210> 745
<211> 365
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Three-Dimensional Structure Of
Cellobiohydrolase From Trichoderma Reesei 365 aa
protein 3CBH_A GI:157836775

<400> 745

```
Ser Gly Thr Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro
 1               5                  10                  15
Trp Ala Asn Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro
            20                  25                  30
```

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

<210> 746
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> 2CBH_A GI:157834734

<400> 746
Thr Gln Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro

```
 1               5                  10                  15
Thr Val Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr
            20                  25                  30
Ser Gln Cys Leu
        35
```

<210> 747
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Three-Dimensional Structures Of Three Engineered Cellulose- Binding Domains Of Cellobiohydrolase I From Trichoderma Reesei, Nmr, 19 Structures 36 aa protein 1AZK_A GI:15783159

<400> 747

```
Thr Gln Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro
 1               5                  10                  15
Thr Val Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Ala
            20                  25                  30
Ser Gln Cys Leu
        35
```

<210> 748
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Three-Dimensional Structures Of Three Engineered Cellulose-Binding Domains Of Cellobiohydrolase I From Trichoderma Reesei, Nmr, 18 Structures 36 aa protein 1AZJ_A GI:15783158

<400> 748

```
Thr Gln Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro
 1               5                  10                  15
Thr Val Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Ala
            20                  25                  30
Ser Gln Cys Leu Thr Gln Ser His Tyr Gly Gln Cys Gly Gly Ile Gly
        35                  40                  45
Tyr Ser Gly Pro Thr Val Cys Ala Ser Gly Thr Thr Cys Gln Val Leu
    50                  55                  60
Asn Pro Ala Tyr Ser Gln Cys Leu
65                  70
```

<210> 749
<211> 36
<212> PRT

<213> Artificial Sequence

<220>
<223> Chain A, Three-Dimensional Structures Of Three
Engineered Cellulose-Binding Domains Of
Cellobiohydrolase I From Trichoderma Reesei, Nmr,
14 Structures 36 aa protein 1AZH_A GI:15783156

<400> 749
Thr Gln Ser His Ala Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro
1 5 10 15
Thr Val Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr
20 25 30
Ser Gln Cys Leu
35

<210> 750
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Three-Dimensional Structures Of Three
Engineered Cellulose-Binding Domains Of
Cellobiohydrolase I From Trichoderma Reesei, Nmr,
23 Structures 36 aa protein 1AZ6_A GI:15783153

<400> 750
Thr Gln Ser His Ala Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro
1 5 10 15
Thr Val Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr
20 25 30
Ser Gln Cys Leu
35

<210> 751
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> cellobiohydrolase II [Trichoderma reesei] 471 aa
protein AAA3421.1 GI:17541

<400> 751
Met Ile Val Gly Ile Leu Thr Thr Leu Ala Thr Leu Ala Thr Leu Ala
1 5 10 15
Ala Ser Val Pro Leu Glu Glu Arg Gln Ala Cys Ser Ser Val Trp Gly
20 25 30
Gln Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly
35 40 45
Ser Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Gly

```
    50                  55                  60
Ala Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg
65                  70                  75                  80
Val Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly
                85                  90                  95
Ser Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr
            100                 105                 110
Ser Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr
        115                 120                 125
Ala Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met
    130                 135                 140
Ala Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu
145                 150                 155                 160
Asp Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile
                165                 170                 175
Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val
            180                 185                 190
Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu
        195                 200                 205
Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp
    210                 215                 220
Thr Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu
225                 230                 235                 240
Val Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr
                245                 250                 255
Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr
            260                 265                 270
Ala Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala
        275                 280                 285
Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala
    290                 295                 300
Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu
305                 310                 315                 320
Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr
                325                 330                 335
Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu
            340                 345                 350
Tyr Ile His Ala Ile Gly Pro Leu Leu Ala Asn His Gly Trp Ser Asn
        355                 360                 365
Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly
    370                 375                 380
Gln Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly
385                 390                 395                 400
Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val
                405                 410                 415
Trp Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala
            420                 425                 430
Pro Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala
        435                 440                 445
Pro Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr
    450                 455                 460
Asn Ala Asn Pro Ser Phe Leu
465                 470
```

<210> 752
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Cellobiohydrolase II core protein, CBH II
cp=3.2.1.91 [T. reesei, Peptide Partial, 38 aa]

<220>
<221> VARIANT
<222> 6, 23, 26, 27, 32
<223> Xaa = Any Amino Acid

<400> 752
Gly Ser Ala Ser Tyr Xaa Gly Asn Pro Phe Val Gly Val Ser Pro Trp
1 5 10 15
Ala Asn Ala Tyr Tyr Ala Xaa Glu Val Xaa Xaa Leu Ala Ile Pro Xaa
20 25 30
Leu Thr Gly Ala Met Ala
35

<210> 753
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> C-Terminal Domain Of Cellobiohydrolase I 1CBH_A
GI:15783535

<400> 753
Thr Gln Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro
1 5 10 15
Thr Val Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr
20 25 30
Ser Gln Cys Leu
35

<210> 754
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> cellobiohydrolase II [Trichoderma reesei] 471 aa
protein AAG3998.1 GI:11692747

<400> 754
Met Ile Val Gly Ile Leu Thr Thr Leu Ala Thr Leu Ala Thr Leu Ala
1 5 10 15

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

```
Pro Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr
    450                 455                 460
Asn Ala Asn Pro Ser Phe Leu
465                 470


<210> 755
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Cellobiohydrolase Cel7a (E223s, A224h,
      L225v, T226a, D262g) Mutant 1EGN_A  GI:14277711

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 755
Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Asp Phe Val
                85                  90                  95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
            100                 105                 110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
        115                 120                 125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
    130                 135                 140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145                 150                 155                 160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                165                 170                 175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
            180                 185                 190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
        195                 200                 205
Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Ser His
    210                 215                 220
Val Ala Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly
225                 230                 235                 240
Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys
                245                 250                 255
Asp Pro Asp Gly Cys Gly Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
```

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

<210> 756
<211> 426
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, Cellobiohydrolase Cel7a With Loop
Deletion 245-252 And Bound Non- Hydrolysable
Cellotetraose 426 aa protein
1Q2E_B GI:39654596

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 756

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

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

<210> 757
<211> 426
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Cellobiohydrolase Cel7a With Loop
Deletion 245-252 And Bound Non- Hydrolysable
Cellotetraose 426 aa protein
1Q2E_A GI:39654595

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 757
Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Asp Phe Val
                85                  90                  95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
            100                 105                 110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
        115                 120                 125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
    130                 135                 140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145                 150                 155                 160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                165                 170                 175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
            180                 185                 190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
        195                 200                 205
Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
    210                 215                 220
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly
225                 230                 235                 240
Asp Gly Cys Gly Gly Gly Thr Cys Asp Pro Asp Gly Cys Asp Trp Asn
                245                 250                 255
Pro Tyr Arg Leu Gly Asn Thr Ser Phe Tyr Gly Pro Gly Ser Ser Phe
            260                 265                 270
Thr Leu Asp Thr Thr Lys Lys Leu Thr Val Val Thr Gln Phe Glu Thr
        275                 280                 285
Ser Gly Ala Ile Asn Arg Tyr Tyr Val Gln Asn Gly Val Thr Phe Gln
    290                 295                 300
Gln Pro Asn Ala Glu Leu Gly Ser Tyr Ser Gly Asn Glu Leu Asn Asp
305                 310                 315                 320
Asp Tyr Cys Thr Ala Glu Glu Ala Glu Phe Gly Gly Ser Ser Phe Ser
                325                 330                 335
Asp Lys Gly Gly Leu Thr Gln Phe Lys Lys Ala Thr Ser Gly Gly Met
            340                 345                 350
Val Leu Val Met Ser Leu Trp Asp Asp Tyr Tyr Ala Asn Met Leu Trp
        355                 360                 365
Leu Asp Ser Thr Tyr Pro Thr Asn Glu Thr Ser Ser Thr Pro Gly Ala

```
    370                 375                 380
Val Arg Gly Ser Cys Ser Thr Ser Ser Gly Val Pro Ala Gln Val Glu
385                 390                 395                 400
Ser Gln Ser Pro Asn Ala Lys Val Thr Phe Ser Asn Ile Lys Phe Gly
                405                 410                 415
Pro Ile Gly Ser Thr Gly Asn Pro Ser Gly
            420                 425


<210> 758
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Cellobiohydrolase Cel7a With Disulphide
      Bridge Added Across Exo-Loop By Mutations D241c
      And D249c
      434 aa protein 1Q2B_A GI:39654594

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 758
Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Asp Phe Val
                85                  90                  95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
            100                 105                 110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
        115                 120                 125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
    130                 135                 140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145                 150                 155                 160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                165                 170                 175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
            180                 185                 190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
        195                 200                 205
Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
    210                 215                 220
```

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

<210> 759
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 5 [Trichoderma reesei QM6a] 438 aa protein XP_6969897.1 GI:589115749

<400> 759

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

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

<210> 760
<211> 418
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 5 [Trichoderma reesei QM6a] 418 aa protein EGR512.1 GI:3452785

<400> 760

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

<210> 761
<211> 344
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 61 [Trichoderma reesei QM6a] 344 aa protein EGR52697.1 GI:34522464

<400> 761
Met Ile Gln Lys Leu Ser Asn Leu Leu Val Thr Ala Leu Ala Val Ala
 1               5                  10                  15
Thr Gly Val Val Gly His Gly His Ile Asn Asp Ile Val Ile Asn Gly
            20                  25                  30
Val Trp Tyr Gln Ala Tyr Asp Pro Thr Thr Phe Pro Tyr Glu Ser Asn
        35                  40                  45
Pro Pro Ile Val Val Gly Trp Thr Ala Ala Asp Leu Asp Asn Gly Phe
    50                  55                  60
Val Ser Pro Asp Ala Tyr Gln Asn Pro Asp Ile Ile Cys His Lys Asn
65                  70                  75                  80
Ala Thr Asn Ala Lys Gly His Ala Ser Val Lys Ala Gly Asp Thr Ile
                85                  90                  95
Leu Phe Gln Trp Val Pro Val Pro Trp Pro His Pro Gly Pro Ile Val
            100                 105                 110
Asp Tyr Leu Ala Asn Cys Asn Gly Asp Cys Glu Thr Val Asp Lys Thr
        115                 120                 125
Thr Leu Glu Phe Phe Lys Ile Asp Gly Val Gly Leu Leu Ser Gly Gly
    130                 135                 140
Asp Pro Gly Thr Trp Ala Ser Asp Val Leu Ile Ser Asn Asn Asn Thr
145                 150                 155                 160
Trp Val Val Lys Ile Pro Asp Asn Leu Ala Pro Gly Asn Tyr Val Leu
                165                 170                 175
Arg His Glu Ile Ile Ala Leu His Ser Ala Gly Gln Ala Asn Gly Ala
            180                 185                 190
Gln Asn Tyr Pro Gln Cys Phe Asn Ile Ala Val Ser Gly Ser Gly Ser
        195                 200                 205
Leu Gln Pro Ser Gly Val Leu Gly Thr Asp Leu Tyr His Ala Thr Asp
    210                 215                 220
Pro Gly Val Leu Ile Asn Ile Tyr Thr Ser Pro Leu Asn Tyr Ile Ile
225                 230                 235                 240
Pro Gly Pro Thr Val Val Ser Gly Leu Pro Thr Ser Val Ala Gln Gly
                245                 250                 255
Ser Ser Ala Ala Thr Ala Thr Ala Ser Ala Thr Val Pro Gly Gly Gly
            260                 265                 270
Ser Gly Pro Thr Ser Arg Thr Thr Thr Thr Ala Arg Thr Thr Gln Ala
        275                 280                 285
Ser Ser Arg Pro Ser Ser Thr Pro Pro Ala Thr Thr Ser Ala Pro Ala
    290                 295                 300
Gly Gly Pro Thr Gln Thr Leu Tyr Gly Gln Cys Gly Gly Ser Gly Tyr
305                 310                 315                 320
Ser Gly Pro Thr Arg Cys Ala Pro Pro Ala Thr Cys Ser Thr Leu Asn
                325                 330                 335

Pro Tyr Tyr Ala Gln Cys Leu Asn
            340


<210> 762
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> endo-1,4-beta-glucanase V [Trichoderma reesei RUT
      C-3] 242 aa protein ETR998.1 GI:572276454

<400> 762
Met Lys Ala Thr Leu Val Leu Gly Ser Leu Ile Val Gly Ala Val Ser
 1               5                  10                  15
Ala Tyr Lys Ala Thr Thr Thr Arg Tyr Tyr Asp Gly Gln Glu Gly Ala
            20                  25                  30
Cys Gly Cys Gly Ser Ser Ser Gly Ala Phe Pro Trp Gln Leu Gly Ile
        35                  40                  45
Gly Asn Gly Val Tyr Thr Ala Ala Gly Ser Gln Ala Leu Phe Asp Thr
    50                  55                  60
Ala Gly Ala Ser Trp Cys Gly Ala Gly Cys Gly Lys Cys Tyr Gln Leu
65                  70                  75                  80
Thr Ser Thr Gly Gln Ala Pro Cys Ser Ser Cys Gly Thr Gly Gly Ala
                85                  90                  95
Ala Gly Gln Ser Ile Ile Val Met Val Thr Asn Leu Cys Pro Asn Asn
            100                 105                 110
Gly Asn Ala Gln Trp Cys Pro Val Val Gly Gly Thr Asn Gln Tyr Gly
        115                 120                 125
Tyr Ser Tyr His Phe Asp Ile Met Ala Gln Asn Glu Ile Phe Gly Asp
    130                 135                 140
Asn Val Val Val Asp Phe Glu Pro Ile Ala Cys Pro Gly Gln Ala Ala
145                 150                 155                 160
Ser Asp Trp Gly Thr Cys Leu Cys Val Gly Gln Gln Glu Thr Asp Pro
                165                 170                 175
Thr Pro Val Leu Gly Asn Asp Thr Gly Ser Thr Pro Pro Gly Ser Ser
            180                 185                 190
Pro Pro Ala Thr Ser Ser Ser Pro Pro Ser Gly Gly Gly Gln Gln Thr
        195                 200                 205
Leu Tyr Gly Gln Cys Gly Gly Ala Gly Trp Thr Gly Pro Thr Thr Cys
    210                 215                 220
Gln Ala Pro Gly Thr Cys Lys Val Gln Asn Gln Trp Tyr Ser Gln Cys
225                 230                 235                 240
Leu Pro



<210> 763
<211> 249
<212> PRT
<213> Artificial Sequence

<220>

<223> Chain A, The Structure Of A Glycoside Hydrolase
Family 61 Member, Cel61b From The Hypocrea
Jecorina 249 aa protein 2VTC_A GI:19844312

<400> 763
Met Lys Ser Cys Ala Ile Leu Ala Ala Leu Gly Cys Leu Ala Gly Ser
1 5 10 15
Val Leu Gly His Gly Gln Val Gln Asn Phe Thr Ile Asn Gly Gln Tyr
20 25 30
Asn Gln Gly Phe Ile Leu Asp Tyr Tyr Tyr Gln Lys Gln Asn Thr Gly
35 40 45
His Phe Pro Asn Val Ala Gly Trp Tyr Ala Glu Asp Leu Asp Leu Gly
50 55 60
Phe Ile Ser Pro Asp Gln Tyr Thr Thr Pro Asp Ile Val Cys His Lys
65 70 75 80
Asn Ala Ala Pro Gly Ala Ile Ser Ala Thr Ala Ala Ala Gly Ser Asn
85 90 95
Ile Val Phe Gln Trp Gly Pro Gly Val Trp Pro His Pro Tyr Gly Pro
100 105 110
Ile Val Thr Tyr Val Val Glu Cys Ser Gly Ser Cys Thr Thr Val Asn
115 120 125
Lys Asn Asn Leu Arg Trp Val Lys Ile Gln Glu Ala Gly Ile Asn Tyr
130 135 140
Asn Thr Gln Val Trp Ala Gln Gln Asp Leu Ile Asn Gln Gly Asn Lys
145 150 155 160
Trp Thr Val Lys Ile Pro Ser Ser Leu Arg Pro Gly Asn Tyr Val Phe
165 170 175
Arg His Glu Leu Leu Ala Ala His Gly Ala Ser Ser Ala Asn Gly Met
180 185 190
Gln Asn Tyr Pro Gln Cys Val Asn Ile Ala Val Thr Gly Ser Gly Thr
195 200 205
Lys Ala Leu Pro Ala Gly Thr Pro Ala Thr Gln Leu Tyr Lys Pro Thr
210 215 220
Asp Pro Gly Ile Leu Phe Asn Pro Tyr Thr Thr Ile Thr Ser Tyr Thr
225 230 235 240
Ile Pro Gly Pro Ala Leu Trp Gln Gly
245

<210> 764
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, The Structure Of A Glycoside Hydrolase
Family 61 Member, Cel61b From The Hypocrea
Jecorina 249 aa protein 2VTC_B GI:198443121

<400> 764
Met Lys Ser Cys Ala Ile Leu Ala Ala Leu Gly Cys Leu Ala Gly Ser
1 5 10 15
Val Leu Gly His Gly Gln Val Gln Asn Phe Thr Ile Asn Gly Gln Tyr
20 25 30

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

<210> 765
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<223> endoglucanase VIII [Trichoderma reesei RUT C-3]
438 aa protein ETR9685.1 GI:572273122

<400> 765

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

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

<210> 766
<211> 378
<212> PRT
<213> Artificial Sequence

<220>
<223> putative endoglucanase [Trichoderma reesei RUT C-3] 378 aa protein ETS3449.1 GI:57228352

<400> 766

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

<210> 767
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> endoglucanase VII [Trichoderma reesei RUT C-3] 249
aa protein ETS3833.1 GI:57228773

<400> 767
Met Lys Ser Cys Ala Ile Leu Ala Ala Leu Gly Cys Leu Ala Gly Ser
 1               5                  10                  15
Val Leu Gly His Gly Gln Val Gln Asn Phe Thr Ile Asn Gly Gln Tyr
            20                  25                  30
Asn Gln Gly Phe Ile Leu Asp Tyr Tyr Tyr Gln Lys Gln Asn Thr Gly
        35                  40                  45
His Phe Pro Asn Val Ala Gly Trp Tyr Ala Glu Asp Leu Asp Leu Gly
    50                  55                  60
Phe Ile Ser Pro Asp Gln Tyr Thr Thr Pro Asp Ile Val Cys His Lys
65                  70                  75                  80
Asn Ala Ala Pro Gly Ala Ile Ser Ala Thr Ala Ala Ala Gly Ser Asn
                85                  90                  95
Ile Val Phe Gln Trp Gly Pro Gly Val Trp Pro His Pro Tyr Gly Pro
            100                 105                 110
Ile Val Thr Tyr Val Ala Glu Cys Ser Gly Ser Cys Thr Thr Val Asn
        115                 120                 125
Lys Asn Asn Leu Arg Trp Val Lys Ile Gln Glu Ala Gly Ile Asn Tyr
    130                 135                 140
Asn Thr Gln Val Trp Ala Gln Gln Asp Leu Ile Asn Gln Gly Asn Lys
145                 150                 155                 160
Trp Thr Val Lys Ile Pro Ser Ser Leu Arg Pro Gly Asn Tyr Val Phe
                165                 170                 175
Arg His Glu Leu Leu Ala Ala His Gly Ala Ser Ser Ala Asn Gly Met
            180                 185                 190
Gln Asn Tyr Pro Gln Cys Val Asn Ile Ala Val Thr Gly Ser Gly Thr
        195                 200                 205
Lys Ala Leu Pro Ala Gly Thr Pro Ala Thr Gln Leu Tyr Lys Pro Thr
    210                 215                 220
Asp Pro Gly Ile Leu Phe Asn Pro Tyr Thr Thr Ile Thr Ser Tyr Thr
225                 230                 235                 240
Ile Pro Gly Pro Ala Leu Trp Gln Gly
                245


<210> 768
<211> 418
<212> PRT
<213> Artificial Sequence

<220>
<223> endoglucanase III [Trichoderma reesei RUT C-3] 418
aa protein ETS4885.1 GI:572281861

<400> 768
Met Asn Lys Ser Val Ala Pro Leu Leu Leu Ala Ala Ser Ile Leu Tyr
 1               5                  10                  15
Gly Gly Ala Ala Ala Gln Gln Thr Val Trp Gly Gln Cys Gly Gly Ile
            20                  25                  30

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

<210> 769
<211> 234

<212> PRT
<213> Artificial Sequence

<220>
<223> putative endoglucanase [Trichoderma reesei RUT
C-3] 234 aa protein ETS538.1 GI:572282294

<400> 769
Met Lys Leu Leu Ser Ile Ala Ser Leu Leu Ser Leu Val Ala Thr Ala
 1               5                  10                  15
Gln Ala His Met Glu Val Ser Trp Pro Pro Val Phe Arg Ser Lys Tyr
            20                  25                  30
Asn Pro Arg Val Pro Gly Asn Leu Ile Asn Tyr Asp Met Thr Ser Pro
        35                  40                  45
Leu Asn Ala Asp Gly Ser Asn Tyr Pro Cys Lys Gly Tyr Gln Val Asp
    50                  55                  60
Val Gly Arg Pro Glu Gly Ala Pro Gly Val Thr Trp Arg Ala Gly Gly
65                  70                  75                  80
Thr Tyr Asn Leu Thr Val Ala Gly Ser Ala Thr His Ser Gly Gly Ser
                85                  90                  95
Cys Gln Ala Ser Leu Ser Tyr Asp Arg Gly Arg Thr Trp Val Val Val
            100                 105                 110
His Ser Trp Ile Gly Gly Cys Pro Leu Thr Pro Thr Trp Asp Phe Thr
        115                 120                 125
Leu Pro Asn Asp Thr Pro Pro Gly Glu Ala Leu Phe Ala Trp Thr Trp
    130                 135                 140
Phe Asn Arg Ile Gly Asn Arg Glu Met Tyr Met Asn Cys Gly Ala Val
145                 150                 155                 160
Thr Ile Arg Pro Ser Gly Arg Ala Ala Arg Ser Pro Ala Asp Ser Ile
                165                 170                 175
Tyr Asn Arg Pro Ala Gln Phe Val Ala Asn Val Asn Asn Gly Cys Ala
            180                 185                 190
Thr Leu Glu Gly Ala Asp Val Leu Phe Pro Ser Pro Gly Pro Asp Thr
        195                 200                 205
Asp Phe Asp Ser Asp Arg Thr Ala Ala Pro Val Gly Lys Cys Gly Ala
    210                 215                 220
Ser Ser Arg Arg Thr Arg Pro Val Arg Ala
225                 230


<210> 770
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Full=Endoglucanase-5 P43317.1 GI:117136

<400> 770
Met Lys Ala Thr Leu Val Leu Gly Ser Leu Ile Val Gly Ala Val Ser
 1               5                  10                  15
Ala Tyr Lys Ala Thr Thr Thr Arg Tyr Tyr Asp Gly Gln Glu Gly Ala
            20                  25                  30
Cys Gly Cys Gly Ser Ser Ser Gly Ala Phe Pro Trp Gln Leu Gly Ile

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

<210> 771
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Active-Site Mutant E212q Determined At Ph
6. With No Ligand Bound In The Active Site 2CEL_A
GI:1942104

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 771

```
Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
```

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

<210> 772
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, Active-Site Mutant E212q Determined At Ph
6. With No Ligand Bound In The Active Site 434 aa
protein 2CEL_B GI:194215

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 772
Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Asp Phe Val
                85                  90                  95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
            100                 105                 110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
        115                 120                 125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
    130                 135                 140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145                 150                 155                 160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                165                 170                 175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
            180                 185                 190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
        195                 200                 205
Cys Cys Ser Gln Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
    210                 215                 220
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly
225                 230                 235                 240
Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys
                245                 250                 255
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
            260                 265                 270
Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
        275                 280                 285
Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr
    290                 295                 300
Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser
305                 310                 315                 320
Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ala
                325                 330                 335
Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe

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

<210> 773
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Active-Site Mutant E212q Determined At Ph
6. With Cellobiose Bound In The Active Site 434 aa
protein 3CEL_A GI:157836779

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 773

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

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

<210> 774
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Active-site Mutant D214n Determined At Ph
6. With No Ligand Bound In The Active Site 434 aa
protein 4CEL_A GI:1941941

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 774

```
Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
```

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

<210> 775
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, Active-site Mutant D214n Determined At Ph
6. With No Ligand Bound In The Active Site 434 aa
protein 4CEL_B GI:1941942

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 775
Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Asp Phe Val
                85                  90                  95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
            100                 105                 110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
        115                 120                 125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
    130                 135                 140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145                 150                 155                 160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                165                 170                 175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
            180                 185                 190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
        195                 200                 205
Cys Cys Ser Glu Met Asn Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
    210                 215                 220
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly
225                 230                 235                 240
Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys
                245                 250                 255
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
            260                 265                 270
Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
        275                 280                 285
Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr

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

<210> 776
<211> 344
<212> PRT
<213> Artificial Sequence

<220>
<223> Cellulase IV O1445.1 GI:21263647

<400> 776

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

```
Gln Asn Tyr Pro Gln Cys Phe Asn Ile Ala Val Ser Gly Ser Gly Ser
        195                 200                 205
Leu Gln Pro Ser Gly Val Leu Gly Thr Asp Leu Tyr His Ala Thr Asp
    210                 215                 220
Pro Gly Val Leu Ile Asn Ile Tyr Thr Ser Pro Leu Asn Tyr Ile Ile
225                 230                 235                 240
Pro Gly Pro Thr Val Val Ser Gly Leu Pro Thr Ser Val Ala Gln Gly
                245                 250                 255
Ser Ser Ala Ala Thr Ala Thr Ala Ser Ala Thr Val Pro Gly Gly Gly
            260                 265                 270
Ser Gly Pro Thr Ser Arg Thr Thr Thr Thr Ala Arg Thr Thr Gln Ala
        275                 280                 285
Ser Ser Arg Pro Ser Ser Thr Pro Pro Ala Thr Thr Ser Ala Pro Ala
    290                 295                 300
Gly Gly Pro Thr Gln Thr Leu Tyr Gly Gln Cys Gly Gly Ser Gly Tyr
305                 310                 315                 320
Ser Gly Pro Thr Arg Cys Ala Pro Pro Ala Thr Cys Ser Thr Leu Asn
                325                 330                 335
Pro Tyr Tyr Ala Gln Cys Leu Asn
            340
```

<210> 777
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> endoglucanase I precursor [Trichoderma reesei RUT
C-3] 459 aa protein ETS775.1 GI:57228411

<400> 777

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

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


<210> 778
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Cbh1 (E217q) In Complex With Cellohexaose
      And Cellobiose 434 aa protein 7CEL_A GI:157837135

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 778
Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
```

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

<210> 779
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Cbh1 (E212q) Cellotetraose Complex 434 aa
protein 5CEL_A GI:1578372

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 779
Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Asp Phe Val
                85                  90                  95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
            100                 105                 110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
        115                 120                 125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
    130                 135                 140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145                 150                 155                 160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                165                 170                 175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
            180                 185                 190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
        195                 200                 205
Cys Cys Ser Gln Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
    210                 215                 220
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly
225                 230                 235                 240
Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys
                245                 250                 255
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
            260                 265                 270
Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
        275                 280                 285

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



<210> 780
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Cbh1 (E212q) Cellopentaose Complex 434 aa
      protein 6CEL_A GI:15783787

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 780
Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Asp Phe Val
                85                  90                  95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
            100                 105                 110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
        115                 120                 125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
```

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

<210> 781
<211> 418
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Endoglucanase EG-II; Short=EGLII;
AltName: Full=Cellulase; AltName:
Full=Endo-1,4-beta-glucanase; Flags: Precursor 418
aa protein P7982.1 GI:121794

<400> 781
Met Asn Lys Ser Val Ala Pro Leu Leu Leu Ala Ala Ser Ile Leu Tyr

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

<210> 782
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName: Full=Endoglucanase EG-1; AltName:
Full=Cellulase; AltName:
Full=Endo-1,4-beta-glucanase; Flags: Precursor
459 aa protein P7981.1 GI:121788

<400> 782
Met Ala Pro Ser Val Thr Leu Pro Leu Thr Thr Ala Ile Leu Ala Ile
 1               5                  10                  15
Ala Arg Leu Val Ala Ala Gln Gln Pro Gly Thr Ser Thr Pro Glu Val
            20                  25                  30
His Pro Lys Leu Thr Thr Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val
        35                  40                  45
Ala Gln Asp Thr Ser Val Val Leu Asp Trp Asn Tyr Arg Trp Met His
    50                  55                  60
Asp Ala Asn Tyr Asn Ser Cys Thr Val Asn Gly Gly Val Asn Thr Thr
65                  70                  75                  80
Leu Cys Pro Asp Glu Ala Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly
                85                  90                  95
Val Asp Tyr Ala Ala Ser Gly Val Thr Thr Ser Gly Ser Ser Leu Thr
            100                 105                 110
Met Asn Gln Tyr Met Pro Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser
        115                 120                 125
Pro Arg Leu Tyr Leu Leu Asp Ser Asp Gly Glu Tyr Val Met Leu Lys
    130                 135                 140
Leu Asn Gly Gln Glu Leu Ser Phe Asp Val Asp Leu Ser Ala Leu Pro
145                 150                 155                 160
Cys Gly Glu Asn Gly Ser Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly
                165                 170                 175
Gly Ala Asn Gln Tyr Asn Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr
            180                 185                 190
Cys Asp Ala Gln Cys Pro Val Gln Thr Trp Arg Asn Gly Thr Leu Asn
        195                 200                 205
Thr Ser His Gln Gly Phe Cys Cys Asn Glu Met Asp Ile Leu Glu Gly
    210                 215                 220
Asn Ser Arg Ala Asn Ala Leu Thr Pro His Ser Cys Thr Ala Thr Ala
225                 230                 235                 240
Cys Asp Ser Ala Gly Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys
                245                 250                 255
Ser Tyr Tyr Gly Pro Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr
            260                 265                 270
Ile Ile Thr Gln Phe Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu
        275                 280                 285
Val Ser Ile Thr Arg Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser
    290                 295                 300
Ala Gln Pro Gly Gly Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala
305                 310                 315                 320
Tyr Gly Gly Leu Ala Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val

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


<210> 783
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> endo-1,4-beta-glucanase V (EGV) [Trichoderma
      reesei]
      242 aa protein CAA83846.1 GI:485864

<400> 783
Met Lys Ala Thr Leu Val Leu Gly Ser Leu Ile Val Gly Ala Val Ser
 1               5                  10                  15
Ala Tyr Lys Ala Thr Thr Thr Arg Tyr Tyr Asp Gly Gln Glu Gly Ala
            20                  25                  30
Cys Gly Cys Gly Ser Ser Ser Gly Ala Phe Pro Trp Gln Leu Gly Ile
        35                  40                  45
Gly Asn Gly Val Tyr Thr Ala Ala Gly Ser Gln Ala Leu Phe Asp Thr
    50                  55                  60
Ala Gly Ala Ser Trp Cys Gly Ala Gly Cys Gly Lys Cys Tyr Gln Leu
65                  70                  75                  80
Thr Ser Thr Gly Gln Ala Pro Cys Ser Ser Cys Gly Thr Gly Gly Ala
                85                  90                  95
Ala Gly Gln Ser Ile Ile Val Met Val Thr Asn Leu Cys Pro Asn Asn
            100                 105                 110
Gly Asn Ala Gln Trp Cys Pro Val Val Gly Gly Thr Asn Gln Tyr Gly
        115                 120                 125
Tyr Ser Tyr His Phe Asp Ile Met Ala Gln Asn Glu Ile Phe Gly Asp
    130                 135                 140
Asn Val Val Val Asp Phe Glu Pro Ile Ala Cys Pro Gly Gln Ala Ala
145                 150                 155                 160
Ser Asp Trp Gly Thr Cys Leu Cys Val Gly Gln Gln Glu Thr Asp Pro
                165                 170                 175
Thr Pro Val Leu Gly Asn Asp Thr Gly Ser Thr Pro Pro Gly Ser Ser
            180                 185                 190
```

```
Pro Pro Ala Thr Ser Ser Ser Pro Pro Ser Gly Gly Gly Gln Gln Thr
        195                 200                 205
Leu Tyr Gly Gln Cys Gly Gly Ala Gly Trp Thr Gly Pro Thr Thr Cys
    210                 215                 220
Gln Ala Pro Gly Thr Cys Lys Val Gln Asn Gln Trp Tyr Ser Gln Cys
225                 230                 235                 240
Leu Pro
```

<210> 784
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-1,4-glucanase [Trichoderma reesei] 234 aa
protein ABV71388.1 GI:15777972

<400> 784

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

<210> 785
<211> 471

<212> PRT
<213> Artificial Sequence

<220>
<223> cellbiohydrolase II [Trichoderma reesei] 471 aa
protein ADC83999.1 GI:289152138

<400> 785
Met Ile Val Gly Ile Leu Thr Thr Leu Ala Thr Leu Ala Thr Leu Ala
 1               5                  10                  15
Ala Ser Val Pro Leu Glu Glu Arg Gln Ala Cys Ser Ser Val Trp Gly
            20                  25                  30
Gln Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly
        35                  40                  45
Ser Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Gly
    50                  55                  60
Ala Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg
65                  70                  75                  80
Val Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly
                85                  90                  95
Ser Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr
            100                 105                 110
Ser Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr
        115                 120                 125
Ala Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met
    130                 135                 140
Ala Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu
145                 150                 155                 160
Asp Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile
                165                 170                 175
Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val
            180                 185                 190
Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu
        195                 200                 205
Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp
    210                 215                 220
Thr Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu
225                 230                 235                 240
Val Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr
                245                 250                 255
Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr
            260                 265                 270
Ala Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala
        275                 280                 285
Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala
    290                 295                 300
Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu
305                 310                 315                 320
Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr
                325                 330                 335
Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu
            340                 345                 350
Tyr Ile His Ala Ile Gly Pro Leu Leu Ala Asn His Gly Trp Ser Asn
        355                 360                 365

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


<210> 786
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> endo-beta-1,4-glucanase [Trichoderma reesei] 234
      aa protein BAA214.1 GI:2116583

<400> 786
Met Lys Phe Leu Gln Val Leu Pro Ala Leu Ile Pro Ala Ala Leu Ala
 1               5                  10                  15
Gln Thr Ser Cys Asp Gln Trp Ala Thr Phe Thr Gly Asn Gly Tyr Thr
            20                  25                  30
Val Ser Asn Asn Leu Trp Gly Ala Ser Ala Gly Ser Gly Phe Gly Cys
        35                  40                  45
Val Thr Ala Val Ser Leu Ser Gly Gly Ala Ser Trp His Ala Asp Trp
    50                  55                  60
Gln Trp Ser Gly Gly Gln Asn Asn Val Lys Ser Tyr Gln Asn Ser Gln
65                  70                  75                  80
Ile Ala Ile Pro Gln Lys Arg Thr Val Asn Ser Ile Ser Ser Met Pro
                85                  90                  95
Thr Thr Ala Ser Trp Ser Tyr Ser Gly Ser Asn Ile Arg Ala Asn Val
            100                 105                 110
Ala Tyr Asp Leu Phe Thr Ala Ala Asn Pro Asn His Val Thr Tyr Ser
        115                 120                 125
Gly Asp Tyr Glu Leu Met Ile Trp Leu Gly Lys Tyr Gly Asp Ile Gly
    130                 135                 140
Pro Ile Gly Ser Ser Gln Gly Thr Val Asn Val Gly Gly Gln Ser Trp
145                 150                 155                 160
Thr Leu Tyr Tyr Gly Tyr Asn Gly Ala Met Gln Val Tyr Ser Phe Val
                165                 170                 175
Ala Gln Thr Asn Thr Thr Asn Tyr Ser Gly Asp Val Lys Asn Phe Phe
            180                 185                 190
Asn Tyr Leu Arg Asp Asn Lys Gly Tyr Asn Ala Ala Gly Gln Tyr Val
        195                 200                 205
Leu Ser Tyr Gln Phe Gly Thr Glu Pro Phe Thr Gly Ser Gly Thr Leu
    210                 215                 220
```

```
Asn Val Ala Ser Trp Thr Ala Ser Ile Asn
225                 230


<210> 787
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Crystal Structure Of Cel5a (Eg2) From
      Hypocrea Jecorina (Trichoderma Reesei) 34 aa
      protein 3QR3_A GI:39981273

<400> 787
Met Gly Val Arg Phe Ala Gly Val Asn Ile Ala Gly Phe Asp Phe Gly
 1               5                  10                  15
Cys Thr Thr Asp Gly Thr Cys Val Thr Ser Lys Val Tyr Pro Pro Leu
            20                  25                  30
Lys Asn Phe Thr Gly Ser Asn Asn Tyr Pro Asp Gly Ile Gly Gln Met
        35                  40                  45
Gln His Phe Val Asn Glu Asp Gly Met Thr Ile Phe Arg Leu Pro Val
    50                  55                  60
Gly Trp Gln Tyr Leu Val Asn Asn Asn Leu Gly Gly Asn Leu Asp Ser
65                  70                  75                  80
Thr Ser Ile Ser Lys Tyr Asp Gln Leu Val Gln Gly Cys Leu Ser Leu
                85                  90                  95
Gly Ala Tyr Cys Ile Val Asp Ile His Asn Tyr Ala Arg Trp Asn Gly
            100                 105                 110
Gly Ile Ile Gly Gln Gly Gly Pro Thr Asn Ala Gln Phe Thr Ser Leu
        115                 120                 125
Trp Ser Gln Leu Ala Ser Lys Tyr Ala Ser Gln Ser Arg Val Trp Phe
    130                 135                 140
Gly Ile Met Asn Glu Pro His Asp Val Asn Ile Asn Thr Trp Ala Ala
145                 150                 155                 160
Thr Val Gln Glu Val Val Thr Ala Ile Arg Asn Ala Gly Ala Thr Ser
                165                 170                 175
Gln Phe Ile Ser Leu Pro Gly Asn Asp Trp Gln Ser Ala Gly Ala Phe
            180                 185                 190
Ile Ser Asp Gly Ser Ala Ala Ala Leu Ser Gln Val Thr Asn Pro Asp
        195                 200                 205
Gly Ser Thr Thr Asn Leu Ile Phe Asp Val His Lys Tyr Leu Asp Ser
    210                 215                 220
Asp Asn Ser Gly Thr His Ala Glu Cys Thr Thr Asn Asn Ile Asp Gly
225                 230                 235                 240
Ala Phe Ser Pro Leu Ala Thr Trp Leu Arg Gln Asn Asn Arg Gln Ala
                245                 250                 255
Ile Leu Thr Glu Thr Gly Gly Gly Asn Val Gln Ser Cys Ile Gln Asp
            260                 265                 270
Met Cys Gln Gln Ile Gln Tyr Leu Asn Gln Asn Ser Asp Val Tyr Leu
        275                 280                 285
Gly Tyr Val Gly Trp Gly Ala Gly Ser Phe Asp Ser Thr Tyr Val Leu
    290                 295                 300
Thr Glu Thr Pro Thr Ser Ser Gly Asn Ser Trp Thr Asp Thr Ser Leu
```

305 310 315 320
Val Ser Ser Cys Leu Ala Arg Lys Gly Gly Ser Gly Ser Gly His His
325 330 335
His His His His
340

<210> 788
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, Crystal Structure Of Cel5a (Eg2) From
Hypocrea Jecorina (Trichoderma Reesei) 34 aa
protein 3QR3_B GI:39981274

<400> 788
Met Gly Val Arg Phe Ala Gly Val Asn Ile Ala Gly Phe Asp Phe Gly
1 5 10 15
Cys Thr Thr Asp Gly Thr Cys Val Thr Ser Lys Val Tyr Pro Pro Leu
20 25 30
Lys Asn Phe Thr Gly Ser Asn Asn Tyr Pro Asp Gly Ile Gly Gln Met
35 40 45
Gln His Phe Val Asn Glu Asp Gly Met Thr Ile Phe Arg Leu Pro Val
50 55 60
Gly Trp Gln Tyr Leu Val Asn Asn Asn Leu Gly Gly Asn Leu Asp Ser
65 70 75 80
Thr Ser Ile Ser Lys Tyr Asp Gln Leu Val Gln Gly Cys Leu Ser Leu
85 90 95
Gly Ala Tyr Cys Ile Val Asp Ile His Asn Tyr Ala Arg Trp Asn Gly
100 105 110
Gly Ile Ile Gly Gln Gly Gly Pro Thr Asn Ala Gln Phe Thr Ser Leu
115 120 125
Trp Ser Gln Leu Ala Ser Lys Tyr Ala Ser Gln Ser Arg Val Trp Phe
130 135 140
Gly Ile Met Asn Glu Pro His Asp Val Asn Ile Asn Thr Trp Ala Ala
145 150 155 160
Thr Val Gln Glu Val Val Thr Ala Ile Arg Asn Ala Gly Ala Thr Ser
165 170 175
Gln Phe Ile Ser Leu Pro Gly Asn Asp Trp Gln Ser Ala Gly Ala Phe
180 185 190
Ile Ser Asp Gly Ser Ala Ala Ala Leu Ser Gln Val Thr Asn Pro Asp
195 200 205
Gly Ser Thr Thr Asn Leu Ile Phe Asp Val His Lys Tyr Leu Asp Ser
210 215 220
Asp Asn Ser Gly Thr His Ala Glu Cys Thr Thr Asn Asn Ile Asp Gly
225 230 235 240
Ala Phe Ser Pro Leu Ala Thr Trp Leu Arg Gln Asn Asn Arg Gln Ala
245 250 255
Ile Leu Thr Glu Thr Gly Gly Gly Asn Val Gln Ser Cys Ile Gln Asp
260 265 270
Met Cys Gln Gln Ile Gln Tyr Leu Asn Gln Asn Ser Asp Val Tyr Leu
275 280 285

```
Gly Tyr Val Gly Trp Gly Ala Gly Ser Phe Asp Ser Thr Tyr Val Leu
    290                 295                 300
Thr Glu Thr Pro Thr Ser Ser Gly Asn Ser Trp Thr Asp Thr Ser Leu
305                 310                 315                 320
Val Ser Ser Cys Leu Ala Arg Lys Gly Gly Ser Gly Ser Gly His His
                325                 330                 335
His His His His
            340


<210> 789
<211> 838
<212> PRT
<213> Artificial Sequence

<220>
<223> Cel74a [Trichoderma reesei] 838 aa protein
      AAP57752.1 GI:317471

<400> 789
Met Lys Val Ser Arg Val Leu Ala Leu Val Leu Gly Ala Val Ile Pro
 1               5                  10                  15
Ala His Ala Ala Phe Ser Trp Lys Asn Val Lys Leu Gly Gly Gly Gly
            20                  25                  30
Gly Phe Val Pro Gly Ile Ile Phe His Pro Lys Thr Lys Gly Val Ala
        35                  40                  45
Tyr Ala Arg Thr Asp Ile Gly Gly Leu Tyr Arg Leu Asn Ala Asp Asp
    50                  55                  60
Ser Trp Thr Ala Val Thr Asp Gly Ile Ala Asp Asn Ala Gly Trp His
65                  70                  75                  80
Asn Trp Gly Ile Asp Ala Val Ala Leu Asp Pro Gln Asp Asp Gln Lys
                85                  90                  95
Val Tyr Ala Ala Val Gly Met Tyr Thr Asn Ser Trp Asp Pro Ser Asn
            100                 105                 110
Gly Ala Ile Ile Arg Ser Ser Asp Arg Gly Ala Thr Trp Ser Phe Thr
        115                 120                 125
Asn Leu Pro Phe Lys Val Gly Gly Asn Met Pro Gly Arg Gly Ala Gly
    130                 135                 140
Glu Arg Leu Ala Val Asp Pro Ala Asn Ser Asn Ile Ile Tyr Phe Gly
145                 150                 155                 160
Ala Arg Ser Gly Asn Gly Leu Trp Lys Ser Thr Asp Gly Gly Val Thr
                165                 170                 175
Phe Ser Lys Val Ser Ser Phe Thr Ala Thr Gly Thr Tyr Ile Pro Asp
            180                 185                 190
Pro Ser Asp Ser Asn Gly Tyr Asn Ser Asp Lys Gln Gly Leu Met Trp
        195                 200                 205
Val Thr Phe Asp Ser Thr Ser Ser Thr Thr Gly Gly Ala Thr Ser Arg
    210                 215                 220
Ile Phe Val Gly Thr Ala Asp Asn Ile Thr Ala Ser Val Tyr Val Ser
225                 230                 235                 240
Thr Asn Ala Gly Ser Thr Trp Ser Ala Val Pro Gly Gln Pro Gly Lys
                245                 250                 255
Tyr Phe Pro His Lys Ala Lys Leu Gln Pro Ala Glu Lys Ala Leu Tyr
            260                 265                 270
```

```
Leu Thr Tyr Ser Asp Gly Thr Gly Pro Tyr Asp Gly Thr Leu Gly Ser
        275                 280                 285
Val Trp Arg Tyr Asp Ile Ala Gly Gly Thr Trp Lys Asp Ile Thr Pro
    290                 295                 300
Val Ser Gly Ser Asp Leu Tyr Phe Gly Phe Gly Gly Leu Gly Leu Asp
305                 310                 315                 320
Leu Gln Lys Pro Gly Thr Leu Val Val Ala Ser Leu Asn Ser Trp Trp
                325                 330                 335
Pro Asp Ala Gln Leu Phe Arg Ser Thr Asp Ser Gly Thr Thr Trp Ser
            340                 345                 350
Pro Ile Trp Ala Trp Ala Ser Tyr Pro Thr Glu Thr Tyr Tyr Tyr Ser
        355                 360                 365
Ile Ser Thr Pro Lys Ala Pro Trp Ile Lys Asn Asn Phe Ile Asp Val
    370                 375                 380
Thr Ser Glu Ser Pro Ser Asp Gly Leu Ile Lys Arg Leu Gly Trp Met
385                 390                 395                 400
Ile Glu Ser Leu Glu Ile Asp Pro Thr Asp Ser Asn His Trp Leu Tyr
                405                 410                 415
Gly Thr Gly Met Thr Ile Phe Gly Gly His Asp Leu Thr Asn Trp Asp
            420                 425                 430
Thr Arg His Asn Val Ser Ile Gln Ser Leu Ala Asp Gly Ile Glu Glu
        435                 440                 445
Phe Ser Val Gln Asp Leu Ala Ser Ala Pro Gly Gly Ser Glu Leu Leu
    450                 455                 460
Ala Ala Val Gly Asp Asp Asn Gly Phe Thr Phe Ala Ser Arg Asn Asp
465                 470                 475                 480
Leu Gly Thr Ser Pro Gln Thr Val Trp Ala Thr Pro Thr Trp Ala Thr
                485                 490                 495
Ser Thr Ser Val Asp Tyr Ala Gly Asn Ser Val Lys Ser Val Val Arg
            500                 505                 510
Val Gly Asn Thr Ala Gly Thr Gln Gln Val Ala Ile Ser Ser Asp Gly
        515                 520                 525
Gly Ala Thr Trp Ser Ile Asp Tyr Ala Ala Asp Thr Ser Met Asn Gly
    530                 535                 540
Gly Thr Val Ala Tyr Ser Ala Asp Gly Asp Thr Ile Leu Trp Ser Thr
545                 550                 555                 560
Ala Ser Ser Gly Val Gln Arg Ser Gln Phe Gln Gly Ser Phe Ala Ser
                565                 570                 575
Val Ser Ser Leu Pro Ala Gly Ala Val Ile Ala Ser Asp Lys Lys Thr
            580                 585                 590
Asn Ser Val Phe Tyr Ala Gly Ser Gly Ser Thr Phe Tyr Val Ser Lys
        595                 600                 605
Asp Thr Gly Ser Ser Phe Thr Arg Gly Pro Lys Leu Gly Ser Ala Gly
    610                 615                 620
Thr Ile Arg Asp Ile Ala Ala His Pro Thr Thr Ala Gly Thr Leu Tyr
625                 630                 635                 640
Val Ser Thr Asp Val Gly Ile Phe Arg Ser Thr Asp Ser Gly Thr Thr
                645                 650                 655
Phe Gly Gln Val Ser Thr Ala Leu Thr Asn Thr Tyr Gln Ile Ala Leu
            660                 665                 670
Gly Val Gly Ser Gly Ser Asn Trp Asn Leu Tyr Ala Phe Gly Thr Gly
        675                 680                 685
Pro Ser Gly Ala Arg Leu Tyr Ala Ser Gly Asp Ser Gly Ala Ser Trp
    690                 695                 700
```

```
Thr Asp Ile Gln Gly Ser Gln Gly Phe Gly Ser Ile Asp Ser Thr Lys
705                 710                 715                 720
Val Ala Gly Ser Gly Ser Thr Ala Gly Gln Val Tyr Val Gly Thr Asn
                725                 730                 735
Gly Arg Gly Val Phe Tyr Ala Gln Gly Thr Val Gly Gly Gly Thr Gly
            740                 745                 750
Gly Thr Ser Ser Ser Thr Lys Gln Ser Ser Ser Ser Thr Ser Ser Ala
        755                 760                 765
Ser Ser Ser Thr Thr Leu Arg Ser Ser Val Val Ser Thr Thr Arg Ala
    770                 775                 780
Ser Thr Val Thr Ser Ser Arg Thr Ser Ser Ala Ala Gly Pro Thr Gly
785                 790                 795                 800
Ser Gly Val Ala Gly His Tyr Ala Gln Cys Gly Gly Ile Gly Trp Thr
                805                 810                 815
Gly Pro Thr Gln Cys Val Ala Pro Tyr Val Cys Gln Lys Gln Asn Asp
            820                 825                 830
Tyr Tyr Tyr Gln Cys Val
        835
```

<210> 790
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Cel61b [Trichoderma reesei] 249 aa protein
AAP57753.1 GI:31747162

<400> 790

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

```
Gln Asn Tyr Pro Gln Cys Val Asn Ile Ala Val Thr Gly Ser Gly Thr
        195                 200                 205
Lys Ala Leu Pro Ala Gly Thr Pro Ala Thr Gln Leu Tyr Lys Pro Thr
    210                 215                 220
Asp Pro Gly Ile Leu Phe Asn Pro Tyr Thr Thr Ile Thr Ser Tyr Thr
225                 230                 235                 240
Ile Pro Gly Pro Ala Leu Trp Gln Gly
                245
```

<210> 791
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<223> Cel5b [Trichoderma reesei] 438 aa protein
AAP57754.1 GI:31747164

<400> 791

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

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


<210> 792
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> endoglucanase I 459 aa protein 132152A GI:22541

<400> 792
Met Ala Pro Ser Val Thr Leu Pro Leu Thr Thr Ala Ile Leu Ala Ile
 1               5                  10                  15
Ala Arg Leu Val Ala Ala Gln Gln Pro Gly Thr Ser Thr Pro Glu Val
            20                  25                  30
His Pro Lys Leu Thr Thr Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val
        35                  40                  45
Ala Gln Asp Thr Ser Val Val Leu Asp Trp Asn Tyr Arg Trp Met His
    50                  55                  60
Asp Ala Asn Tyr Asn Ser Cys Thr Val Asn Gly Gly Val Asn Thr Thr
65                  70                  75                  80
Leu Cys Pro Asp Glu Ala Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly
                85                  90                  95
Val Asp Tyr Ala Ala Ser Gly Val Thr Thr Ser Gly Ser Ser Leu Thr
            100                 105                 110
Met Asn Gln Tyr Met Pro Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser
        115                 120                 125
Pro Arg Leu Tyr Leu Leu Asp Ser Asp Gly Glu Tyr Val Met Leu Lys
    130                 135                 140
Leu Asn Gly Gln Glu Leu Ser Phe Asp Val Asp Leu Ser Ala Leu Pro
145                 150                 155                 160
Cys Gly Glu Asn Gly Ser Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly
```

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


<210> 793
<211> 344
<212> PRT
<213> Artificial Sequence

<220>
<223> endoglucanase IV [Trichoderma reesei] 344 aa
      protein CAA71999.1 GI:2315274

<400> 793
Met Ile Gln Lys Leu Ser Asn Leu Leu Val Thr Ala Leu Ala Val Ala
 1               5                  10                  15
Thr Gly Val Val Gly His Gly His Ile Asn Asp Ile Val Ile Asn Gly
            20                  25                  30
Val Trp Tyr Gln Ala Tyr Asp Pro Thr Thr Phe Pro Tyr Glu Ser Asn
```

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


<210> 794
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> endoglucanase I [Trichoderma reesei] 459 aa
      protein ADM8177.1 GI:3329711

<400> 794
Met Ala Pro Ser Val Thr Leu Pro Leu Thr Thr Ala Ile Leu Ala Ile
 1               5                  10                  15
Ala Arg Leu Val Ala Ala Gln Gln Pro Gly Thr Ser Thr Pro Glu Val
```

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

450 455

<210> 795
<211> 418
<212> PRT
<213> Artificial Sequence

<220>
<223> endoglucanase II precursor [Trichoderma reesei]
418 aa protein AAA34213.1 GI:17549

<400> 795
Met Asn Lys Ser Val Ala Pro Leu Leu Leu Ala Ala Ser Ile Leu Tyr
1 5 10 15
Gly Gly Ala Val Ala Gln Gln Thr Val Trp Gly Gln Cys Gly Gly Ile
20 25 30
Gly Trp Ser Gly Pro Thr Asn Cys Ala Pro Gly Ser Ala Cys Ser Thr
35 40 45
Leu Asn Pro Tyr Tyr Ala Gln Cys Ile Pro Gly Ala Thr Thr Ile Thr
50 55 60
Thr Ser Thr Arg Pro Pro Ser Gly Pro Thr Thr Thr Thr Arg Ala Thr
65 70 75 80
Ser Thr Ser Ser Ser Thr Pro Pro Thr Ser Ser Gly Val Arg Phe Ala
85 90 95
Gly Val Asn Ile Ala Gly Phe Asp Phe Gly Cys Thr Thr Asp Gly Thr
100 105 110
Cys Val Thr Ser Lys Val Tyr Pro Pro Leu Lys Asn Phe Thr Gly Ser
115 120 125
Asn Asn Tyr Pro Asp Gly Ile Gly Gln Met Gln His Phe Val Asn Glu
130 135 140
Asp Gly Met Thr Ile Phe Arg Leu Pro Val Gly Trp Gln Tyr Leu Val
145 150 155 160
Asn Asn Asn Leu Gly Gly Asn Leu Asp Ser Thr Ser Ile Ser Lys Tyr
165 170 175
Asp Gln Leu Val Gln Gly Cys Leu Ser Leu Gly Ala Tyr Cys Ile Val
180 185 190
Asp Ile His Asn Tyr Ala Arg Trp Asn Gly Gly Ile Ile Gly Gln Gly
195 200 205
Gly Pro Thr Asn Ala Gln Phe Thr Ser Leu Trp Ser Gln Leu Ala Ser
210 215 220
Lys Tyr Ala Ser Gln Ser Arg Val Trp Phe Gly Ile Met Asn Glu Pro
225 230 235 240
His Asp Val Asn Ile Asn Thr Trp Ala Ala Thr Val Gln Glu Val Val
245 250 255
Thr Ala Ile Arg Asn Ala Gly Ala Thr Ser Gln Phe Ile Ser Leu Pro
260 265 270
Gly Asn Asp Trp Gln Ser Ala Gly Ala Phe Ile Ser Asp Gly Ser Ala
275 280 285
Ala Ala Leu Ser Gln Val Thr Asn Pro Asp Gly Ser Thr Thr Asn Leu
290 295 300
Ile Phe Asp Val His Lys Tyr Leu Asp Ser Asp Asn Ser Gly Thr His
305 310 315 320
Ala Glu Cys Thr Thr Asn Asn Ile Asp Gly Ala Phe Ser Pro Leu Ala

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                325                 330                 335
Thr Trp Leu Arg Gln Asn Asn Arg Gln Ala Ile Leu Thr Glu Thr Gly
            340                 345                 350
Gly Gly Asn Val Gln Ser Cys Ile Gln Asp Met Cys Gln Gln Ile Gln
        355                 360                 365
Tyr Leu Asn Gln Asn Ser Asp Val Tyr Leu Gly Tyr Val Gly Trp Gly
    370                 375                 380
Ala Gly Ser Phe Asp Ser Thr Tyr Val Leu Thr Glu Thr Pro Thr Ser
385                 390                 395                 400
Ser Gly Asn Ser Trp Thr Asp Thr Ser Leu Val Ser Ser Cys Leu Ala
                405                 410                 415
Arg Lys
```

<210> 796
<211> 418
<212> PRT
<213> Artificial Sequence

<220>
<223> endoglucanase II [Trichoderma reesei] 418 aa
protein ABA64553.1 GI:77176916

<400> 796

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

<210> 797
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, The X-Ray Crystal Structure Of The
Trichoderma Reesei Family 12 Endoglucanase 3,
Cel12a, At 1.9 A Resolution 218 aa protein 1H8V_A
GI:14278359

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 797
Xaa Thr Ser Cys Asp Gln Trp Ala Thr Phe Thr Gly Asn Gly Tyr Thr
1 5 10 15
Val Ser Asn Asn Leu Trp Gly Ala Ser Ala Gly Ser Gly Phe Gly Cys
20 25 30
Val Thr Ala Val Ser Leu Ser Gly Gly Ala Ser Trp His Ala Asp Trp
35 40 45
Gln Trp Ser Gly Gly Gln Asn Asn Val Lys Ser Tyr Gln Asn Ser Gln
50 55 60
Ile Ala Ile Pro Gln Lys Arg Thr Val Asn Ser Ile Ser Ser Met Pro
65 70 75 80

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Thr Thr Ala Ser Trp Ser Tyr Ser Gly Ser Asn Ile Arg Ala Asn Val
                85                  90                  95
Ala Tyr Asp Leu Phe Thr Ala Ala Asn Pro Asn His Val Thr Tyr Ser
            100                 105                 110
Gly Asp Tyr Glu Leu Met Ile Trp Leu Gly Lys Tyr Gly Asp Ile Gly
        115                 120                 125
Pro Ile Gly Ser Ser Gln Gly Thr Val Asn Val Gly Gly Gln Ser Trp
    130                 135                 140
Thr Leu Tyr Tyr Gly Tyr Asn Gly Ala Met Gln Val Tyr Ser Phe Val
145                 150                 155                 160
Ala Gln Thr Asn Thr Thr Asn Tyr Ser Gly Asp Val Lys Asn Phe Phe
                165                 170                 175
Asn Tyr Leu Arg Asp Asn Lys Gly Tyr Asn Ala Ala Gly Gln Tyr Val
            180                 185                 190
Leu Ser Tyr Gln Phe Gly Thr Glu Pro Phe Thr Gly Ser Gly Thr Leu
        195                 200                 205
Asn Val Ala Ser Trp Thr Ala Ser Ile Asn
    210                 215


<210> 798
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, The X-Ray Crystal Structure Of The
      Trichoderma Reesei Family 12 Endoglucanase 3,
      Cel12a, At 1.9 A Resolution 218 aa protein 1H8V_B
      GI:142783

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 798
Xaa Thr Ser Cys Asp Gln Trp Ala Thr Phe Thr Gly Asn Gly Tyr Thr
 1               5                  10                  15
Val Ser Asn Asn Leu Trp Gly Ala Ser Ala Gly Ser Gly Phe Gly Cys
            20                  25                  30
Val Thr Ala Val Ser Leu Ser Gly Gly Ala Ser Trp His Ala Asp Trp
        35                  40                  45
Gln Trp Ser Gly Gly Gln Asn Asn Val Lys Ser Tyr Gln Asn Ser Gln
    50                  55                  60
Ile Ala Ile Pro Gln Lys Arg Thr Val Asn Ser Ile Ser Ser Met Pro
65                  70                  75                  80
Thr Thr Ala Ser Trp Ser Tyr Ser Gly Ser Asn Ile Arg Ala Asn Val
                85                  90                  95
Ala Tyr Asp Leu Phe Thr Ala Ala Asn Pro Asn His Val Thr Tyr Ser
            100                 105                 110
Gly Asp Tyr Glu Leu Met Ile Trp Leu Gly Lys Tyr Gly Asp Ile Gly
        115                 120                 125
Pro Ile Gly Ser Ser Gln Gly Thr Val Asn Val Gly Gly Gln Ser Trp
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    130                 135                 140
Thr Leu Tyr Tyr Gly Tyr Asn Gly Ala Met Gln Val Tyr Ser Phe Val
145                 150                 155                 160
Ala Gln Thr Asn Thr Thr Asn Tyr Ser Gly Asp Val Lys Asn Phe Phe
                165                 170                 175
Asn Tyr Leu Arg Asp Asn Lys Gly Tyr Asn Ala Ala Gly Gln Tyr Val
            180                 185                 190
Leu Ser Tyr Gln Phe Gly Thr Glu Pro Phe Thr Gly Ser Gly Thr Leu
        195                 200                 205
Asn Val Ala Ser Trp Thr Ala Ser Ile Asn
    210                 215


<210> 799
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain C, The X-Ray Crystal Structure Of The
      Trichoderma Reesei Family 12 Endoglucanase 3,
      Cel12a, At 1.9 A  Resolution 218 aa protein 1H8V_C
      GI:14278361

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 799
Xaa Thr Ser Cys Asp Gln Trp Ala Thr Phe Thr Gly Asn Gly Tyr Thr
 1               5                  10                  15
Val Ser Asn Asn Leu Trp Gly Ala Ser Ala Gly Ser Gly Phe Gly Cys
            20                  25                  30
Val Thr Ala Val Ser Leu Ser Gly Gly Ala Ser Trp His Ala Asp Trp
        35                  40                  45
Gln Trp Ser Gly Gly Gln Asn Asn Val Lys Ser Tyr Gln Asn Ser Gln
    50                  55                  60
Ile Ala Ile Pro Gln Lys Arg Thr Val Asn Ser Ile Ser Ser Met Pro
65                  70                  75                  80
Thr Thr Ala Ser Trp Ser Tyr Ser Gly Ser Asn Ile Arg Ala Asn Val
                85                  90                  95
Ala Tyr Asp Leu Phe Thr Ala Ala Asn Pro Asn His Val Thr Tyr Ser
            100                 105                 110
Gly Asp Tyr Glu Leu Met Ile Trp Leu Gly Lys Tyr Gly Asp Ile Gly
        115                 120                 125
Pro Ile Gly Ser Ser Gln Gly Thr Val Asn Val Gly Gly Gln Ser Trp
    130                 135                 140
Thr Leu Tyr Tyr Gly Tyr Asn Gly Ala Met Gln Val Tyr Ser Phe Val
145                 150                 155                 160
Ala Gln Thr Asn Thr Thr Asn Tyr Ser Gly Asp Val Lys Asn Phe Phe
                165                 170                 175
Asn Tyr Leu Arg Asp Asn Lys Gly Tyr Asn Ala Ala Gly Gln Tyr Val
            180                 185                 190
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Leu Ser Tyr Gln Phe Gly Thr Glu Pro Phe Thr Gly Ser Gly Thr Leu
        195                 200                 205
Asn Val Ala Ser Trp Thr Ala Ser Ile Asn
    210                 215


<210> 800
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain D, The X-Ray Crystal Structure Of The
      Trichoderma Reesei Family 12 Endoglucanase 3,
      Cel12a, At 1.9 A Resolution 218 aa protein 1H8V_D
      GI:14278362

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 800
Xaa Thr Ser Cys Asp Gln Trp Ala Thr Phe Thr Gly Asn Gly Tyr Thr
 1               5                  10                  15
Val Ser Asn Asn Leu Trp Gly Ala Ser Ala Gly Ser Gly Phe Gly Cys
            20                  25                  30
Val Thr Ala Val Ser Leu Ser Gly Gly Ala Ser Trp His Ala Asp Trp
        35                  40                  45
Gln Trp Ser Gly Gly Gln Asn Asn Val Lys Ser Tyr Gln Asn Ser Gln
    50                  55                  60
Ile Ala Ile Pro Gln Lys Arg Thr Val Asn Ser Ile Ser Ser Met Pro
65                  70                  75                  80
Thr Thr Ala Ser Trp Ser Tyr Ser Gly Ser Asn Ile Arg Ala Asn Val
                85                  90                  95
Ala Tyr Asp Leu Phe Thr Ala Ala Asn Pro Asn His Val Thr Tyr Ser
            100                 105                 110
Gly Asp Tyr Glu Leu Met Ile Trp Leu Gly Lys Tyr Gly Asp Ile Gly
        115                 120                 125
Pro Ile Gly Ser Ser Gln Gly Thr Val Asn Val Gly Gly Gln Ser Trp
    130                 135                 140
Thr Leu Tyr Tyr Gly Tyr Asn Gly Ala Met Gln Val Tyr Ser Phe Val
145                 150                 155                 160
Ala Gln Thr Asn Thr Thr Asn Tyr Ser Gly Asp Val Lys Asn Phe Phe
                165                 170                 175
Asn Tyr Leu Arg Asp Asn Lys Gly Tyr Asn Ala Ala Gly Gln Tyr Val
            180                 185                 190
Leu Ser Tyr Gln Phe Gly Thr Glu Pro Phe Thr Gly Ser Gly Thr Leu
        195                 200                 205
Asn Val Ala Ser Trp Thr Ala Ser Ile Asn
    210                 215


<210> 801
```

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

<220>
<223> Chain E, The X-Ray Crystal Structure Of The
Trichoderma Reesei Family 12 Endoglucanase 3,
Cel12a, At 1.9 A Resolution 218 aa protein 1H8V_E
GI:14278363

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 801
Xaa Thr Ser Cys Asp Gln Trp Ala Thr Phe Thr Gly Asn Gly Tyr Thr
1 5 10 15
Val Ser Asn Asn Leu Trp Gly Ala Ser Ala Gly Ser Gly Phe Gly Cys
20 25 30
Val Thr Ala Val Ser Leu Ser Gly Gly Ala Ser Trp His Ala Asp Trp
35 40 45
Gln Trp Ser Gly Gly Gln Asn Asn Val Lys Ser Tyr Gln Asn Ser Gln
50 55 60
Ile Ala Ile Pro Gln Lys Arg Thr Val Asn Ser Ile Ser Ser Met Pro
65 70 75 80
Thr Thr Ala Ser Trp Ser Tyr Ser Gly Ser Asn Ile Arg Ala Asn Val
85 90 95
Ala Tyr Asp Leu Phe Thr Ala Ala Asn Pro Asn His Val Thr Tyr Ser
100 105 110
Gly Asp Tyr Glu Leu Met Ile Trp Leu Gly Lys Tyr Gly Asp Ile Gly
115 120 125
Pro Ile Gly Ser Ser Gln Gly Thr Val Asn Val Gly Gly Gln Ser Trp
130 135 140
Thr Leu Tyr Tyr Gly Tyr Asn Gly Ala Met Gln Val Tyr Ser Phe Val
145 150 155 160
Ala Gln Thr Asn Thr Thr Asn Tyr Ser Gly Asp Val Lys Asn Phe Phe
165 170 175
Asn Tyr Leu Arg Asp Asn Lys Gly Tyr Asn Ala Ala Gly Gln Tyr Val
180 185 190
Leu Ser Tyr Gln Phe Gly Thr Glu Pro Phe Thr Gly Ser Gly Thr Leu
195 200 205
Asn Val Ala Ser Trp Thr Ala Ser Ile Asn
210 215

<210> 802
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain F, The X-Ray Crystal Structure Of The
Trichoderma Reesei Family 12 Endoglucanase 3,

Cel12a, At 1.9 A Resolution 218 aa protein 1H8V_F
GI:14278364

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 802
Xaa Thr Ser Cys Asp Gln Trp Ala Thr Phe Thr Gly Asn Gly Tyr Thr
 1               5                  10                  15
Val Ser Asn Asn Leu Trp Gly Ala Ser Ala Gly Ser Gly Phe Gly Cys
            20                  25                  30
Val Thr Ala Val Ser Leu Ser Gly Gly Ala Ser Trp His Ala Asp Trp
        35                  40                  45
Gln Trp Ser Gly Gly Gln Asn Asn Val Lys Ser Tyr Gln Asn Ser Gln
    50                  55                  60
Ile Ala Ile Pro Gln Lys Arg Thr Val Asn Ser Ile Ser Ser Met Pro
65                  70                  75                  80
Thr Thr Ala Ser Trp Ser Tyr Ser Gly Ser Asn Ile Arg Ala Asn Val
                85                  90                  95
Ala Tyr Asp Leu Phe Thr Ala Ala Asn Pro Asn His Val Thr Tyr Ser
            100                 105                 110
Gly Asp Tyr Glu Leu Met Ile Trp Leu Gly Lys Tyr Gly Asp Ile Gly
        115                 120                 125
Pro Ile Gly Ser Ser Gln Gly Thr Val Asn Val Gly Gly Gln Ser Trp
    130                 135                 140
Thr Leu Tyr Tyr Gly Tyr Asn Gly Ala Met Gln Val Tyr Ser Phe Val
145                 150                 155                 160
Ala Gln Thr Asn Thr Thr Asn Tyr Ser Gly Asp Val Lys Asn Phe Phe
                165                 170                 175
Asn Tyr Leu Arg Asp Asn Lys Gly Tyr Asn Ala Ala Gly Gln Tyr Val
            180                 185                 190
Leu Ser Tyr Gln Phe Gly Thr Glu Pro Phe Thr Gly Ser Gly Thr Leu
        195                 200                 205
Asn Val Ala Ser Trp Thr Ala Ser Ile Asn
    210                 215


<210> 803
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> endoglucanase I precursor [Trichoderma reesei] 459
aa protein AAA34212.1 GI:17547

<400> 803
Met Ala Pro Ser Val Thr Leu Pro Leu Thr Thr Ala Ile Leu Ala Ile
 1               5                  10                  15
Ala Arg Leu Val Ala Ala Gln Gln Pro Gly Thr Ser Thr Pro Glu Val
            20                  25                  30
His Pro Lys Leu Thr Thr Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val

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

<210> 804
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Solution Structure Of The Cellulose-
binding Domain Of Endoglucanase I From Trichoderma
Reesei And Its Interaction With Cello-oligo-
saccharides 38 aa protein 4BMF_A GI:5743

<400> 804
Ser Cys Thr Gln Thr His Trp Gly Gln Cys Gly Gly Ile Gly Tyr Ser
 1               5                  10                  15
Gly Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys Gln Tyr Ser Asn Asp
            20                  25                  30
Tyr Tyr Ser Gln Cys Leu
        35


<210> 805
<211> 371
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Endoglucanase I From Trichoderma Reesei
371 aa protein 1EG1_A GI:239236

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 805
Xaa Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys Leu Thr Thr
 1               5                  10                  15
Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp Thr Ser Val
            20                  25                  30
Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn Tyr Asn Ser
        35                  40                  45
Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro Asp Glu Ala
    50                  55                  60
Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala Ser
65                  70                  75                  80
Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln Tyr Met Pro
                85                  90                  95
Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu Leu
            100                 105                 110
Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly Gln Glu Leu
        115                 120                 125
Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly Ser
    130                 135                 140

```
Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr Asn
145                 150                 155                 160
Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys Pro
                165                 170                 175
Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His Gln Gly Phe
            180                 185                 190
Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn Ala
        195                 200                 205
Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly Cys
    210                 215                 220
Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro Gly
225                 230                 235                 240
Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe Asn
                245                 250                 255
Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg Lys
            260                 265                 270
Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly Asp
        275                 280                 285
Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala Thr
    290                 295                 300
Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile Trp
305                 310                 315                 320
Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala Gly
                325                 330                 335
Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Ile Leu Ala Asn Asn
            340                 345                 350
Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile Gly
        355                 360                 365
Ser Thr Thr
    370


<210> 806
<211> 371
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain C, Endoglucanase I From Trichoderma Reesei
      371 aa protein 1EG1_C GI:239237

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 806
Xaa Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys Leu Thr Thr
 1               5                  10                  15
Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp Thr Ser Val
            20                  25                  30
Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn Tyr Asn Ser
        35                  40                  45
Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro Asp Glu Ala
```

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

<210> 807
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> endoglucanase [Trichoderma reesei RUT C-3] 764 aa
protein ETS6856.1 GI:572283882

<400> 807

```
Met Arg Ser Phe Ser Leu Leu Gly Ser Leu Ser Leu Leu Thr Ser Leu
```

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

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


<210> 808
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> endoglucanase, partial [Trichoderma reesei] 242 aa
      protein AHK2346.1 GI:58829453

<400> 808
Met Lys Ala Thr Leu Val Leu Gly Ser Leu Ile Val Gly Ala Val Ser
```

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

<210> 809
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Hypocrea Jecorina Cel7a E212q Mutant In
Complex With P-nitrophenyl Cellobioside 434 aa
protein 4UWT_A GI:922664681

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 809

```
Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
```

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

<210> 810

<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, O-nitrophenyl Cellobioside As An Active
Site Probe For Family 7 Cellobiohydrolases 434 aa
protein 4VZ_A GI:931139719

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 810
Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe Val
                85                  90                  95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
            100                 105                 110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
        115                 120                 125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
    130                 135                 140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145                 150                 155                 160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                165                 170                 175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
            180                 185                 190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
        195                 200                 205
Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
    210                 215                 220
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly
225                 230                 235                 240
Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys
                245                 250                 255
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
            260                 265                 270
Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
        275                 280                 285
Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr
    290                 295                 300
Val Gln Asp Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser

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

<210> 811
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Hypocrea Jecorina Cel7a (wild Type)
Soaked With Xylopentaose 434 aa protein 4D5Q_A
GI:783282859

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 811
Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
1 5 10 15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
20 25 30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
35 40 45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
50 55 60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65 70 75 80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe Val
85 90 95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
100 105 110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
115 120 125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
130 135 140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr

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

<210> 812
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Cbh1 In Complex With S-propranolol 434 aa
protein 1DY4_A GI:1284415

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 812

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

Ser Gly

<210> 813
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 6 [Trichoderma reesei QM6a] 471 aa protein XP_696258.1 GI:58911115

<400> 813
Met Ile Val Gly Ile Leu Thr Thr Leu Ala Thr Leu Ala Thr Leu Ala
 1               5                  10                  15
Ala Ser Val Pro Leu Glu Glu Arg Gln Ala Cys Ser Ser Val Trp Gly
            20                  25                  30
Gln Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly
        35                  40                  45
Ser Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Gly
    50                  55                  60
Ala Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg
65                  70                  75                  80
Val Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly
                85                  90                  95
Ser Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr
            100                 105                 110
Ser Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr
        115                 120                 125
Ala Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met
    130                 135                 140
Ala Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu
145                 150                 155                 160
Asp Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile
                165                 170                 175
Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val
            180                 185                 190
Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu
        195                 200                 205
Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp
    210                 215                 220
Thr Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu
225                 230                 235                 240
Val Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr
                245                 250                 255
Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr
            260                 265                 270
Ala Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala
        275                 280                 285
Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala
    290                 295                 300
Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu
305                 310                 315                 320

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

<210> 814
<211> 514
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 7 [Trichoderma reesei QM6a] 514 aa protein XP_6969224.1 GI:58911443

<400> 814

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

```
Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln
            180                 185                 190
Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly
        195                 200                 205
Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly
    210                 215                 220
Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu
225                 230                 235                 240
Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu
                245                 250                 255
Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr
            260                 265                 270
Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr
        275                 280                 285
Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys
    290                 295                 300
Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr
305                 310                 315                 320
Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly
                325                 330                 335
Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu
            340                 345                 350
Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln
        355                 360                 365
Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp
    370                 375                 380
Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr
385                 390                 395                 400
Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr
                405                 410                 415
Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys
            420                 425                 430
Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn
        435                 440                 445
Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr
    450                 455                 460
Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln
465                 470                 475                 480
Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val
                485                 490                 495
Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln
            500                 505                 510
Cys Leu
```

<210> 815
<211> 514
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 7 [Trichoderma reesei QM6a] 514 aa protein EGR44817.1 GI:34514556

<400> 815
```
Met Tyr Arg Lys Leu Ala Val Ile Ser Ala Phe Leu Ala Thr Ala Arg
 1               5                  10                  15
Ala Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr
            20                  25                  30
Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser
        35                  40                  45
Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser
    50                  55                  60
Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp
65                  70                  75                  80
Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala
                85                  90                  95
Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe
            100                 105                 110
Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met
        115                 120                 125
Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe
    130                 135                 140
Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala
145                 150                 155                 160
Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro
                165                 170                 175
Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln
            180                 185                 190
Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly
        195                 200                 205
Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly
    210                 215                 220
Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu
225                 230                 235                 240
Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu
                245                 250                 255
Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr
            260                 265                 270
Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr
        275                 280                 285
Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys
    290                 295                 300
Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr
305                 310                 315                 320
Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly
                325                 330                 335
Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu
            340                 345                 350
Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln
        355                 360                 365
Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp
    370                 375                 380
Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr
385                 390                 395                 400
Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr
                405                 410                 415
```

```
Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys
            420                 425                 430
Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn
        435                 440                 445
Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr
    450                 455                 460
Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln
465                 470                 475                 480
Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val
                485                 490                 495
Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln
            500                 505                 510
Cys Leu
```

<210> 816
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> glycoside hydrolase family 6 [Trichoderma reesei QM6a] 471 aa protein EGR5117.1 GI:3452782

<400> 816

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

```
Thr Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu
225                 230                 235                 240
Val Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr
                245                 250                 255
Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr
            260                 265                 270
Ala Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala
        275                 280                 285
Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala
    290                 295                 300
Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu
305                 310                 315                 320
Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr
                325                 330                 335
Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu
            340                 345                 350
Tyr Ile His Ala Ile Gly Pro Leu Leu Ala Asn His Gly Trp Ser Asn
        355                 360                 365
Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly
    370                 375                 380
Gln Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly
385                 390                 395                 400
Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val
                405                 410                 415
Trp Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala
            420                 425                 430
Pro Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala
        435                 440                 445
Pro Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr
    450                 455                 460
Asn Ala Asn Pro Ser Phe Leu
465                 470


<210> 817
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Hypocrea Jecorina Cellobiohydrolase Cel7a
      E212q Soaked With Xylotriose 434 aa protein 4D5I_A
      GI:783282849

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 817
Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30
```

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

<210> 818
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Hypocrea Jecorina Cellobiohydrolase Cel7a
E217q Soaked With Xylopentaose 434 aa protein
4D5P_A GI:783282856

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 818
Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Asp Phe Val
                85                  90                  95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
            100                 105                 110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
        115                 120                 125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
    130                 135                 140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145                 150                 155                 160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                165                 170                 175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
            180                 185                 190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
        195                 200                 205
Cys Cys Ser Glu Met Asp Ile Trp Gln Ala Asn Ser Ile Ser Glu Ala
    210                 215                 220
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly
225                 230                 235                 240
Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys
                245                 250                 255
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
            260                 265                 270
Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
        275                 280                 285
Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr
    290                 295                 300

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

<210> 819
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Hypocrea Jecorina Cel7a In Complex With
(R)-Dihydroxy- Phenanthrenolol 434 aa protein
2V3I_A GI:19356563

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 819

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

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

<210> 820
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Hypocrea Jecorina Cel7a In Complex With
(S)-Dihydroxy- Phenanthrenolol 434 aa protein
2V3R_A GI:19356564

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 820
Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe Val
                85                  90                  95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
            100                 105                 110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
        115                 120                 125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
    130                 135                 140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145                 150                 155                 160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                165                 170                 175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
            180                 185                 190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
        195                 200                 205
Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
    210                 215                 220
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly
225                 230                 235                 240
Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys
                245                 250                 255
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
            260                 265                 270
Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
        275                 280                 285
Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr
    290                 295                 300
Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser
305                 310                 315                 320
Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ala
                325                 330                 335
Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe
            340                 345                 350
Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp
        355                 360                 365
Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn
    370                 375                 380
Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser
385                 390                 395                 400
Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys Val
                405                 410                 415

```
Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Pro
            420                 425                 430
Ser Gly
```

<210> 821
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Michaelis Complex Of Hypocrea Jecorina
Cel7a E217q Mutant With Cellononaose Spanning The
Active Site 434 aa protein 4C4C_A GI:57215318

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 821

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

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

<210> 822
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Covalent Glycosyl-enzyme Intermediate Of
Hypocrea Jecorina Cel7a E217q Mutant Trapped Using
Dnp-2-deoxy-2-fluoro-cellotrioside 434 aa protein
4C4D_A GI:572153181

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 822

```
Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Asp Phe Val
```

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

<210> 823
<211> 365
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Cel6a D175a Mutant 365 aa protein 1HGW_A

GI:1865599

<400> 823
Ser Gly Thr Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro
 1               5                  10                  15
Trp Ala Asn Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro
            20                  25                  30
Ser Leu Thr Gly Ala Met Ala Thr Ala Ala Ala Ala Val Ala Lys Val
        35                  40                  45
Pro Ser Phe Met Trp Leu Asp Thr Leu Asp Lys Thr Pro Leu Met Glu
    50                  55                  60
Gln Thr Leu Ala Asp Ile Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr
65                  70                  75                  80
Ala Gly Gln Phe Val Val Tyr Asp Leu Pro Asp Arg Ala Cys Ala Ala
                85                  90                  95
Leu Ala Ser Asn Gly Glu Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys
            100                 105                 110
Tyr Lys Asn Tyr Ile Asp Thr Ile Arg Gln Ile Val Val Glu Tyr Ser
        115                 120                 125
Asp Ile Arg Thr Leu Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Leu
    130                 135                 140
Val Thr Asn Leu Gly Thr Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr
145                 150                 155                 160
Leu Glu Cys Ile Asn Tyr Ala Val Thr Gln Leu Asn Leu Pro Asn Val
                165                 170                 175
Ala Met Tyr Leu Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala
            180                 185                 190
Asn Gln Asp Pro Ala Ala Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala
        195                 200                 205
Ser Ser Pro Arg Ala Leu Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr
    210                 215                 220
Asn Gly Trp Asn Ile Thr Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala
225                 230                 235                 240
Val Tyr Asn Glu Lys Leu Tyr Ile His Ala Ile Gly Pro Leu Leu Ala
                245                 250                 255
Asn His Gly Trp Ser Asn Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser
            260                 265                 270
Gly Lys Gln Pro Thr Gly Gln Gln Gln Trp Gly Asp Trp Cys Asn Val
        275                 280                 285
Ile Gly Thr Gly Phe Gly Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser
    290                 295                 300
Leu Leu Asp Ser Phe Val Trp Val Lys Pro Gly Gly Glu Cys Asp Gly
305                 310                 315                 320
Thr Ser Asp Ser Ser Ala Pro Arg Phe Asp Ser His Cys Ala Leu Pro
                325                 330                 335
Asp Ala Leu Gln Pro Ala Pro Gln Ala Gly Ala Trp Phe Gln Ala Tyr
            340                 345                 350
Phe Val Gln Leu Leu Thr Asn Ala Asn Pro Ser Phe Leu
        355                 360                 365

<210> 824
<211> 365
<212> PRT

<213> Artificial Sequence

<220>
<223> Chain B, Cel6a D175a Mutant 365 aa protein 1HGW_B
GI:1865591

<400> 824
```
Ser Gly Thr Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro
 1               5                  10                  15
Trp Ala Asn Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro
            20                  25                  30
Ser Leu Thr Gly Ala Met Ala Thr Ala Ala Ala Ala Val Ala Lys Val
        35                  40                  45
Pro Ser Phe Met Trp Leu Asp Thr Leu Asp Lys Thr Pro Leu Met Glu
    50                  55                  60
Gln Thr Leu Ala Asp Ile Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr
65                  70                  75                  80
Ala Gly Gln Phe Val Val Tyr Asp Leu Pro Asp Arg Ala Cys Ala Ala
                85                  90                  95
Leu Ala Ser Asn Gly Glu Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys
            100                 105                 110
Tyr Lys Asn Tyr Ile Asp Thr Ile Arg Gln Ile Val Val Glu Tyr Ser
        115                 120                 125
Asp Ile Arg Thr Leu Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Leu
    130                 135                 140
Val Thr Asn Leu Gly Thr Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr
145                 150                 155                 160
Leu Glu Cys Ile Asn Tyr Ala Val Thr Gln Leu Asn Leu Pro Asn Val
                165                 170                 175
Ala Met Tyr Leu Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala
            180                 185                 190
Asn Gln Asp Pro Ala Ala Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala
        195                 200                 205
Ser Ser Pro Arg Ala Leu Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr
    210                 215                 220
Asn Gly Trp Asn Ile Thr Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala
225                 230                 235                 240
Val Tyr Asn Glu Lys Leu Tyr Ile His Ala Ile Gly Pro Leu Leu Ala
                245                 250                 255
Asn His Gly Trp Ser Asn Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser
            260                 265                 270
Gly Lys Gln Pro Thr Gly Gln Gln Gln Trp Gly Asp Trp Cys Asn Val
        275                 280                 285
Ile Gly Thr Gly Phe Gly Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser
    290                 295                 300
Leu Leu Asp Ser Phe Val Trp Val Lys Pro Gly Gly Glu Cys Asp Gly
305                 310                 315                 320
Thr Ser Asp Ser Ser Ala Pro Arg Phe Asp Ser His Cys Ala Leu Pro
                325                 330                 335
Asp Ala Leu Gln Pro Ala Pro Gln Ala Gly Ala Trp Phe Gln Ala Tyr
            340                 345                 350
Phe Val Gln Leu Leu Thr Asn Ala Asn Pro Ser Phe Leu
        355                 360                 365
```

<210> 825
<211> 365
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Cel6a D221a Mutant 365 aa protein 1HGY_A
GI:18655911

<400> 825
Ser Gly Thr Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro
 1               5                  10                  15
Trp Ala Asn Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro
            20                  25                  30
Ser Leu Thr Gly Ala Met Ala Thr Ala Ala Ala Ala Val Ala Lys Val
        35                  40                  45
Pro Ser Phe Met Trp Leu Asp Thr Leu Asp Lys Thr Pro Leu Met Glu
    50                  55                  60
Gln Thr Leu Ala Asp Ile Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr
65                  70                  75                  80
Ala Gly Gln Phe Val Val Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala
                85                  90                  95
Leu Ala Ser Asn Gly Glu Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys
            100                 105                 110
Tyr Lys Asn Tyr Ile Asp Thr Ile Arg Gln Ile Val Val Glu Tyr Ser
        115                 120                 125
Asp Ile Arg Thr Leu Leu Val Ile Glu Pro Ala Ser Leu Ala Asn Leu
    130                 135                 140
Val Thr Asn Leu Gly Thr Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr
145                 150                 155                 160
Leu Glu Cys Ile Asn Tyr Ala Val Thr Gln Leu Asn Leu Pro Asn Val
                165                 170                 175
Ala Met Tyr Leu Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala
            180                 185                 190
Asn Gln Asp Pro Ala Ala Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala
        195                 200                 205
Ser Ser Pro Arg Ala Leu Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr
    210                 215                 220
Asn Gly Trp Asn Ile Thr Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala
225                 230                 235                 240
Val Tyr Asn Glu Lys Leu Tyr Ile His Ala Ile Gly Pro Leu Leu Ala
                245                 250                 255
Asn His Gly Trp Ser Asn Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser
            260                 265                 270
Gly Lys Gln Pro Thr Gly Gln Gln Gln Trp Gly Asp Trp Cys Asn Val
        275                 280                 285
Ile Gly Thr Gly Phe Gly Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser
    290                 295                 300
Leu Leu Asp Ser Phe Val Trp Val Lys Pro Gly Gly Glu Cys Asp Gly
305                 310                 315                 320
Thr Ser Asp Ser Ser Ala Pro Arg Phe Asp Ser His Cys Ala Leu Pro
                325                 330                 335
Asp Ala Leu Gln Pro Ala Pro Gln Ala Gly Ala Trp Phe Gln Ala Tyr

```
            340                 345                 350
Phe Val Gln Leu Leu Thr Asn Ala Asn Pro Ser Phe Leu
        355                 360                 365


<210> 826
<211> 365
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, Cel6a D221a Mutant 365 aa protein 1HGY_B
      GI:18655912

<400> 826
Ser Gly Thr Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro
 1               5                  10                  15
Trp Ala Asn Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro
            20                  25                  30
Ser Leu Thr Gly Ala Met Ala Thr Ala Ala Ala Ala Val Ala Lys Val
        35                  40                  45
Pro Ser Phe Met Trp Leu Asp Thr Leu Asp Lys Thr Pro Leu Met Glu
    50                  55                  60
Gln Thr Leu Ala Asp Ile Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr
65                  70                  75                  80
Ala Gly Gln Phe Val Val Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala
                85                  90                  95
Leu Ala Ser Asn Gly Glu Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys
            100                 105                 110
Tyr Lys Asn Tyr Ile Asp Thr Ile Arg Gln Ile Val Val Glu Tyr Ser
        115                 120                 125
Asp Ile Arg Thr Leu Leu Val Ile Glu Pro Ala Ser Leu Ala Asn Leu
    130                 135                 140
Val Thr Asn Leu Gly Thr Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr
145                 150                 155                 160
Leu Glu Cys Ile Asn Tyr Ala Val Thr Gln Leu Asn Leu Pro Asn Val
                165                 170                 175
Ala Met Tyr Leu Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala
            180                 185                 190
Asn Gln Asp Pro Ala Ala Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala
        195                 200                 205
Ser Ser Pro Arg Ala Leu Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr
    210                 215                 220
Asn Gly Trp Asn Ile Thr Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala
225                 230                 235                 240
Val Tyr Asn Glu Lys Leu Tyr Ile His Ala Ile Gly Pro Leu Leu Ala
                245                 250                 255
Asn His Gly Trp Ser Asn Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser
            260                 265                 270
Gly Lys Gln Pro Thr Gly Gln Gln Gln Trp Gly Asp Trp Cys Asn Val
        275                 280                 285
Ile Gly Thr Gly Phe Gly Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser
    290                 295                 300
Leu Leu Asp Ser Phe Val Trp Val Lys Pro Gly Gly Glu Cys Asp Gly
```

305 310 315 320
Thr Ser Asp Ser Ser Ala Pro Arg Phe Asp Ser His Cys Ala Leu Pro
325 330 335
Asp Ala Leu Gln Pro Ala Pro Gln Ala Gly Ala Trp Phe Gln Ala Tyr
340 345 350
Phe Val Gln Leu Leu Thr Asn Ala Asn Pro Ser Phe Leu
355 360 365

<210> 827
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<223> cellobiohydrolase,beta glucan 49 aa protein 13195A
GI:223874

<220>
<221> VARIANT
<222> 348, 349
<223> Xaa = Any Amino Acid

<400> 827
Glu Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
1 5 10 15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
20 25 30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
35 40 45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
50 55 60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Thr Ser
65 70 75 80
Ala Tyr Ser Ser Glx Pro Gly Gly Gly Gly Gly Val Val Ile Phe Phe
85 90 95
Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala Ser Asp Thr Thr Tyr
100 105 110
Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser Phe Asp Val Asp Val
115 120 125
Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu Tyr Phe Val Ser Met
130 135 140
Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr Asn Thr Ala Gly Ala
145 150 155 160
Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys Pro Arg Asp Leu Lys
165 170 175
Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp Glu Pro Ser Ser Asn
180 185 190
Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser Cys Cys Ser Glu Met
195 200 205
Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala Leu Thr Pro His Pro
210 215 220
Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly Asp Gly Cys Gly Gly
225 230 235 240

```
Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys Asp Pro Asp Gly Cys
                245                 250                 255
Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser Phe Tyr Gly Pro Gly
            260                 265                 270
Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu Thr Val Val Thr Gln
        275                 280                 285
Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr Val Gln Asp Gly Val
    290                 295                 300
Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser Tyr Ser Gly Asn Glu
305                 310                 315                 320
Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ala Glu Phe Gly Gly Ser
                325                 330                 335
Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe Xaa Xaa Ala Thr Ser
            340                 345                 350
Gly Gly Met Val Leu Val Met Ser Leu Trp Asp Asp Tyr Tyr Ala Asn
        355                 360                 365
Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn Glu Thr Ser Ser Thr
    370                 375                 380
Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser Ser Gly Val Pro Ala
385                 390                 395                 400
Gln Val Glu Ser Gln Ser Pro Asn Ala Lys Val Thr Phe Ser Asn Ile
                405                 410                 415
Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Pro Ser Gly Gly Asn Pro
            420                 425                 430
Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr Thr Thr Thr Thr Ser Ser
        435                 440                 445
Ser Glx Pro Pro Pro Gly Ala His Arg Arg Tyr Gly Gln Cys Gly Gly
    450                 455                 460
Ile Gly Tyr Ser Gly Pro Thr Val Cys Ala Ser Gly Thr Thr Cys Gln
465                 470                 475                 480
Val Leu Asn Pro Tyr Tyr Ser Gln Cys Leu
                485                 490


<210> 828
<211> 365
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Cel6a (y169f) With A Non-hydrolysable
      Cellotetraose 365 aa protein 1QJW_A GI:6137482

<400> 828
Ser Gly Thr Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro
 1               5                  10                  15
Trp Ala Asn Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro
            20                  25                  30
Ser Leu Thr Gly Ala Met Ala Thr Ala Ala Ala Ala Val Ala Lys Val
        35                  40                  45
Pro Ser Phe Met Trp Leu Asp Thr Leu Asp Lys Thr Pro Leu Met Glu
    50                  55                  60
Gln Thr Leu Ala Asp Ile Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr
65                  70                  75                  80
```

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

<210> 829
<211> 365
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, Cel6a (y169f) With A Non-hydrolysable
Cellotetraose 365 aa protein 1QJW_B GI:6137483

<400> 829

```
Ser Gly Thr Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro
 1               5                  10                  15
Trp Ala Asn Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro
            20                  25                  30
Ser Leu Thr Gly Ala Met Ala Thr Ala Ala Ala Ala Val Ala Lys Val
        35                  40                  45
```

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

<210> 830
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Cel6a In Complex With M-iodobenzyl
Beta-d-glucopyranosyl- Beta(1,4)-d-xylopyranoside
363 aa protein 1QK_A GI:6137484

<400> 830
```
Thr Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala
```

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

<210> 831
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, Cel6a In Complex With M-iodobenzyl

Beta-d-glucopyranosyl- Beta(1,4)-d-xylopyranoside
363 aa protein 1QK_B GI:6137485

<400> 831

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

<210> 832
<211> 363

<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Wild Type Cel6a With A Non-hydrolysable
Cellotetraose 363 aa protein 1QK2_A GI:6137486

<400> 832
Thr Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala
 1               5                  10                  15
Asn Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu
            20                  25                  30
Thr Gly Ala Met Ala Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser
        35                  40                  45
Phe Met Trp Leu Asp Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr
    50                  55                  60
Leu Ala Asp Ile Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly
65                  70                  75                  80
Gln Phe Val Val Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala
                85                  90                  95
Ser Asn Gly Glu Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys
            100                 105                 110
Asn Tyr Ile Asp Thr Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile
        115                 120                 125
Arg Thr Leu Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr
    130                 135                 140
Asn Leu Gly Thr Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu
145                 150                 155                 160
Cys Ile Asn Tyr Ala Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met
                165                 170                 175
Tyr Leu Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln
            180                 185                 190
Asp Pro Ala Ala Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser
        195                 200                 205
Pro Arg Ala Leu Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly
    210                 215                 220
Trp Asn Ile Thr Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr
225                 230                 235                 240
Asn Glu Lys Leu Tyr Ile His Ala Ile Gly Pro Leu Leu Ala Asn His
                245                 250                 255
Gly Trp Ser Asn Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys
            260                 265                 270
Gln Pro Thr Gly Gln Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly
        275                 280                 285
Thr Gly Phe Gly Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu
    290                 295                 300
Asp Ser Phe Val Trp Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser
305                 310                 315                 320
Asp Ser Ser Ala Pro Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala
                325                 330                 335
Leu Gln Pro Ala Pro Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val
            340                 345                 350
Gln Leu Leu Thr Asn Ala Asn Pro Ser Phe Leu
        355                 360

<210> 833
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, Wild Type Cel6a With A Non-hydrolysable
Cellotetraose 363 aa protein 1QK2_B GI:6137487

<400> 833
Thr Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala
 1               5                  10                  15
Asn Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu
            20                  25                  30
Thr Gly Ala Met Ala Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser
        35                  40                  45
Phe Met Trp Leu Asp Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr
    50                  55                  60
Leu Ala Asp Ile Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly
65                  70                  75                  80
Gln Phe Val Val Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala
                85                  90                  95
Ser Asn Gly Glu Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys
            100                 105                 110
Asn Tyr Ile Asp Thr Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile
        115                 120                 125
Arg Thr Leu Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr
    130                 135                 140
Asn Leu Gly Thr Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu
145                 150                 155                 160
Cys Ile Asn Tyr Ala Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met
                165                 170                 175
Tyr Leu Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln
            180                 185                 190
Asp Pro Ala Ala Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser
        195                 200                 205
Pro Arg Ala Leu Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly
    210                 215                 220
Trp Asn Ile Thr Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr
225                 230                 235                 240
Asn Glu Lys Leu Tyr Ile His Ala Ile Gly Pro Leu Leu Ala Asn His
                245                 250                 255
Gly Trp Ser Asn Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys
            260                 265                 270
Gln Pro Thr Gly Gln Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly
        275                 280                 285
Thr Gly Phe Gly Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu
    290                 295                 300
Asp Ser Phe Val Trp Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser
305                 310                 315                 320
Asp Ser Ser Ala Pro Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala
                325                 330                 335

```
Leu Gln Pro Ala Pro Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val
            340                 345                 350
Gln Leu Leu Thr Asn Ala Asn Pro Ser Phe Leu
        355                 360
```

<210> 834
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName:Full=Exoglucanase 2;AltName:Full=1,4-beta-
cellobiohydrolase;AltName:Full=Exocellobiohydrolas
e II;Short=CBHII;AltName:Full=Exoglucanase II;
Flags:Precursor 471 aa protein P7987.1 GI:121855

<400> 834

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

```
Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala
    290                 295                 300
Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu
305                 310                 315                 320
Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr
                325                 330                 335
Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu
            340                 345                 350
Tyr Ile His Ala Ile Gly Pro Leu Leu Ala Asn His Gly Trp Ser Asn
        355                 360                 365
Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly
    370                 375                 380
Gln Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly
385                 390                 395                 400
Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val
                405                 410                 415
Trp Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala
            420                 425                 430
Pro Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala
        435                 440                 445
Pro Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr
    450                 455                 460
Asn Ala Asn Pro Ser Phe Leu
465                 470
```

<210> 835
<211> 513
<212> PRT
<213> Artificial Sequence

<220>
<223> RecName:Full=Exoglucanase 1;AltName:Full=1,4-beta-
cellobiohydrolase;AltName:Full=Exocellobiohydrolas
e I; Short=CBHI;AltName:Full=Exoglucanase I;
Flags:Precursor 513 aa protein P62694.1 GI:542144

<400> 835

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

```
Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe
    130                 135                 140
Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala
145                 150                 155                 160
Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro
                165                 170                 175
Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln
            180                 185                 190
Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly
        195                 200                 205
Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly
    210                 215                 220
Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu
225                 230                 235                 240
Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu
                245                 250                 255
Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr
            260                 265                 270
Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr
        275                 280                 285
Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys
    290                 295                 300
Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr
305                 310                 315                 320
Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly
                325                 330                 335
Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu
            340                 345                 350
Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln
        355                 360                 365
Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp
    370                 375                 380
Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr
385                 390                 395                 400
Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr
                405                 410                 415
Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys
            420                 425                 430
Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn
        435                 440                 445
Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Arg Gly Thr Thr Thr Thr
    450                 455                 460
Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln Ser
465                 470                 475                 480
His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val Cys
                485                 490                 495
Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln Cys
            500                 505                 510
Leu
```

<210> 836
<211> 471

<212> PRT
<213> Artificial Sequence

<220>
<223> unnamed protein product [Trichoderma reesei]
      471 aa protein CAV28333.1 GI:21829938

<400> 836
Met Ile Val Gly Ile Leu Thr Thr Leu Ala Thr Leu Ala Thr Leu Ala
 1               5                  10                  15
Ala Ser Val Pro Leu Glu Glu Arg Gln Ala Cys Ser Ser Val Trp Gly
            20                  25                  30
Gln Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly
        35                  40                  45
Ser Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Gly
    50                  55                  60
Ala Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg
65                  70                  75                  80
Val Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly
                85                  90                  95
Ser Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr
            100                 105                 110
Ser Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr
        115                 120                 125
Ala Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met
    130                 135                 140
Ala Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu
145                 150                 155                 160
Asp Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile
                165                 170                 175
Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val
            180                 185                 190
Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu
        195                 200                 205
Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp
    210                 215                 220
Thr Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu
225                 230                 235                 240
Val Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr
                245                 250                 255
Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr
            260                 265                 270
Ala Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala
        275                 280                 285
Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala
    290                 295                 300
Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu
305                 310                 315                 320
Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr
                325                 330                 335
Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu
            340                 345                 350
Tyr Ile His Ala Ile Gly Pro Leu Leu Ala Asn His Gly Trp Ser Asn
        355                 360                 365

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


<210> 837
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> cellobiohydrolase II 471 aa protein 134188A
      GI:225475

<400> 837
Met Ile Val Gly Ile Leu Thr Thr Leu Ala Thr Leu Ala Thr Leu Ala
 1               5                  10                  15
Ala Ser Val Pro Leu Glu Glu Arg Gln Ala Cys Ser Ser Val Trp Gly
            20                  25                  30
Gln Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly
        35                  40                  45
Ser Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Gly
    50                  55                  60
Ala Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg
65                  70                  75                  80
Val Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly
                85                  90                  95
Ser Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr
            100                 105                 110
Ser Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr
        115                 120                 125
Ala Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met
    130                 135                 140
Ala Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu
145                 150                 155                 160
Asp Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile
                165                 170                 175
Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val
            180                 185                 190
Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu
        195                 200                 205
Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp
    210                 215                 220
```

```
Thr Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu
225                 230                 235                 240
Val Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr
                245                 250                 255
Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr
            260                 265                 270
Ala Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala
        275                 280                 285
Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala
    290                 295                 300
Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu
305                 310                 315                 320
Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr
                325                 330                 335
Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu
            340                 345                 350
Tyr Ile His Ala Ile Gly Pro Leu Leu Ala Asn His Gly Trp Ser Asn
        355                 360                 365
Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly
    370                 375                 380
Gln Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly
385                 390                 395                 400
Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val
                405                 410                 415
Trp Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala
            420                 425                 430
Pro Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala
        435                 440                 445
Pro Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr
    450                 455                 460
Asn Ala Asn Pro Ser Phe Leu
465                 470


<210> 838
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> unnamed [Trichoderma reesei] 471 aa protein
      AAA72922.1 GI:17543

<400> 838
Met Ile Val Gly Ile Leu Thr Thr Leu Ala Thr Leu Ala Thr Leu Ala
 1               5                  10                  15
Ala Ser Val Pro Leu Glu Glu Arg Gln Ala Cys Ser Ser Val Trp Gly
            20                  25                  30
Gln Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly
        35                  40                  45
Ser Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Gly
    50                  55                  60
Ala Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg
65                  70                  75                  80
```

```
Val Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly
                85                  90                  95
Ser Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr
            100                 105                 110
Ser Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr
        115                 120                 125
Ala Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met
    130                 135                 140
Ala Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu
145                 150                 155                 160
Asp Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile
                165                 170                 175
Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val
            180                 185                 190
Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu
        195                 200                 205
Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp
    210                 215                 220
Thr Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu
225                 230                 235                 240
Val Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr
                245                 250                 255
Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr
            260                 265                 270
Ala Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala
        275                 280                 285
Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala
    290                 295                 300
Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu
305                 310                 315                 320
Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr
                325                 330                 335
Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu
            340                 345                 350
Tyr Ile His Ala Ile Gly Arg Leu Leu Ala Asn His Gly Trp Ser Asn
        355                 360                 365
Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly
    370                 375                 380
Gln Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly
385                 390                 395                 400
Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val
                405                 410                 415
Trp Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala
            420                 425                 430
Pro Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala
        435                 440                 445
Ala Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr
    450                 455                 460
Asn Ala Asn Pro Ser Phe Leu
465                 470
```

<210> 839
<211> 434

<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Hypocrea Jecorina Cellobiohydrolase Cel7a
E217q Soaked With Xylotriose 434 aa protein 4D5J_A
GI:783282851

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 839
Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Asp Phe Val
                85                  90                  95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
            100                 105                 110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
        115                 120                 125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
    130                 135                 140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145                 150                 155                 160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                165                 170                 175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
            180                 185                 190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
        195                 200                 205
Cys Cys Ser Glu Met Asp Ile Trp Gln Ala Asn Ser Ile Ser Glu Ala
    210                 215                 220
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly
225                 230                 235                 240
Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys
                245                 250                 255
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
            260                 265                 270
Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
        275                 280                 285
Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr
    290                 295                 300
Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser
305                 310                 315                 320

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

<210> 840
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Hypocrea Jecorina Cellobiohydrolase Cel7a
E212q Soaked With Xylopentaose 434 aa protein
4D5O_A GI:783282853

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 840

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Xaa Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
 1               5                  10                  15
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Asp Phe Val
                85                  90                  95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
            100                 105                 110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
        115                 120                 125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
    130                 135                 140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145                 150                 155                 160
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```
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                165                 170                 175
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
            180                 185                 190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
        195                 200                 205
Cys Cys Ser Gln Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
    210                 215                 220
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly
225                 230                 235                 240
Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys
                245                 250                 255
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
            260                 265                 270
Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
        275                 280                 285
Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr
    290                 295                 300
Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser
305                 310                 315                 320
Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ala
                325                 330                 335
Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe
            340                 345                 350
Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp
        355                 360                 365
Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn
    370                 375                 380
Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser
385                 390                 395                 400
Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys Val
                405                 410                 415
Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Pro
            420                 425                 430
Ser Gly
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<210> 841
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Hypocrea Jecorina Cellobiohydrolase Cel7a
E217q Soaked With Xylotetraose 434 aa protein
4D5V_A GI:783282861

<220>
<221> VARIANT
<222> 1
<223> Xaa = Any Amino Acid

<400> 841

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

Ser Gly

<210> 842
<211> 365
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Cellobiohydrolase Ii, Catalytic Domain,
Mutant Y169f 365 aa protein 1CB2_A GI:182776

<400> 842
Ser Gly Thr Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro
 1               5                  10                  15
Trp Ala Asn Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro
            20                  25                  30
Ser Leu Thr Gly Ala Met Ala Thr Ala Ala Ala Ala Val Ala Lys Val
        35                  40                  45
Pro Ser Phe Met Trp Leu Asp Thr Leu Asp Lys Thr Pro Leu Met Glu
    50                  55                  60
Gln Thr Leu Ala Asp Ile Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr
65                  70                  75                  80
Ala Gly Gln Phe Val Val Phe Asp Leu Pro Asp Arg Asp Cys Ala Ala
                85                  90                  95
Leu Ala Ser Asn Gly Glu Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys
            100                 105                 110
Tyr Lys Asn Tyr Ile Asp Thr Ile Arg Gln Ile Val Val Glu Tyr Ser
        115                 120                 125
Asp Ile Arg Thr Leu Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Leu
    130                 135                 140
Val Thr Asn Leu Gly Thr Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr
145                 150                 155                 160
Leu Glu Cys Ile Asn Tyr Ala Val Thr Gln Leu Asn Leu Pro Asn Val
                165                 170                 175
Ala Met Tyr Leu Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala
            180                 185                 190
Asn Gln Asp Pro Ala Ala Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala
        195                 200                 205
Ser Ser Pro Arg Ala Leu Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr
    210                 215                 220
Asn Gly Trp Asn Ile Thr Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala
225                 230                 235                 240
Val Tyr Asn Glu Lys Leu Tyr Ile His Ala Ile Gly Pro Leu Leu Ala
                245                 250                 255
Asn His Gly Trp Ser Asn Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser
            260                 265                 270
Gly Lys Gln Pro Thr Gly Gln Gln Gln Trp Gly Asp Trp Cys Asn Val
        275                 280                 285
Ile Gly Thr Gly Phe Gly Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser
    290                 295                 300
Leu Leu Asp Ser Phe Val Trp Val Lys Pro Gly Gly Glu Cys Asp Gly
305                 310                 315                 320

```
Thr Ser Asp Ser Ser Ala Pro Arg Phe Asp Ser His Cys Ala Leu Pro
                325                 330                 335
Asp Ala Leu Gln Pro Ala Pro Gln Ala Gly Ala Trp Phe Gln Ala Tyr
            340                 345                 350
Phe Val Gln Leu Leu Thr Asn Ala Asn Pro Ser Phe Leu
        355                 360                 365


<210> 843
<211> 365
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, Cellobiohydrolase Ii, Catalytic Domain,
      Mutant Y169f 365 aa protein 1CB2_B GI:182777

<400> 843
Ser Gly Thr Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro
 1               5                  10                  15
Trp Ala Asn Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro
            20                  25                  30
Ser Leu Thr Gly Ala Met Ala Thr Ala Ala Ala Ala Val Ala Lys Val
        35                  40                  45
Pro Ser Phe Met Trp Leu Asp Thr Leu Asp Lys Thr Pro Leu Met Glu
    50                  55                  60
Gln Thr Leu Ala Asp Ile Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr
65                  70                  75                  80
Ala Gly Gln Phe Val Val Phe Asp Leu Pro Asp Arg Asp Cys Ala Ala
                85                  90                  95
Leu Ala Ser Asn Gly Glu Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys
            100                 105                 110
Tyr Lys Asn Tyr Ile Asp Thr Ile Arg Gln Ile Val Val Glu Tyr Ser
        115                 120                 125
Asp Ile Arg Thr Leu Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Leu
    130                 135                 140
Val Thr Asn Leu Gly Thr Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr
145                 150                 155                 160
Leu Glu Cys Ile Asn Tyr Ala Val Thr Gln Leu Asn Leu Pro Asn Val
                165                 170                 175
Ala Met Tyr Leu Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala
            180                 185                 190
Asn Gln Asp Pro Ala Ala Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala
        195                 200                 205
Ser Ser Pro Arg Ala Leu Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr
    210                 215                 220
Asn Gly Trp Asn Ile Thr Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala
225                 230                 235                 240
Val Tyr Asn Glu Lys Leu Tyr Ile His Ala Ile Gly Pro Leu Leu Ala
                245                 250                 255
Asn His Gly Trp Ser Asn Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser
            260                 265                 270
Gly Lys Gln Pro Thr Gly Gln Gln Gln Trp Gly Asp Trp Cys Asn Val
        275                 280                 285
```

```
Ile Gly Thr Gly Phe Gly Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser
    290                 295                 300
Leu Leu Asp Ser Phe Val Trp Val Lys Pro Gly Gly Glu Cys Asp Gly
305                 310                 315                 320
Thr Ser Asp Ser Ser Ala Pro Arg Phe Asp Ser His Cys Ala Leu Pro
                325                 330                 335
Asp Ala Leu Gln Pro Ala Pro Gln Ala Gly Ala Trp Phe Gln Ala Tyr
            340                 345                 350
Phe Val Gln Leu Leu Thr Asn Ala Asn Pro Ser Phe Leu
        355                 360                 365
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<210> 844

<400> 844
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<210> 845
<211> 2469
<212> DNA
<213> Artificial Sequence

<220>
<223> SS2c-G1 Mating pheromone a-factor

<400> 845
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gacgacgatg aagcaattgc tgtagctaac aattcagcct caaaatttga aaatgcaaga 180
aatcacttcc gtaataacag attccatagg aagcaatctt ccgacttatt cttggctata 240
caatgcgaga aagagatcat taggaatggt gctaagaatg aaggtactac caaagtgaaa 300
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cttccatata gccttccctt tcatccaggg agaatgtggt gtcattgtag aatggtttat 840
ctgccaatgt cgtatcttta tggtaagaga tttgttggtc caatcactcc aatagtttta 900
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catttcgtca agcatagtca gattcaagag gattgtccag gtgatccaaa cgtatggttc 1440
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gattgcacag ctgagggatt gaaagcttca ctgatgttat ctaagttgcc ttctaaaatt 1560
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ttgattaacc ctgccgaaac atttggtgat atcgtaattg actacagtta tgtggaatgc 1740
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gacgggtctt ggtatggttg ttggggtgtc tgttttactt atgctggttg gtttggcatc 1920
aaaggcttag tagctgctgg tagaacatac aataattgtg ttgccattag aaaggcttgt 1980
aacttcctgt tgtcaaaaga attgcctggc ggtggttggg gcgaaagcta cctaagttgc 2040
caaaacaaag tttataccaa tctggaggga aacaagccac acttagtcaa tactgcatgg 2100
gtcatgatgg ccttgattga agcaggacaa ggggaaagag atccagctcc gttgcataga 2160
gctgccagat tgctaatcaa tagtcaattg gagtcaggtg actttccaca acaagaaatc 2220
atgggtgtgt ttaataagaa ctgtatgata acatatgccg catacagaaa catattccct 2280
atatgggctc taggtgaata ctcccatcgt gtcttggata tgggaagtgc agctcctgga 2340
agtggaagtg gttcaggaat gcaaccatct accgctaccg ccgctccaaa agaaaagacc 2400
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attgcttag 2469

<210> 846
<211> 822
<212> PRT
<213> Artificial Sequence

<220>
<223> SS2c-G10 Full Gene AA seq

<400> 846
Met Trp Arg Leu Lys Val Gly Lys Glu Ser Val Gly Glu Lys Glu Glu
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Lys Trp Ile Lys Ser Ile Ser Asn His Leu Gly Arg Gln Val Trp Glu
            20                  25                  30
Phe Cys Ser Gly Glu Asn Glu Asn Asp Asp Asp Glu Ala Ile Ala Val
        35                  40                  45
Ala Asn Asn Ser Ala Ser Lys Phe Glu Asn Ala Arg Asn His Phe Arg
    50                  55                  60
Asn Asn Arg Phe His Arg Lys Gln Ser Ser Asp Leu Phe Leu Ala Ile
65                  70                  75                  80
Gln Cys Glu Lys Glu Ile Ile Arg Asn Gly Ala Lys Asn Glu Gly Thr
                85                  90                  95
Thr Lys Val Lys Glu Gly Glu Asp Val Lys Lys Glu Ala Val Lys Asn
            100                 105                 110
Thr Leu Glu Arg Ala Leu Ser Phe Tyr Ser Ala Val Gln Thr Ser Asp
        115                 120                 125
Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro Met Phe Leu Leu Pro Gly
    130                 135                 140
Leu Val Ile Ala Leu Tyr Val Thr Gly Val Leu Asn Ser Val Leu Ser
145                 150                 155                 160
Lys His His Arg Gln Glu Met Cys Arg Tyr Ile Tyr Asn His Gln Asn
                165                 170                 175
Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly Ser Ser Thr Met Phe
            180                 185                 190
Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu Leu Gly Glu Ala Ala
        195                 200                 205
Asp Gly Gly Glu His Gly Ala Met Thr Lys Ala Arg Ser Trp Ile Leu
    210                 215                 220
Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser Trp Gly Lys Leu Trp Leu
225                 230                 235                 240

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Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn Pro Leu Pro Pro
                245                 250                 255
Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro Phe His Pro Gly Arg Met
            260                 265                 270
Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly
        275                 280                 285
Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu Ser Leu Arg Lys
    290                 295                 300
Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile Asp Trp Asn Arg Ser Arg
305                 310                 315                 320
Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met Gln
                325                 330                 335
Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu Pro Leu Phe Ser
            340                 345                 350
Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met Lys Ile Ala Met
        355                 360                 365
Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile Cys Leu Gly
    370                 375                 380
Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro
385                 390                 395                 400
Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile Pro Asp Tyr Leu
                405                 410                 415
Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn Gly Ser Gln
            420                 425                 430
Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile Ser Thr Lys Leu
        435                 440                 445
Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His His Phe Val Lys
    450                 455                 460
His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro Asn Val Trp Phe
465                 470                 475                 480
Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His Gly
                485                 490                 495
Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ser Leu Met
            500                 505                 510
Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro Leu Glu Lys Asn
        515                 520                 525
Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Glu Asn
    530                 535                 540
Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu Glu
545                 550                 555                 560
Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr Ser
                565                 570                 575
Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Ala Leu Phe Lys
            580                 585                 590
Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Ala Ala Ile Ala
        595                 600                 605
Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys Thr Asp Gly Ser Trp
    610                 615                 620
Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly Ile
625                 630                 635                 640
Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Val Ala Ile
                645                 650                 655
Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly Gly
            660                 665                 670
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Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu
        675                 680                 685
Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp Val Met Met Ala
    690                 695                 700
Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala Pro Leu His Arg
705                 710                 715                 720
Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser Gly Asp Phe Pro
                725                 730                 735
Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr
            740                 745                 750
Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Ser
        755                 760                 765
His Arg Val Leu Asp Met Gly Ser Ala Ala Pro Gly Ser Gly Ser Gly
    770                 775                 780
Ser Gly Met Gln Pro Ser Thr Ala Thr Ala Ala Pro Lys Glu Lys Thr
785                 790                 795                 800
Ser Ser Glu Lys Lys Asp Asn Tyr Ile Ile Lys Gly Val Phe Trp Asp
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Pro Ala Cys Val Ile Ala
            820
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<210> 847

<400> 847
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<210> 848
<211> 2469
<212> DNA
<213> Artificial Sequence

<220>
<223> SS2c-G10 Full gene NT Seq STEP 1

<400> 848
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gacgacgatg aagcaattgc tgtagctaac aattcagcct caaaatttga aaatgcaaga 180
aatcacttcc gtaataacag attccatagg aagcaatctt ccgacttatt cttggctata 240
caatgcgaga aagagatcat taggaatggt gctaagaatg aaggtactac caaagtgaaa 300
gaaggtgaag atgttaagaa agaagccgta aaaaatacac tagaaagagc attgtcgttc 360
tattctgctg tacagacctc tgacggtaat tgggcatcag acttgggagg acctatgttc 420
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tcgttgagaa aagagttata taccattccg taccacgaga ttgattggaa tagatccaga 960
aacacgtgtg ctaaggagga cttatattac cctcacccta agatgcaaga tatcctatgg 1020
ggcagtatct accatgtcta cgaaccgcta ttttcaggtt ggccaggtaa gagattgagg 1080
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gatggaatga gaatgcaggg ttataatggt tcacagcttt gggacactgc attcagcata 1320
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Phe Cys Ser Gly Glu Asn Glu Asn Asp Asp Asp Glu Ala Ile Ala Val
        35                  40                  45
Ala Asn Asn Ser Ala Ser Lys Phe Glu Asn Ala Arg Asn His Phe Arg
    50                  55                  60
Asn Asn Arg Phe His Arg Lys Gln Ser Ser Asp Leu Phe Leu Ala Ile
65                  70                  75                  80
Gln Cys Glu Lys Glu Ile Ile Arg Asn Gly Ala Lys Asn Glu Gly Thr
                85                  90                  95
Thr Lys Val Lys Glu Gly Glu Asp Val Lys Lys Glu Ala Val Lys Asn
            100                 105                 110
Thr Leu Glu Arg Ala Leu Ser Phe Tyr Ser Ala Val Gln Thr Ser Asp
        115                 120                 125
Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro Met Phe Leu Leu Pro Gly
    130                 135                 140
Leu Val Ile Ala Leu Tyr Val Thr Gly Val Leu Asn Ser Val Leu Ser
145                 150                 155                 160

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Lys His His Arg Gln Glu Met Cys Arg Tyr Ile Tyr Asn His Gln Asn
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Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly Ser Ser Thr Met Phe
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Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu Leu Gly Glu Ala Ala
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Asp Gly Gly Glu His Gly Ala Met Thr Lys Ala Arg Ser Trp Ile Leu
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Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser Trp Gly Lys Leu Trp Leu
225                 230                 235                 240
Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn Pro Leu Pro Pro
                245                 250                 255
Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro Phe His Pro Gly Arg Met
            260                 265                 270
Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly
        275                 280                 285
Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu Ser Leu Arg Lys
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Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile Asp Trp Asn Arg Ser Arg
305                 310                 315                 320
Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met Gln
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Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu Pro Leu Phe Ser
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Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met Lys Ile Ala Met
        355                 360                 365
Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile Cys Leu Gly
    370                 375                 380
Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro
385                 390                 395                 400
Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile Pro Asp Tyr Leu
                405                 410                 415
Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn Gly Ser Gln
            420                 425                 430
Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile Ser Thr Lys Leu
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Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His His Phe Val Lys
    450                 455                 460
His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro Asn Val Trp Phe
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Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His Gly
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Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ser Leu Met
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Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro Leu Glu Lys Asn
        515                 520                 525
Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Glu Asn
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Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu Glu
545                 550                 555                 560
Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr Ser
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Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Ala Leu Phe Lys
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Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Ala Ala Ile Ala
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Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly Ile
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Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Val Ala Ile
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Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly Gly
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Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu
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Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp Val Met Met Ala
690 695 700
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Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser Gly Asp Phe Pro
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Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr
740 745 750
Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Ser
755 760 765
His Arg Val Leu Asp Met Gly Ser Ala Ala Pro Gly Ser Gly Ser Gly
770 775 780
Ser Gly Met Gln Pro Ser Thr Ala Thr Ala Ala Pro Lys Glu Lys Thr
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Phe Cys Ser Gly Glu Asn Glu Asn Asp Asp Asp Glu Ala Ile Ala Val
        35                  40                  45

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Ala Asn Asn Ser Ala Ser Lys Phe Glu Asn Ala Arg Asn His Phe Arg
    50                  55                  60
Asn Asn Arg Phe His Arg Lys Gln Ser Ser Asp Leu Phe Leu Ala Ile
65                  70                  75                  80
Gln Cys Glu Lys Glu Ile Ile Arg Asn Gly Ala Lys Asn Glu Gly Thr
                85                  90                  95
Thr Lys Val Lys Glu Gly Glu Asp Val Lys Lys Glu Ala Val Lys Asn
            100                 105                 110
Thr Leu Glu Arg Ala Leu Ser Phe Tyr Ser Ala Val Gln Thr Ser Asp
        115                 120                 125
Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro Met Phe Leu Leu Pro Gly
    130                 135                 140
Leu Val Ile Ala Leu Tyr Val Thr Gly Val Leu Asn Ser Val Leu Ser
145                 150                 155                 160
Lys His His Arg Gln Glu Met Cys Arg Tyr Ile Tyr Asn His Gln Asn
                165                 170                 175
Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly Ser Ser Thr Met Phe
            180                 185                 190
Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu Leu Gly Glu Ala Ala
        195                 200                 205
Asp Gly Gly Glu His Gly Ala Met Thr Lys Ala Arg Ser Trp Ile Leu
    210                 215                 220
Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser Trp Gly Lys Leu Trp Leu
225                 230                 235                 240
Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn Pro Leu Pro Pro
                245                 250                 255
Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro Phe His Pro Gly Arg Met
            260                 265                 270
Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly
        275                 280                 285
Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu Ser Leu Arg Lys
    290                 295                 300
Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile Asp Trp Asn Arg Ser Arg
305                 310                 315                 320
Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met Gln
                325                 330                 335
Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu Pro Leu Phe Ser
            340                 345                 350
Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met Lys Ile Ala Met
        355                 360                 365
Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile Cys Leu Gly
    370                 375                 380
Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro
385                 390                 395                 400
Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile Pro Asp Tyr Leu
                405                 410                 415
Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn Gly Ser Gln
            420                 425                 430
Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile Ser Thr Lys Leu
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Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His His Phe Val Lys
    450                 455                 460
His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro Asn Val Trp Phe
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Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro Leu Glu Lys Asn
        515                 520                 525
Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Glu Asn
    530                 535                 540
Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu Glu
545                 550                 555                 560
Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr Ser
                565                 570                 575
Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Ala Leu Phe Lys
            580                 585                 590
Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Ala Ala Ile Ala
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Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys Thr Asp Gly Ser Trp
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Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly Ile
625                 630                 635                 640
Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Val Ala Ile
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Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly Gly
            660                 665                 670
Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu
        675                 680                 685
Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp Val Met Met Ala
    690                 695                 700
Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala Pro Leu His Arg
705                 710                 715                 720
Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser Gly Asp Phe Pro
                725                 730                 735
Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr
            740                 745                 750
Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Ser
        755                 760                 765
His Arg Val Leu Asp Met Gly Ser Ala Ala Pro Gly Ser Gly Ser Gly
    770                 775                 780
Ser Gly Met Ser Ala Ser Thr Thr Ser Leu Glu Glu Tyr Gln Lys Thr
785                 790                 795                 800
Phe Leu Glu Leu Gly Leu Glu Cys Lys Ala Leu Arg Phe Gly Ser Phe
                805                 810                 815
Lys Leu Asn Ser Gly Arg Gln Ser Pro Tyr Phe Phe Asn Leu Ser Leu
            820                 825                 830
Phe Asn Ser Gly Lys Leu Leu Ala Asn Leu Ala Thr Ala Tyr Ala Thr
        835                 840                 845
Ala Ile Ile Gln Ser Glu Leu Lys Phe Asp Val Ile Phe Gly Pro Ala
    850                 855                 860
Tyr Lys Gly Ile Pro Leu Ala Ala Ile Val Cys Val Lys Leu Ala Glu
865                 870                 875                 880
Ile Gly Gly Thr Lys Phe Gln Gly Ile Gln Tyr Ala Phe Asn Arg Lys
                885                 890                 895
Lys Val Lys Asp His Gly Glu Gly Gly Ile Ile Val Gly Ala Ser Leu
            900                 905                 910
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Glu Asp Lys Arg Val Leu Ile Ile Asp Asp Val Met Thr Ala Gly Thr
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Ala Ile Asn Glu Ala Phe Glu Ile Ile Ser Ile Ala Gln Gly Arg Val
930 935 940
Val Gly Cys Ile Val Ala Leu Asp Arg Gln Glu Val Ile His Glu Ser
945 950 955 960
Asp Pro Glu Arg Thr Ser Ala Thr Gln Ser Val Ser Lys Arg Tyr Asn
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Val Pro Val Leu Ser Ile Val Ser Leu Thr Gln Val Val Gln Phe Met
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<212> PRT
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<220>
<223> SS2d-G11 Full Gene AA seq

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Phe Cys Ser Gly Glu Asn Glu Asn Asp Asp Asp Glu Ala Ile Ala Val
        35                  40                  45
Ala Asn Asn Ser Ala Ser Lys Phe Glu Asn Ala Arg Asn His Phe Arg
    50                  55                  60
Asn Asn Arg Phe His Arg Lys Gln Ser Ser Asp Leu Phe Leu Ala Ile
65                  70                  75                  80
Gln Cys Glu Lys Glu Ile Ile Arg Asn Gly Ala Lys Asn Glu Gly Thr
                85                  90                  95
Thr Lys Val Lys Glu Gly Glu Asp Val Lys Lys Glu Ala Val Lys Asn
            100                 105                 110
Thr Leu Glu Arg Ala Leu Ser Phe Tyr Ser Ala Val Gln Thr Ser Asp
        115                 120                 125
Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro Met Phe Leu Leu Pro Gly

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Leu Val Ile Ala Leu Tyr Val Thr Gly Val Leu Asn Ser Val Leu Ser
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Lys His His Arg Gln Glu Met Cys Arg Tyr Ile Tyr Asn His Gln Asn
                165                 170                 175
Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly Ser Ser Thr Met Phe
            180                 185                 190
Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu Leu Gly Glu Ala Ala
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Asp Gly Gly Glu His Gly Ala Met Thr Lys Ala Arg Ser Trp Ile Leu
    210                 215                 220
Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser Trp Gly Lys Leu Trp Leu
225                 230                 235                 240
Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn Pro Leu Pro Pro
                245                 250                 255
Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro Phe His Pro Gly Arg Met
            260                 265                 270
Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly
        275                 280                 285
Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu Ser Leu Arg Lys
    290                 295                 300
Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile Asp Trp Asn Arg Ser Arg
305                 310                 315                 320
Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met Gln
                325                 330                 335
Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu Pro Leu Phe Ser
            340                 345                 350
Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met Lys Ile Ala Met
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Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile Cys Leu Gly
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Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro
385                 390                 395                 400
Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile Pro Asp Tyr Leu
                405                 410                 415
Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn Gly Ser Gln
            420                 425                 430
Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile Ser Thr Lys Leu
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Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His His Phe Val Lys
    450                 455                 460
His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro Asn Val Trp Phe
465                 470                 475                 480
Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His Gly
                485                 490                 495
Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ser Leu Met
            500                 505                 510
Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro Leu Glu Lys Asn
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Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Glu Asn
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Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly Ile
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Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly Gly
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Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu
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Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp Val Met Met Ala
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Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala Pro Leu His Arg
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Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser Gly Asp Phe Pro
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Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr
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Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Ser
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His Arg Val Leu Asp Met Gly Ser Ala Ala Pro Gly Ser Gly Ser Gly
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Ser Gly Met Thr Glu Leu Asp Tyr Gln Gly Thr Ala Glu Ala Ala Ser
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Thr Ser Tyr Ser Arg Asn Gln Thr Asp Leu Lys Pro Phe Pro Ser Ala
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Gly Ser Ala Ser Ser Ser Ile Lys Thr Thr Glu Pro Val Lys Asp His
            820                 825                 830
Arg Arg Arg Arg Ser Ser Ser Ile Ile Ser His Val Glu Pro Glu Thr
        835                 840                 845
Phe Glu Asp Glu Asn Asp Gln Gln Leu Leu Pro Asn Met Asn Ala Thr
    850                 855                 860
Trp Val Asp Gln Arg Gly Ala Trp Ile Ile His Val Val Ile Ile Ile
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Leu Leu Lys Leu Phe Tyr Asn Leu Phe Pro Gly Val Thr Thr Glu Trp
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Ser Trp Thr Leu Thr Asn Met Thr Tyr Val Ile Gly Ser Tyr Val Met
            900                 905                 910
Phe His Leu Ile Lys Gly Thr Pro Phe Asp Phe Asn Gly Gly Ala Tyr
        915                 920                 925
Asp Asn Leu Thr Met Trp Glu Gln Ile Asp Asp Glu Thr Leu Tyr Thr
    930                 935                 940
Pro Ser Arg Lys Phe Leu Ile Ser Val Pro Ile Ala Leu Phe Leu Val
945                 950                 955                 960
Ser Thr His Tyr Ala His Tyr Asp Leu Lys Leu Phe Ser Trp Asn Cys
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Phe Leu Thr Thr Phe Gly Ala Val Val Pro Lys Leu Pro Val Thr His
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gaagttcacg gtggttcacc atggggtgcg ggtaccattg caggcagtga cggttcaaga 2880
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<212> PRT
<213> Artificial Sequence

<220>
<223> SS2e-A7a Full Gene AA seq

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

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Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu Ser Leu Arg Lys
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Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile Asp Trp Asn Arg Ser Arg
305                 310                 315                 320
Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met Gln
                325                 330                 335
Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu Pro Leu Phe Ser
            340                 345                 350
Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met Lys Ile Ala Met
        355                 360                 365
Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile Cys Leu Gly
    370                 375                 380
Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro
385                 390                 395                 400
Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile Pro Asp Tyr Leu
                405                 410                 415
Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn Gly Ser Gln
            420                 425                 430
Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile Ser Thr Lys Leu
        435                 440                 445
Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His His Phe Val Lys
    450                 455                 460
His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro Asn Val Trp Phe
465                 470                 475                 480
Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His Gly
                485                 490                 495
Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ser Leu Met
            500                 505                 510
Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro Leu Glu Lys Asn
        515                 520                 525
Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Glu Asn
    530                 535                 540
Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu Glu
545                 550                 555                 560
Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr Ser
                565                 570                 575
Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Ala Leu Phe Lys
            580                 585                 590
Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Ala Ala Ile Ala
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Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys Thr Asp Gly Ser Trp
    610                 615                 620
Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly Ile
625                 630                 635                 640
Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Val Ala Ile
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Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly Gly
            660                 665                 670
Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu
        675                 680                 685
Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp Val Met Met Ala
    690                 695                 700
Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala Pro Leu His Arg
705                 710                 715                 720
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Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser Gly Asp Phe Pro
725 730 735
Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr
740 745 750
Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Ser
755 760 765
His Arg Val Leu Asp Met Gly Ser Ala Ala Pro Gly Ser Gly Ser Gly
770 775 780
Ser Gly Met Pro Arg Val Ala Ile Ile Ile Tyr Thr Leu Tyr Gly His
785 790 795 800
Val Ala Ala Thr Ala Glu Ala Glu Lys Lys Gly Ile Glu Ala Ala Gly
805 810 815
Gly Ser Ala Asp Ile Tyr Gln Val Glu Glu Thr Leu Ser Pro Glu Val
820 825 830
Val Lys Ala Leu Gly Gly Ala Pro Lys Pro Asp Tyr Pro Ile Ala Thr
835 840 845
Gln Asp Thr Leu Thr Glu Tyr Asp Ala Phe Leu Phe Gly Ile Pro Thr
850 855 860
Arg Phe Gly Asn Phe Pro Ala Gln Trp Lys Ala Phe Trp Asp Arg Thr
865 870 875 880
Gly Gly Leu Trp Ala Lys Gly Ala Leu His Gly Lys Val Ala Gly Cys
885 890 895
Phe Val Ser Thr Gly Thr Gly Gly Gly Asn Glu Ala Thr Ile Met Asn
900 905 910
Ser Leu Ser Thr Leu Ala His His Gly Ile Ile Phe Val Pro Leu Gly
915 920 925
Tyr Lys Asn Val Phe Ala Glu Leu Thr Asn Met Asp Glu Val His Gly
930 935 940
Gly Ser Pro Trp Gly Ala Gly Thr Ile Ala Gly Ser Asp Gly Ser Arg
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<400> 857
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<212> PRT
<213> Artificial Sequence

<220>
<223> SS4d-G5 Full Gene AA seq

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

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Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met Gln
                325                 330                 335
Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu Pro Leu Phe Ser
            340                 345                 350
Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met Lys Ile Ala Met
        355                 360                 365
Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile Cys Leu Gly
    370                 375                 380
Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro
385                 390                 395                 400
Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile Pro Asp Tyr Leu
                405                 410                 415
Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn Gly Ser Gln
            420                 425                 430
Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile Ser Thr Lys Leu
        435                 440                 445
Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His His Phe Val Lys
    450                 455                 460
His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro Asn Val Trp Phe
465                 470                 475                 480
Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His Gly
                485                 490                 495
Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ser Leu Met
            500                 505                 510
Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro Leu Glu Lys Asn
        515                 520                 525
Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Glu Asn
    530                 535                 540
Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu Glu
545                 550                 555                 560
Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr Ser
                565                 570                 575
Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Ala Leu Phe Lys
            580                 585                 590
Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Ala Ala Ile Ala
        595                 600                 605
Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys Thr Asp Gly Ser Trp
    610                 615                 620
Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly Ile
625                 630                 635                 640
Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Val Ala Ile
                645                 650                 655
Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly Gly
            660                 665                 670
Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu
        675                 680                 685
Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp Val Met Met Ala
    690                 695                 700
Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala Pro Leu His Arg
705                 710                 715                 720
Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser Gly Asp Phe Pro
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Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr
            740                 745                 750
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        755                 760                 765
His Arg Val Leu Asp Met Gly Ser Ala Ala Pro Gly Ser Gly Ser Gly
    770                 775                 780
Ser Gly Met Gly Lys Asn Val Leu Leu Leu Gly Ser Gly Phe Val Ala
785                 790                 795                 800
Gln Pro Val Ile Asp Thr Leu Ala Ala Asn Asp Asp Ile Asn Val Thr
                805                 810                 815
Val Ala Cys Arg Thr Leu Ala Asn Ala Gln Ala Leu Ala Lys Pro Ser
            820                 825                 830
Gly Ser Lys Ala Ile Ser Leu Asp Val Thr Asp Asp Ser Ala Leu Asp
        835                 840                 845
Lys Val Leu Ala Asp Asn Asp Val Val Ile Ser Leu Ile Pro Tyr Thr
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Phe His Pro Asn Val Val Lys Ser Ala Ile Arg Thr Lys Thr Asp Val
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Val Thr Ser Ser Tyr Ile Ser Pro Ala Leu Arg Glu Leu Glu Pro Glu
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Ile Val Lys Ala Gly Ile Thr Val Met Asn Glu Ile Gly Leu Asp Pro
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Gly Ile Asp His Leu Tyr Ala Val Lys Thr Ile Asp Glu Val His Arg
        915                 920                 925
Ala Gly Gly Lys Leu Lys Ser Phe Leu Ser Tyr Cys Gly Gly Leu Pro
    930                 935                 940
Ala Pro Glu Asp Ser Asp Asn Pro Leu Gly Tyr Lys Phe Ser Trp Ser
945                 950                 955                 960
Ser Arg Gly Val Leu Leu Ala Leu Arg Asn Ser Ala Lys Tyr Trp Lys
                965                 970                 975
Asp Gly Lys Ile Glu Thr Val Ser Ser Glu Asp Leu Met Ala Thr Ala
            980                 985                 990
Lys Pro Tyr Phe Ile Tyr Pro Gly Tyr Ala Phe Val Cys Tyr Pro Asn
        995                 1000                1005
Arg Asp Ser Thr Leu Phe Lys Asp Leu Tyr His Ile Pro Glu Ala Glu
    1010                1015                1020
Thr Val Ile Arg Gly Thr Leu Arg Tyr Gln Gly Phe Pro Glu Phe Val
1025                1030                1035                1040
Lys Ala Leu Val Asp Met Gly Met Leu Lys Asp Asp Ala Asn Glu Ile
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Phe Ser Lys Pro Ile Ala Trp Asn Glu Ala Leu Lys Gln Tyr Leu Gly
            1060                1065                1070
Ala Lys Ser Thr Ser Lys Glu Asp Leu Ile Ala Ser Ile Asp Ser Lys
        1075                1080                1085
Ala Thr Trp Lys Asp Asp Glu Asp Arg Glu Arg Ile Leu Ser Gly Phe
    1090                1095                1100
Ala Trp Leu Gly Leu Phe Ser Asp Ala Lys Ile Thr Pro Arg Gly Asn
1105                1110                1115                1120
Ala Leu Asp Thr Leu Cys Ala Arg Leu Glu Glu Leu Met Gln Tyr Glu
                1125                1130                1135
Asp Asn Glu Arg Asp Met Val Val Leu Gln His Lys Phe Gly Ile Glu
            1140                1145                1150
Trp Ala Asp Gly Thr Thr Glu Thr Arg Thr Ser Thr Leu Val Asp Tyr
        1155                1160                1165
Gly Lys Val Gly Gly Tyr Ser Ser Met Ala Ala Thr Val Gly Tyr Pro
    1170                1175                1180
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Val Ala Ile Ala Thr Lys Phe Val Leu Asp Gly Thr Ile Lys Gly Pro
1185 1190 1195 1200
Gly Leu Leu Ala Pro Tyr Ser Pro Glu Ile Asn Asp Pro Ile Met Lys
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<211> 3336
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<213> Artificial Sequence

<220>
<223> SS4d-C7 Full gene NT Seq

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gacgacgatg aagcaattgc tgtagctaac aattcagcct caaaatttga aaatgcaaga 180
aatcacttcc gtaataacag attccatagg aagcaatctt ccgacttatt cttggctata 240
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ttaaggttac taggagaagc ggcagatggc ggtgagcatg gtgcgatgac caaagcaagg 660
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aaagaaattg atgccgctat tgctaaagcc gcaaattttc tggagaatat gcagaaaaca 1860
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gtcatgatgg ccttgattga agcaggacaa ggggaaagag atccagctcc gttgcataga 2160
gctgccagat tgctaatcaa tagtcaattg gagtcaggtg actttccaca acaagaaatc 2220
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            20                  25                  30
Phe Cys Ser Gly Glu Asn Glu Asn Asp Asp Asp Glu Ala Ile Ala Val
        35                  40                  45
Ala Asn Asn Ser Ala Ser Lys Phe Glu Asn Ala Arg Asn His Phe Arg
    50                  55                  60
Asn Asn Arg Phe His Arg Lys Gln Ser Ser Asp Leu Phe Leu Ala Ile
65                  70                  75                  80
Gln Cys Glu Lys Glu Ile Ile Arg Asn Gly Ala Lys Asn Glu Gly Thr
                85                  90                  95
Thr Lys Val Lys Glu Gly Glu Asp Val Lys Lys Glu Ala Val Lys Asn
            100                 105                 110
Thr Leu Glu Arg Ala Leu Ser Phe Tyr Ser Ala Val Gln Thr Ser Asp
        115                 120                 125
Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro Met Phe Leu Leu Pro Gly
    130                 135                 140
Leu Val Ile Ala Leu Tyr Val Thr Gly Val Leu Asn Ser Val Leu Ser
145                 150                 155                 160
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Lys His His Arg Gln Glu Met Cys Arg Tyr Ile Tyr Asn His Gln Asn
                165                 170                 175
Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly Ser Ser Thr Met Phe
            180                 185                 190
Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu Leu Gly Glu Ala Ala
        195                 200                 205
Asp Gly Gly Glu His Gly Ala Met Thr Lys Ala Arg Ser Trp Ile Leu
    210                 215                 220
Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser Trp Gly Lys Leu Trp Leu
225                 230                 235                 240
Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn Pro Leu Pro Pro
                245                 250                 255
Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro Phe His Pro Gly Arg Met
            260                 265                 270
Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly
        275                 280                 285
Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu Ser Leu Arg Lys
    290                 295                 300
Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile Asp Trp Asn Arg Ser Arg
305                 310                 315                 320
Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met Gln
                325                 330                 335
Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu Pro Leu Phe Ser
            340                 345                 350
Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met Lys Ile Ala Met
        355                 360                 365
Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile Cys Leu Gly
    370                 375                 380
Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro
385                 390                 395                 400
Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile Pro Asp Tyr Leu
                405                 410                 415
Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn Gly Ser Gln
            420                 425                 430
Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile Ser Thr Lys Leu
        435                 440                 445
Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His His Phe Val Lys
    450                 455                 460
His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro Asn Val Trp Phe
465                 470                 475                 480
Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His Gly
                485                 490                 495
Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ser Leu Met
            500                 505                 510
Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro Leu Glu Lys Asn
        515                 520                 525
Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Glu Asn
    530                 535                 540
Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu Glu
545                 550                 555                 560
Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr Ser
                565                 570                 575
Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Ala Leu Phe Lys
            580                 585                 590
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Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Ala Ala Ile Ala
        595                 600                 605
Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys Thr Asp Gly Ser Trp
    610                 615                 620
Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly Ile
625                 630                 635                 640
Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Val Ala Ile
                645                 650                 655
Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly Gly
            660                 665                 670
Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu
        675                 680                 685
Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp Val Met Met Ala
    690                 695                 700
Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala Pro Leu His Arg
705                 710                 715                 720
Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser Gly Asp Phe Pro
                725                 730                 735
Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr
            740                 745                 750
Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Ser
        755                 760                 765
His Arg Val Leu Asp Met Gly Ser Ala Ala Pro Gly Ser Gly Ser Gly
    770                 775                 780
Ser Gly Met Ser Arg Leu Pro Leu Lys Gln Phe Leu Ala Asp Asn Pro
785                 790                 795                 800
Lys Lys Val Leu Val Leu Asp Gly Gly Gln Gly Thr Glu Leu Glu Asn
                805                 810                 815
Arg Gly Ile Lys Val Ala Asn Pro Val Trp Ser Thr Ile Pro Phe Ile
            820                 825                 830
Ser Glu Ser Phe Trp Ser Asp Glu Ser Ser Ala Asn Arg Lys Ile Val
        835                 840                 845
Lys Glu Met Phe Asn Asp Phe Leu Asn Ala Gly Ala Glu Ile Leu Met
    850                 855                 860
Thr Thr Thr Tyr Gln Thr Ser Tyr Lys Ser Val Ser Glu Asn Thr Pro
865                 870                 875                 880
Ile Arg Thr Leu Ser Glu Tyr Asn Asn Leu Leu Asn Arg Ile Val Asp
                885                 890                 895
Phe Ser Arg Asn Cys Ile Gly Glu Asp Lys Tyr Leu Ile Gly Cys Ile
            900                 905                 910
Gly Pro Trp Gly Ala His Ile Cys Arg Glu Phe Thr Gly Asp Tyr Gly
        915                 920                 925
Ala Glu Pro Glu Asn Ile Asp Phe Tyr Gln Tyr Phe Lys Pro Gln Leu
    930                 935                 940
Glu Asn Phe Asn Lys Asn Asp Lys Leu Asp Leu Ile Gly Phe Glu Thr
945                 950                 955                 960
Ile Pro Asn Ile His Glu Leu Lys Ala Ile Leu Ser Trp Asp Glu Ser
                965                 970                 975
Ile Leu Ser Arg Pro Phe Tyr Ile Gly Leu Ser Val His Glu His Gly
            980                 985                 990
Val Leu Arg Asp Gly Thr Thr Met Glu Glu Ile Ala Gln Val Ile Lys
        995                 1000                1005
Asp Leu Gly Asp Lys Ile Asn Pro Asn Phe Ser Phe Leu Gly Ile Asn
    1010                1015                1020
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Cys Val Ser Phe Asn Gln Ser Pro Asp Ile Leu Glu Ser Leu His Gln
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Ala Leu Pro Asn Met Ala Leu Leu Ala Tyr Pro Asn Ser Gly Glu Val
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Tyr Asp Thr Glu Lys Lys Ile Trp Leu Pro Asn Ser Asp Lys Leu Asn
1060 1065 1070
Ser Trp Asp Thr Val Val Lys Gln Tyr Ile Ser Ser Gly Ala Arg Ile
1075 1080 1085
Ile Gly Gly Cys Cys Arg Thr Ser Pro Lys Asp Ile Gln Glu Ile Ser
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<211> 2391
<212> DNA
<213> Artificial Sequence

<220>
<223> SS3b-D8 Full gene NT Seq

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attaaaagca ttagtaacca tttgggcaga caagtctggg agttttgctc tggtgaaaat 180
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gaaatcatgg gtgtgtttaa taagaactgt atgataacat atgccgcata cagaaacata 2340
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<211> 796
<212> PRT
<213> Artificial Sequence

<220>
<223> SS3b-D8 Full Gene AA seq

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

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        275                 280                 285
Phe His Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr Leu Pro
    290                 295                 300
Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr Pro Ile
305                 310                 315                 320
Val Leu Ser Leu Arg Lys Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile
                325                 330                 335
Asp Trp Asn Arg Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr
            340                 345                 350
Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His Val
        355                 360                 365
Tyr Glu Pro Leu Phe Ser Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys
    370                 375                 380
Ala Met Lys Ile Ala Met Glu His Ile His Tyr Glu Asp Glu Asn Ser
385                 390                 395                 400
Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu Cys
                405                 410                 415
Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Phe His Leu Gln
            420                 425                 430
Arg Ile Pro Asp Tyr Leu Trp Leu Ala Glu Asp Gly Met Arg Met Gln
        435                 440                 445
Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala
    450                 455                 460
Ile Ile Ser Thr Lys Leu Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys
465                 470                 475                 480
Ala His His Phe Val Lys His Ser Gln Ile Gln Glu Asp Cys Pro Gly
                485                 490                 495
Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp Pro Phe
            500                 505                 510
Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly
        515                 520                 525
Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Lys Ile Val Gly
    530                 535                 540
Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val Leu Leu
545                 550                 555                 560
Ser Leu Gln Asn Glu Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg
                565                 570                 575
Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp
            580                 585                 590
Ile Val Ile Asp Tyr Ser Tyr Val Glu Cys Thr Ser Ala Thr Met Glu
        595                 600                 605
Ala Leu Ala Leu Phe Lys Lys Leu His Pro Gly His Arg Thr Lys Glu
    610                 615                 620
Ile Asp Ala Ala Ile Ala Lys Ala Ala Asn Phe Leu Glu Asn Met Gln
625                 630                 635                 640
Lys Thr Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr
                645                 650                 655
Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr
            660                 665                 670
Asn Asn Cys Val Ala Ile Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys
        675                 680                 685
Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn
    690                 695                 700
Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val Asn Thr
```

705 710 715 720
Ala Trp Val Met Met Ala Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp
725 730 735
Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu
740 745 750
Glu Ser Gly Asp Phe Pro Gln Gln Glu Ile Met Gly Val Phe Asn Lys
755 760 765
Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp
770 775 780
Ala Leu Gly Glu Tyr Ser His Arg Val Leu Asp Met
785 790 795

<210> 865
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> SS3b-D8 Fusion AA seq

<400> 865
Met Ser Gln Glu Phe Glu Thr Pro Ala Val
1 5 10

<210> 866
<211> 2394
<212> DNA
<213> Artificial Sequence

<220>
<223> SS2c-A10a Full gene NT Seq

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gacgacgatg aagcaattgc tgtagctaac aattcagcct caaaatttga aaatgcaaga 180
aatcacttcc gtaataacag attccatagg aagcaatctt ccgacttatt cttggctata 240
caatgcgaga aagagatcat taggaatggt gctaagaatg aaggtactac caaagtgaaa 300
gaaggtgaag atgttaagaa agaagccgta aaaaatacac tagaaagagc attgtcgttc 360
tattctgctg tacagacctc tgacggtaat tgggcatcag acttgggagg acctatgttc 420
cttttaccag ggctagttat tgcgctatac gttacaggcg ttcttaacag tgtgttgtca 480
aaacatcaca ggcaagaaat gtgtcgttac atctataatc accaaaacga agatggaggg 540
tggggtttac atatagaagg ctcttctact atgtttgggt ctgcactgaa ttacgttgcg 600
ttaaggttac taggagaagc ggcagatggc ggtgagcatg gtgcgatgac caaagcaagg 660
tcctggatat tggaaagagg aggtgccaca gcaataactt cctggggcaa actttggctt 720
tccgtattag gagtgtatga atggtcggga aacaatccat tgccacccga attttggtta 780
cttccatata gccttccctt tcatccaggg agaatgtggt gtcattgtag aatggtttat 840
ctgccaatgt cgtatcttta tggtaagaga tttgttggtc caatcactcc aatagtttta 900
tcgttgagaa aagagttata taccattccg taccacgaga ttgattggaa tagatccaga 960
aacacgtgtg ctaaggagga cttatattac cctcacccta agatgcaaga tatcctatgg 1020
ggcagtatct accatgtcta cgaaccgcta ttttcaggtt ggccaggtaa gagattgagg 1080
gaaaaggcca tgaaaattgc aatggaacat atccattacg aagatgagaa ttccaggtac 1140

atatgccttg gacccgtgaa caaagttcta aatatgctgt gttgctgggt tgaggatcct 1200
tactctgatg ctttcaagtt tcacttgcag agaattcctg actatctatg gttagctgaa 1260
gatggaatga gaatgcaggg ttataatggt tcacagcttt gggacactgc attcagcata 1320
caagcgataa tctcaacgaa attgattgat acgtttggtc cgacattacg taaagcacac 1380
catttcgtca agcatagtca gattcaagag gattgtccag gtgatccaaa cgtatggttc 1440
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gattgcacag ctgagggatt gaaagcttca ctgatgttat ctaagttgcc ttctaaaatt 1560
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ttgattaacc ctgccgaaac atttggtgat atcgtaattg actacagtta tgtggaatgc 1740
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aacttcctgt tgtcaaaaga attgcctggc ggtggttggg gcgaaagcta cctaagttgc 2040
caaaacaaag tttataccaa tctggaggga aacaagccac acttagtcaa tactgcatgg 2100
gtcatgatgg ccttgattga agcaggacaa ggggaaagag atccagctcc gttgcataga 2160
gctgccagat tgctaatcaa tagtcaattg gagtcaggtg actttccaca acaagaaatc 2220
atgggtgtgt ttaataagaa ctgtatgata acatatgccg catacagaaa catattccct 2280
atatgggctc taggtgaata ctcccatcgt gtcttggata tgggaagtgc agctcctgga 2340
agtggaagtg gttcaggaat gaattcgaat gaagacatca tacctgaact ataa 2394

<210> 867

<400> 867
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<210> 868
<211> 2394
<212> DNA
<213> Artificial Sequence

<220>
<223> SS2c-A10a Full gene NT Seq

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gacgacgatg aagcaattgc tgtagctaac aattcagcct caaaatttga aaatgcaaga 180
aatcacttcc gtaataacag attccatagg aagcaatctt ccgacttatt cttggctata 240
caatgcgaga aagagatcat taggaatggt gctaagaatg aaggtactac caaagtgaaa 300
gaaggtgaag atgttaagaa agaagccgta aaaaatacac tagaaagagc attgtcgttc 360
tattctgctg tacagacctc tgacggtaat tgggcatcag acttgggagg acctatgttc 420
cttttaccag ggctagttat tgcgctatac gttacaggcg ttcttaacag tgtgttgtca 480
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tggggtttac atatagaagg ctcttctact atgtttgggt ctgcactgaa ttacgttgcg 600
ttaaggttac taggagaagc ggcagatggc ggtgagcatg gtgcgatgac caaagcaagg 660
tcctggatat tggaaagagg aggtgccaca gcaataactt cctggggcaa actttggctt 720
tccgtattag gagtgtatga atggtcggga aacaatccat tgccacccga attttggtta 780
cttccatata gccttccctt tcatccaggg agaatgtggt gtcattgtag aatggtttat 840
ctgccaatgt cgtatcttta tggtaagaga tttgttggtc caatcactcc aatagtttta 900
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aacacgtgtg ctaaggagga cttatattac cctcacccta agatgcaaga tatcctatgg 1020
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tactctgatg ctttcaagtt tcacttgcag agaattcctg actatctatg gttagctgaa 1260
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gattgcacag ctgagggatt gaaagcttca ctgatgttat ctaagttgcc ttctaaaatt 1560
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ttgattaacc ctgccgaaac atttggtgat atcgtaattg actacagtta tgtggaatgc 1740
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gacgggtctt ggtatggttg ttggggtgtc tgttttactt atgctggttg gtttggcatc 1920
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aacttcctgt tgtcaaaaga attgcctggc ggtggttggg gcgaaagcta cctaagttgc 2040
caaaacaaag tttataccaa tctggaggga aacaagccac acttagtcaa tactgcatgg 2100
gtcatgatgg ccttgattga agcaggacaa ggggaaagag atccagctcc gttgcataga 2160
gctgccagat tgctaatcaa tagtcaattg gagtcaggtg actttccaca acaagaaatc 2220
atgggtgtgt ttaataagaa ctgtatgata acatatgccg catacagaaa catattccct 2280
atatgggctc taggtgaata ctcccatcgt gtcttggata tgggaagtgc agctcctgga 2340
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<210> 869
<211> 797
<212> PRT
<213> Artificial Sequence

<220>
<223> SS2c-A10a Full Gene AA seq

<400> 869
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 1               5                  10                  15
Lys Trp Ile Lys Ser Ile Ser Asn His Leu Gly Arg Gln Val Trp Glu
            20                  25                  30
Phe Cys Ser Gly Glu Asn Glu Asn Asp Asp Asp Glu Ala Ile Ala Val
        35                  40                  45
Ala Asn Asn Ser Ala Ser Lys Phe Glu Asn Ala Arg Asn His Phe Arg
    50                  55                  60
Asn Asn Arg Phe His Arg Lys Gln Ser Ser Asp Leu Phe Leu Ala Ile
65                  70                  75                  80
Gln Cys Glu Lys Glu Ile Ile Arg Asn Gly Ala Lys Asn Glu Gly Thr
                85                  90                  95
Thr Lys Val Lys Glu Gly Glu Asp Val Lys Lys Glu Ala Val Lys Asn
            100                 105                 110
Thr Leu Glu Arg Ala Leu Ser Phe Tyr Ser Ala Val Gln Thr Ser Asp
        115                 120                 125
Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro Met Phe Leu Leu Pro Gly
    130                 135                 140
Leu Val Ile Ala Leu Tyr Val Thr Gly Val Leu Asn Ser Val Leu Ser
145                 150                 155                 160
Lys His His Arg Gln Glu Met Cys Arg Tyr Ile Tyr Asn His Gln Asn
                165                 170                 175

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Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly Ser Ser Thr Met Phe
            180                 185                 190
Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu Leu Gly Glu Ala Ala
        195                 200                 205
Asp Gly Gly Glu His Gly Ala Met Thr Lys Ala Arg Ser Trp Ile Leu
    210                 215                 220
Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser Trp Gly Lys Leu Trp Leu
225                 230                 235                 240
Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn Pro Leu Pro Pro
                245                 250                 255
Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro Phe His Pro Gly Arg Met
            260                 265                 270
Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly
        275                 280                 285
Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu Ser Leu Arg Lys
    290                 295                 300
Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile Asp Trp Asn Arg Ser Arg
305                 310                 315                 320
Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met Gln
                325                 330                 335
Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu Pro Leu Phe Ser
            340                 345                 350
Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met Lys Ile Ala Met
        355                 360                 365
Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile Cys Leu Gly
    370                 375                 380
Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro
385                 390                 395                 400
Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile Pro Asp Tyr Leu
                405                 410                 415
Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn Gly Ser Gln
            420                 425                 430
Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile Ser Thr Lys Leu
        435                 440                 445
Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His His Phe Val Lys
    450                 455                 460
His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro Asn Val Trp Phe
465                 470                 475                 480
Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His Gly
                485                 490                 495
Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ser Leu Met
            500                 505                 510
Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro Leu Glu Lys Asn
        515                 520                 525
Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Glu Asn
    530                 535                 540
Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu Glu
545                 550                 555                 560
Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr Ser
                565                 570                 575
Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Ala Leu Phe Lys
            580                 585                 590
Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Ala Ala Ile Ala
        595                 600                 605
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Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys Thr Asp Gly Ser Trp
    610                 615                 620
Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly Ile
625                 630                 635                 640
Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Val Ala Ile
                645                 650                 655
Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly Gly
            660                 665                 670
Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu
        675                 680                 685
Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp Val Met Met Ala
    690                 695                 700
Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala Pro Leu His Arg
705                 710                 715                 720
Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser Gly Asp Phe Pro
                725                 730                 735
Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr
            740                 745                 750
Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Ser
        755                 760                 765
His Arg Val Leu Asp Met Gly Ser Ala Ala Pro Gly Ser Gly Ser Gly
    770                 775                 780
Ser Gly Met Asn Ser Asn Glu Asp Ile Ile Pro Glu Leu
785                 790                 795
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<210> 870
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> SS2c-A10a Fusion AA seq

<400> 870
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Met Asn Ser Asn Glu Asp Ile Ile Pro Glu Leu
 1               5                  10
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<210> 871
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequence A  CYP87D18 DNA (codon
optimized)

<400> 871
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aacaagtgga gagattccaa gttcaatggt gttctacctc ctggaactat ggggctacca 120
ttgataggag agacaattca gttgtcaaga ccatctgaca gtttggatgt gcatcccttt 180
atccagaaga aagtcgaacg ttatggtccg atatttaaaa cctgtttggc aggcagacca 240
gttgttgttt cagcggatgc agagttcaat aattacatta tgttacaaga aggtagagct 300
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gtagaaatgt ggtatttgga cacactgtct aaattcttcg ggttggatac agagtggtta 360
aaagccttag gcttaatcca caagtacata agatccatta ccctaaacca ttttggtgct 420
gaagcattga gagaaagatt cttgccattt atagaggcat cgtctatgga agcgttacat 480
tcttggtcca ctcaacccag tgtggaggtc aagaatgcaa gtgctttgat ggtattcaga 540
acgtctgtaa acaaaatgtt tggagaagat gctaagaaat tatcaggaaa tattccaggt 600
aaattcacaa agctgctggg tggctttcta tctctaccgt taaattttcc cggcactact 660
tatcacaagt gcttaaaaga catgaaagaa atccagaaga aattacgtga agttgtagat 720
gatagacttg ccaatgttgg gccagatgtt gaggactttc tagggcaagc gttgaaagac 780
aaagaatccg agaaattcat aagcgaagaa tttatcatcc aattgctatt ttcaataagc 840
tttgcttcgt tcgaatcgat cagcacgacg ttgacattga ttttgaagct acttgacgaa 900
catcctgagg ttgtaaagga attagaagcc gaacatgaag ctatcagaaa agctagagct 960
gatccagatg gtccaattac ctgggaagaa tacaaatcta tgaccttcac acttcaagtc 1020
ataaacgaaa cacttaggtt aggctcagtg actcctgcct tattgaggaa aactgttaaa 1080
gatctgcaag tcaagggtta cattattcct gaaggatgga ctataatgtt ggtaactgca 1140
tctaggcatc gtgatccaaa ggtctacaaa gatccgcaca tattcaatcc ttggagatgg 1200
aaagacctgg actcaattac cattcaaaag aactttatgc cattcggtgg tggtttaagg 1260
cattgtgcag gagctgaata ctccaaagtg tatctgtgta cttttcttca cattctttgc 1320
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tttgaggatg gtttgcacgt caagtttact cctaaagagt aa 1422

<210> 872
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequence B CYP87D18 Protein

<400> 872
Met Trp Thr Val Val Leu Gly Leu Ala Thr Leu Phe Val Ala Tyr Tyr
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Ile His Trp Ile Asn Lys Trp Arg Asp Ser Lys Phe Asn Gly Val Leu
            20                  25                  30
Pro Pro Gly Thr Met Gly Leu Pro Leu Ile Gly Glu Thr Ile Gln Leu
        35                  40                  45
Ser Arg Pro Ser Asp Ser Leu Asp Val His Pro Phe Ile Gln Lys Lys
    50                  55                  60
Val Glu Arg Tyr Gly Pro Ile Phe Lys Thr Cys Leu Ala Gly Arg Pro
65                  70                  75                  80
Val Val Val Ser Ala Asp Ala Glu Phe Asn Asn Tyr Ile Met Leu Gln
                85                  90                  95
Glu Gly Arg Ala Val Glu Met Trp Tyr Leu Asp Thr Leu Ser Lys Phe
            100                 105                 110
Phe Gly Leu Asp Thr Glu Trp Leu Lys Ala Leu Gly Leu Ile His Lys
        115                 120                 125
Tyr Ile Arg Ser Ile Thr Leu Asn His Phe Gly Ala Glu Ala Leu Arg
    130                 135                 140
Glu Arg Phe Leu Pro Phe Ile Glu Ala Ser Ser Met Glu Ala Leu His
145                 150                 155                 160
Ser Trp Ser Thr Gln Pro Ser Val Glu Val Lys Asn Ala Ser Ala Leu
                165                 170                 175
Met Val Phe Arg Thr Ser Val Asn Lys Met Phe Gly Glu Asp Ala Lys
            180                 185                 190
Lys Leu Ser Gly Asn Ile Pro Gly Lys Phe Thr Lys Leu Leu Gly Gly

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        195                 200                 205
Phe Leu Ser Leu Pro Leu Asn Phe Pro Gly Thr Thr Tyr His Lys Cys
    210                 215                 220
Leu Lys Asp Met Lys Glu Ile Gln Lys Lys Leu Arg Glu Val Val Asp
225                 230                 235                 240
Asp Arg Leu Ala Asn Val Gly Pro Asp Val Glu Asp Phe Leu Gly Gln
                245                 250                 255
Ala Leu Lys Asp Lys Glu Ser Glu Lys Phe Ile Ser Glu Glu Phe Ile
            260                 265                 270
Ile Gln Leu Leu Phe Ser Ile Ser Phe Ala Ser Phe Glu Ser Ile Ser
        275                 280                 285
Thr Thr Leu Thr Leu Ile Leu Lys Leu Leu Asp Glu His Pro Glu Val
    290                 295                 300
Val Lys Glu Leu Glu Ala Glu His Glu Ala Ile Arg Lys Ala Arg Ala
305                 310                 315                 320
Asp Pro Asp Gly Pro Ile Thr Trp Glu Glu Tyr Lys Ser Met Thr Phe
                325                 330                 335
Thr Leu Gln Val Ile Asn Glu Thr Leu Arg Leu Gly Ser Val Thr Pro
            340                 345                 350
Ala Leu Leu Arg Lys Thr Val Lys Asp Leu Gln Val Lys Gly Tyr Ile
        355                 360                 365
Ile Pro Glu Gly Trp Thr Ile Met Leu Val Thr Ala Ser Arg His Arg
    370                 375                 380
Asp Pro Lys Val Tyr Lys Asp Pro His Ile Phe Asn Pro Trp Arg Trp
385                 390                 395                 400
Lys Asp Leu Asp Ser Ile Thr Ile Gln Lys Asn Phe Met Pro Phe Gly
                405                 410                 415
Gly Gly Leu Arg His Cys Ala Gly Ala Glu Tyr Ser Lys Val Tyr Leu
            420                 425                 430
Cys Thr Phe Leu His Ile Leu Cys Thr Lys Tyr Arg Trp Thr Lys Leu
        435                 440                 445
Gly Gly Gly Arg Ile Ala Arg Ala His Ile Leu Ser Phe Glu Asp Gly
    450                 455                 460
Leu His Val Lys Phe Thr Pro Lys Glu
465                 470
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<210> 873
<211> 2106
<212> DNA
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequence C SgCPR DNA (codon optimized)

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gttgccatct tgaccacttc tattgctgtt atgattggtt gcttcgttgt cttgatgtgg 180
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
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tgttctcatt tggaattcaa catttccggt tccgctttga attacgaaac tggtgatcat 1020
gttggtgtct actgtgaaaa cttgactgaa actgttgatg aagccttgaa cttgttgggt 1080
ttgtctccag aaacttactt ctctatctac accgataacg aagatggtac tccattgggt 1140
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gctgatttgt tgaactctcc aaaaaagtct gctttgttgg ctttagctgc tcatgcttct 1260
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gctaaaccac cattaggtgt ttttttgct gctgttgctc caagattgca acctagattc 1440
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gtttacgata agatgccaac tggtagaatt cataagggtg tttgttctac ctggatgaag 1560
aattctgttc caatggaaaa gtcccatgaa tgttcttggg ctccaatttt cgttagacaa 1620
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ggtttggctc cttttagagg ttttttacaa gaaagattgg ccttgaaaga atccggtgtt 1740
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gaagatgaat tgaacaactt cgttgaaacc ggtgctttgt ccgaattggt tattgctttt 1860
tctagagaag gtcctaccaa agaatacgtc caacataaga tggctgaaaa ggcttctgat 1920
atctggaact tgatttctga aggtgcttac ttgtacgttt gtggtgatgc taaaggtatg 1980
gctaaggatg ttcatagaac cttgcatacc atcatgcaag aacaaggttc tttggattct 2040
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tggtaa 2106

<210> 874
<211> 701
<212> PRT
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequence D SgCPR Protein

<400> 874
Met Lys Val Ser Pro Phe Glu Phe Met Ser Ala Ile Ile Lys Gly Arg
 1               5                  10                  15
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

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        115                 120                 125
Leu Asp Asp Tyr Ala Ala Asp Asp Asp Gln Tyr Glu Glu Lys Leu Lys
    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
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
    530                 535                 540
Leu Pro Ala Glu Ser Lys Val Pro Ile Ile Met Val Gly Pro Gly Thr
```

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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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<210> 875
<211> 1461
<212> DNA
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequence E CYP51G1 (codon optimized)

<400> 875
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atggaacctg aaaacaagtt cttcaatgtt gggttattga tcgtagttac gttggttttg 60
gctaaactaa tttctgcggt cattaattcc aggtctaaga agagagtacc tccaaccgtc 120
aaaggttttc cacttgtagg tggcttggtt agatttctta aagggccaat tgtgatgttg 180
agagaagaat atcccaaaca tggatccgta ttcactctga atttactaca taagaagatt 240
acctttctga ttggaccaga agtttctgca catttcttta aggcttcaga gagtgattta 300
tcacagcaag aagtctacca atttaacgtg cccacttttg gtccgggcgt tgttttcgat 360
gtcgactact cggtaaggca agaacaattc agattcttta ccgaagcatt gagagttaca 420
aaactgaagg gctatgttga ccaaatggtg aaagaagcag aagattactt ttcaaaatgg 480
ggtgattcag gagaggttga tctaaaatgc gaacttgaac acttgatcat attaaccgca 540
tctagatgtt tgttgggaag agaagttcgt gaccagttat ttgctgatgt aagtgcccta 600
tttcatgact tggataacgg tatgctgcca atatccgtga tgttcccata cttgcctata 660
cccgctcata ggagaagaga tcaagcgaga tcaaaattgg ctgatatctt tgtcaacatc 720
atatcctctc gtaaatgtac tggcacttct gaaaatgaca tgttacaatg ctttataaac 780
tctaaataca aagatggcag accaactact gattctgaaa tcacagggtt attgatagcc 840
gcattattcg ctgggcaaca tacgagctcg attactagca catggacagg cgcatatttg 900
ttatgtcaca aagagtatat gagtgccgtt cttgaagagc agcagaaaca aatggagaag 960
catggtgacg aaattgatca cgatattcta tccgaaatgg acaatttgta ccgttgcatc 1020
aaagaagccc taagactaca tccacccttg attatgctta tgaggtcgag tcataccgat 1080
tttagcgtta cgacaagaga aggaaaagag tatgatattc cgaagggaca tattatagcc 1140
acaagtccag ctttcgcaaa tcgtttacct cacgtgtata aagaccctga cagatttgat 1200
ccagataggt ttgctccagg tagagatgag gataaggctg ctggaccttt ctcctacata 1260
tcatttggtg gtggtagaca cggttgttta ggtgaacctt ttgcgtattt acaaatcaag 1320
gcaatctggt cacacttact gagaaatttt gagttagagt tgattagtcc tttcccggaa 1380
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attgactgga atgccatggt tgtgggtgtc aagggtaaag tgatggtcag gtataagaga 1440
agaaagctta gcgtatctta g 1461

<210> 876
<211> 486
<212> PRT
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequence F CYP51G1 Protein

<400> 876
Met Glu Pro Glu Asn Lys Phe Phe Asn Val Gly Leu Leu Ile Val Val
 1               5                  10                  15
Thr Leu Val Leu Ala Lys Leu Ile Ser Ala Val Ile Asn Ser Arg Ser
            20                  25                  30
Lys Lys Arg Val Pro Pro Thr Val Lys Gly Phe Pro Leu Val Gly Gly
        35                  40                  45
Leu Val Arg Phe Leu Lys Gly Pro Ile Val Met Leu Arg Glu Glu Tyr
    50                  55                  60
Pro Lys His Gly Ser Val Phe Thr Leu Asn Leu Leu His Lys Lys Ile
65                  70                  75                  80
Thr Phe Leu Ile Gly Pro Glu Val Ser Ala His Phe Phe Lys Ala Ser
                85                  90                  95
Glu Ser Asp Leu Ser Gln Gln Glu Val Tyr Gln Phe Asn Val Pro Thr
            100                 105                 110
Phe Gly Pro Gly Val Val Phe Asp Val Asp Tyr Ser Val Arg Gln Glu
        115                 120                 125
Gln Phe Arg Phe Phe Thr Glu Ala Leu Arg Val Thr Lys Leu Lys Gly
    130                 135                 140
Tyr Val Asp Gln Met Val Lys Glu Ala Glu Asp Tyr Phe Ser Lys Trp
145                 150                 155                 160
Gly Asp Ser Gly Glu Val Asp Leu Lys Cys Glu Leu Glu His Leu Ile
                165                 170                 175
Ile Leu Thr Ala Ser Arg Cys Leu Leu Gly Arg Glu Val Arg Asp Gln
            180                 185                 190
Leu Phe Ala Asp Val Ser Ala Leu Phe His Asp Leu Asp Asn Gly Met
        195                 200                 205
Leu Pro Ile Ser Val Met Phe Pro Tyr Leu Pro Ile Pro Ala His Arg
    210                 215                 220
Arg Arg Asp Gln Ala Arg Ser Lys Leu Ala Asp Ile Phe Val Asn Ile
225                 230                 235                 240
Ile Ser Ser Arg Lys Cys Thr Gly Thr Ser Glu Asn Asp Met Leu Gln
                245                 250                 255
Cys Phe Ile Asn Ser Lys Tyr Lys Asp Gly Arg Pro Thr Thr Asp Ser
            260                 265                 270
Glu Ile Thr Gly Leu Leu Ile Ala Ala Leu Phe Ala Gly Gln His Thr
        275                 280                 285
Ser Ser Ile Thr Ser Thr Trp Thr Gly Ala Tyr Leu Leu Cys His Lys
    290                 295                 300
Glu Tyr Met Ser Ala Val Leu Glu Glu Gln Gln Lys Gln Met Glu Lys
305                 310                 315                 320
His Gly Asp Glu Ile Asp His Asp Ile Leu Ser Glu Met Asp Asn Leu
                325                 330                 335

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Tyr Arg Cys Ile Lys Glu Ala Leu Arg Leu His Pro Pro Leu Ile Met
            340                 345                 350
Leu Met Arg Ser Ser His Thr Asp Phe Ser Val Thr Thr Arg Glu Gly
        355                 360                 365
Lys Glu Tyr Asp Ile Pro Lys Gly His Ile Ile Ala Thr Ser Pro Ala
    370                 375                 380
Phe Ala Asn Arg Leu Pro His Val Tyr Lys Asp Pro Asp Arg Phe Asp
385                 390                 395                 400
Pro Asp Arg Phe Ala Pro Gly Arg Asp Glu Asp Lys Ala Ala Gly Pro
                405                 410                 415
Phe Ser Tyr Ile Ser Phe Gly Gly Gly Arg His Gly Cys Leu Gly Glu
            420                 425                 430
Pro Phe Ala Tyr Leu Gln Ile Lys Ala Ile Trp Ser His Leu Leu Arg
        435                 440                 445
Asn Phe Glu Leu Glu Leu Ile Ser Pro Phe Pro Glu Ile Asp Trp Asn
    450                 455                 460
Ala Met Val Val Gly Val Lys Gly Lys Val Met Val Arg Tyr Lys Arg
465                 470                 475                 480
Arg Lys Leu Ser Val Ser
                485
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<210> 877
<211> 1515
<212> DNA
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequence G CYP71B97 (codon optimized)

<400> 877

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aaactaccat tgttaggcca tctgcactta ttgggttctt tgcctcattg ctccttatgt 180
gaactgtcta gaaaatatgg tcctgtcatg ttgttaaaat taggctcagt acctaccgta 240
gtcatatcta gcgctgcagc cgctagagag gtgttgaaag tacacgatct agcatgttgc 300
tctcgtccga gattggctgc ttccggtaga ttctcgtaca attttctgga tctgaactta 360
agcccatatg gtgagagatg gagagaactg aggaaaattt gcgtattggt tttgctgagt 420
gctagacgtg ttcagagctt ccaacagata agagaagaag aggtgggatt attacttaaa 480
tccattagtc aagtttccag tagtgccact ccagttgatc tatctgagaa atcctattct 540
ttgacagcta acattatcac tagaatcgcg tttgggaagt cattcagagg tggcgaatta 600
gacaatgaaa actttcaaca agtcatccac agagcatcga ttgccttagg ttccttttct 660
gtgacaaact tctttccttc agtagggtgg attatcgaca gattaaccgg tgtacatggc 720
agattggaga agagttttgc tgaattagac accttctttc agcatatcat tgatgatcgt 780
atcaattttg tcgcaacaag ccaaaccgaa gaaaacatta tagacgtact attgaaaatg 840
gaaagagaac gttcaaaatt tgatgtccta caactgaata gggactgcat aaaagccttg 900
ataatggata tatttcttgc cggtgtagat actggagcag ggacaattgt gtgggcattg 960
actgaattgg tgagaaatcc cagagtgatg aagaagttgc aagacgaaat aaggtcgtgt 1020
gtgaaagagg atcaagtcaa ggaacgtgat ttagagaaac ttcagtactt aaagatggtc 1080
gttaaagaag ttttaagatt gcatgctcca gttcctttgt tattgccgag agagacaatg 1140
tctcatttca aactaaatgg ttatgacatt gatccgaaaa ctcacttgca tgtcaatgtt 1200
tgggcgattg gtagggaccc agattcttgg tctgatccag aagaattctt cccagaaaga 1260
ttcgcaggat caagtattga ttacaaagga cataattttg aattgctgcc atttggtggt 1320
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ggcagaagga tctgtcccgg tatgaacatg gggacagttg cggttgaact tgcactaacg 1380
aacctattac tttgttttga ttggactcta cctgatggca tgaaagagga agatgttgac 1440
atggaagaag atggtggact tgctattgct aagaaatctc ccctaaaatt agttccagtt 1500
aggtgtctta attag 1515

<210> 878
<211> 504
<212> PRT
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequence H CYP71B97 Protein

<400> 878
Met Leu Ser Leu Ala Ile Trp Val Ser Leu Leu Phe Leu Leu Ser Ser
 1               5                  10                  15
Leu Leu Leu Leu Lys Thr Lys Lys Lys Val Ala Pro Gln Lys Lys Lys
            20                  25                  30
Lys Gln Phe Pro Pro Gly Pro Pro Lys Leu Pro Leu Leu Gly His Leu
        35                  40                  45
His Leu Leu Gly Ser Leu Pro His Cys Ser Leu Cys Glu Leu Ser Arg
    50                  55                  60
Lys Tyr Gly Pro Val Met Leu Leu Lys Leu Gly Ser Val Pro Thr Val
65                  70                  75                  80
Val Ile Ser Ser Ala Ala Ala Ala Arg Glu Val Leu Lys Val His Asp
                85                  90                  95
Leu Ala Cys Cys Ser Arg Pro Arg Leu Ala Ala Ser Gly Arg Phe Ser
            100                 105                 110
Tyr Asn Phe Leu Asp Leu Asn Leu Ser Pro Tyr Gly Glu Arg Trp Arg
        115                 120                 125
Glu Leu Arg Lys Ile Cys Val Leu Val Leu Leu Ser Ala Arg Arg Val
    130                 135                 140
Gln Ser Phe Gln Gln Ile Arg Glu Glu Glu Val Gly Leu Leu Leu Lys
145                 150                 155                 160
Ser Ile Ser Gln Val Ser Ser Ser Ala Thr Pro Val Asp Leu Ser Glu
                165                 170                 175
Lys Ser Tyr Ser Leu Thr Ala Asn Ile Ile Thr Arg Ile Ala Phe Gly
            180                 185                 190
Lys Ser Phe Arg Gly Gly Glu Leu Asp Asn Glu Asn Phe Gln Gln Val
        195                 200                 205
Ile His Arg Ala Ser Ile Ala Leu Gly Ser Phe Ser Val Thr Asn Phe
    210                 215                 220
Phe Pro Ser Val Gly Trp Ile Ile Asp Arg Leu Thr Gly Val His Gly
225                 230                 235                 240
Arg Leu Glu Lys Ser Phe Ala Glu Leu Asp Thr Phe Phe Gln His Ile
                245                 250                 255
Ile Asp Asp Arg Ile Asn Phe Val Ala Thr Ser Gln Thr Glu Glu Asn
            260                 265                 270
Ile Ile Asp Val Leu Leu Lys Met Glu Arg Glu Arg Ser Lys Phe Asp
        275                 280                 285
Val Leu Gln Leu Asn Arg Asp Cys Ile Lys Ala Leu Ile Met Asp Ile
    290                 295                 300
Phe Leu Ala Gly Val Asp Thr Gly Ala Gly Thr Ile Val Trp Ala Leu
305                 310                 315                 320

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

<210> 879
<211> 1518
<212> DNA
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequence I CYP73A152 (codon optimized)

<400> 879
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atagccatta gcaaattaag gggtaaaagg tttaaactgc caccaggtcc gttacctgtc 120
cctatctttg gcaactggtt acaggttggt gatgatttga accacagaaa tctaacgggt 180
ttagccaaga aatttgggga tattttcttg ttaagaatgg gccaaagaaa cttagtggta 240
gtttcatctc ctgaacttgc caaagaagtg cttcatacac aaggagtgga gtttggatct 300
agaacaagaa atgtagtgtt cgacatattt accggaaaag gtcaagatat ggttttcaca 360
gtatatggtg aacattggcg taaaatgcgt agaataatga ctgtaccatt cttcaccaac 420
aaggttgtcc aacaatatag gcatggatgg gaagcagaag cagctagcgt tgttgaagat 480
gtgaagaaga atccggaatc tgctactact ggtattgtgt tacgtcgtag acttcaattg 540
atgatgtaca ataacatgta tcgtataatg tttgacagaa gatttgagtc cgaggatgat 600
cccctatttc acaaattgag agcactgaat ggtgagagat ctaggttggc tcaatcgttc 660
gagtacaact atggagactt catccctatt ttaagacctt tcttgagagg ctatttgaaa 720
atttgcaagg aagtcaagga cactaggtta cagttgttta aagactactt tgttgaagaa 780
agaaagaaat tggcgaacgt gaaaactacc acaaatgagg gcttaaaatg tgcgatcgat 840
cacattctgg acgcacaaca gaaaggtgaa atcaatgaag ataacgtttt atacattgtt 900
gagaatatta atgtagctgc cattgaaact acgttgtggt cgatagaatg gggaattgca 960
gagcttgtca atcatcctga aatccaaaga aagctgagaa atgagatgga tacagtctta 1020
ggctcaggtg ttcctatcac tgaaccagat acacataagt tgccctattt acaagctgtc 1080

ataaaagaaa ctcttagact tagaatggct ataccttgc tagttccaca tatgaatcta 1140
catgatgcca aactgggtgg ttacgacatt ccagcagaat ccaagattct agtaaacgct 1200
tggtggttag ccaataatcc agctaattgg aagaatccag aagaattcag accagagaga 1260
ttcttggaag aagaatccaa agttgaagct aatgggaacg actttagata tttaccgttc 1320
ggtgtaggaa gaaggagttg tccagggata attttagcgc tacctatcct agctatcacc 1380
ataggcagac tggttcagaa ctttgaattg ttacctccac cagggcaaag taagctggat 1440
acaagtgaga agggtggtca gttttcattg catattctta aacactcaac cattgtcgtt 1500
aaacccaggg cattttag 1518

<210> 880
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequence J CYP73A152 Protein

<400> 880
Met Asp Leu Leu Leu Leu Glu Lys Thr Leu Leu Gly Leu Phe Ile Ala
 1               5                  10                  15
Val Val Leu Ala Ile Ala Ile Ser Lys Leu Arg Gly Lys Arg Phe Lys
            20                  25                  30
Leu Pro Pro Gly Pro Leu Pro Val Pro Ile Phe Gly Asn Trp Leu Gln
        35                  40                  45
Val Gly Asp Asp Leu Asn His Arg Asn Leu Thr Gly Leu Ala Lys Lys
    50                  55                  60
Phe Gly Asp Ile Phe Leu Leu Arg Met Gly Gln Arg Asn Leu Val Val
65                  70                  75                  80
Val Ser Ser Pro Glu Leu Ala Lys Glu Val Leu His Thr Gln Gly Val
                85                  90                  95
Glu Phe Gly Ser Arg Thr Arg Asn Val Val Phe Asp Ile Phe Thr Gly
            100                 105                 110
Lys Gly Gln Asp Met Val Phe Thr Val Tyr Gly Glu His Trp Arg Lys
        115                 120                 125
Met Arg Arg Ile Met Thr Val Pro Phe Phe Thr Asn Lys Val Val Gln
    130                 135                 140
Gln Tyr Arg His Gly Trp Glu Ala Glu Ala Ala Ser Val Val Glu Asp
145                 150                 155                 160
Val Lys Lys Asn Pro Glu Ser Ala Thr Thr Gly Ile Val Leu Arg Arg
                165                 170                 175
Arg Leu Gln Leu Met Met Tyr Asn Asn Met Tyr Arg Ile Met Phe Asp
            180                 185                 190
Arg Arg Phe Glu Ser Glu Asp Asp Pro Leu Phe His Lys Leu Arg Ala
        195                 200                 205
Leu Asn Gly Glu Arg Ser Arg Leu Ala Gln Ser Phe Glu Tyr Asn Tyr
    210                 215                 220
Gly Asp Phe Ile Pro Ile Leu Arg Pro Phe Leu Arg Gly Tyr Leu Lys
225                 230                 235                 240
Ile Cys Lys Glu Val Lys Asp Thr Arg Leu Gln Leu Phe Lys Asp Tyr
                245                 250                 255
Phe Val Glu Glu Arg Lys Lys Leu Ala Asn Val Lys Thr Thr Thr Asn
            260                 265                 270
Glu Gly Leu Lys Cys Ala Ile Asp His Ile Leu Asp Ala Gln Gln Lys
        275                 280                 285

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Gly Glu Ile Asn Glu Asp Asn Val Leu Tyr Ile Val Glu Asn Ile Asn
    290                 295                 300
Val Ala Ala Ile Glu Thr Thr Leu Trp Ser Ile Glu Trp Gly Ile Ala
305                 310                 315                 320
Glu Leu Val Asn His Pro Glu Ile Gln Arg Lys Leu Arg Asn Glu Met
                325                 330                 335
Asp Thr Val Leu Gly Ser Gly Val Pro Ile Thr Glu Pro Asp Thr His
            340                 345                 350
Lys Leu Pro Tyr Leu Gln Ala Val Ile Lys Glu Thr Leu Arg Leu Arg
        355                 360                 365
Met Ala Ile Pro Leu Leu Val Pro His Met Asn Leu His Asp Ala Lys
    370                 375                 380
Leu Gly Gly Tyr Asp Ile Pro Ala Glu Ser Lys Ile Leu Val Asn Ala
385                 390                 395                 400
Trp Trp Leu Ala Asn Asn Pro Ala Asn Trp Lys Asn Pro Glu Glu Phe
                405                 410                 415
Arg Pro Glu Arg Phe Leu Glu Glu Glu Ser Lys Val Glu Ala Asn Gly
            420                 425                 430
Asn Asp Phe Arg Tyr Leu Pro Phe Gly Val Gly Arg Arg Ser Cys Pro
        435                 440                 445
Gly Ile Ile Leu Ala Leu Pro Ile Leu Ala Ile Thr Ile Gly Arg Leu
    450                 455                 460
Val Gln Asn Phe Glu Leu Leu Pro Pro Pro Gly Gln Ser Lys Leu Asp
465                 470                 475                 480
Thr Ser Glu Lys Gly Gly Gln Phe Ser Leu His Ile Leu Lys His Ser
                485                 490                 495
Thr Ile Val Val Lys Pro Arg Ala Phe
            500                 505
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<210> 881
<211> 1494
<212> DNA
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequence K CYP80C13 (codon optimized)

<400> 881
atgttaaaag atccctttg ctttcccttt ctacctctgt tgagtttggc tgttcttctg 60
ttcttactat tgagaaggat ctgctctaaa tctaagccta gacctttgcc tccgggtcct 120
actccatggc ctgtggtcgg aaatctattg caaataggca caaatcccca tatttcgatc 180
actcaatttt ctcaaactta cggtccgttg atttccttgc gtttgggaac tagcttattg 240
gtcgttgcat cgtcaccagc tgctgctact gccgttctta gaacacatga tagattactt 300
agtgcgagat atatgttcca gacgattcct gacaaacgta aacatgccca attgtcctta 360
tctacatcgc cattctgcga tgaccattgg aagtcattga gaagcatttg tagagcaaac 420
ttattcacgt ccaaggctat agagtcacaa ggaggtctta gaagaagaaa gatgaaagag 480
atggtggaat ttctacaatc caaacaaggt acggttgtag gtgttaggga cttagtgttt 540
accaccgttt tcaacatctt atccaacttg gtgttctcaa gagacttagt tggctatgta 600
ggtgaaggtt tcaatgggat taagtcatct tttcaccgtt ctatgaaatt agggttaaca 660
cctaatctgg cagactttta tccaatactg gaagggttcg atcttcaagg actacagaag 720
aaggctgtac tatataacaa aggagttgat tctacatggg aaatcctagt caaagaaagg 780
agagaattac acaggaacaa cttggtagtt tcaccgaatg acttcttgga tgttttgata 840
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cagaatcaat tcagtgatga tcagatcaac tacttgatta ccgaggttct aacagctggt 900
attgatacaa ccacttctac cgttgaatgg gctatggcgg aactgttaaa gaataaggat 960
ttaactgaga aagtcagggt cgaattggaa agagagatga aaatcaagga aaatgcgatt 1020
gatgagagtc agattagtca atttcagttt cttcaacagt gtgtcaaaga aactttgaga 1080
ctttatccac cagtgccatt tctgttacca agactagcac cagaaccttg tgaagtgatg 1140
ggttacagta ttccgaaaga tacctcgata tttgttaacg catggggcat tggtagagat 1200
ccatctatat gggaggaacc ctcagcattc aaaccagaaa gatttgtcaa ttcagactta 1260
gactttaaag cctatgatta cagattcttg ccttttggtg gaggcagaag atcttgtcca 1320
ggccttttga tgacaactgt acaagtacca ttgataattg ccacgttaat ccacaatttt 1380
gactggagcc tacctaatgg cggtgatttg gcccaattgg atttaagcgg tcaaatgggt 1440
gtatccttac aaaaggaaaa gccactgttg cttattccca ggaaacgtac ttag 1494

<210> 882
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequence L CYP80C13 Protein

<400> 882
Met Leu Lys Asp Pro Phe Cys Phe Pro Phe Leu Pro Leu Leu Ser Leu
 1               5                  10                  15
Ala Val Leu Leu Phe Leu Leu Leu Arg Arg Ile Cys Ser Lys Ser Lys
            20                  25                  30
Pro Arg Pro Leu Pro Pro Gly Pro Thr Pro Trp Pro Val Val Gly Asn
        35                  40                  45
Leu Leu Gln Ile Gly Thr Asn Pro His Ile Ser Ile Thr Gln Phe Ser
    50                  55                  60
Gln Thr Tyr Gly Pro Leu Ile Ser Leu Arg Leu Gly Thr Ser Leu Leu
65                  70                  75                  80
Val Val Ala Ser Ser Pro Ala Ala Ala Thr Ala Val Leu Arg Thr His
                85                  90                  95
Asp Arg Leu Leu Ser Ala Arg Tyr Met Phe Gln Thr Ile Pro Asp Lys
            100                 105                 110
Arg Lys His Ala Gln Leu Ser Leu Ser Thr Ser Pro Phe Cys Asp Asp
        115                 120                 125
His Trp Lys Ser Leu Arg Ser Ile Cys Arg Ala Asn Leu Phe Thr Ser
    130                 135                 140
Lys Ala Ile Glu Ser Gln Gly Gly Leu Arg Arg Arg Lys Met Lys Glu
145                 150                 155                 160
Met Val Glu Phe Leu Gln Ser Lys Gln Gly Thr Val Val Gly Val Arg
                165                 170                 175
Asp Leu Val Phe Thr Thr Val Phe Asn Ile Leu Ser Asn Leu Val Phe
            180                 185                 190
Ser Arg Asp Leu Val Gly Tyr Val Gly Glu Gly Phe Asn Gly Ile Lys
        195                 200                 205
Ser Ser Phe His Arg Ser Met Lys Leu Gly Leu Thr Pro Asn Leu Ala
    210                 215                 220
Asp Phe Tyr Pro Ile Leu Glu Gly Phe Asp Leu Gln Gly Leu Gln Lys
225                 230                 235                 240
Lys Ala Val Leu Tyr Asn Lys Gly Val Asp Ser Thr Trp Glu Ile Leu
                245                 250                 255
Val Lys Glu Arg Arg Glu Leu His Arg Asn Asn Leu Val Val Ser Pro

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            260                 265                 270
Asn Asp Phe Leu Asp Val Leu Ile Gln Asn Gln Phe Ser Asp Asp Gln
        275                 280                 285
Ile Asn Tyr Leu Ile Thr Glu Val Leu Thr Ala Gly Ile Asp Thr Thr
    290                 295                 300
Thr Ser Thr Val Glu Trp Ala Met Ala Glu Leu Leu Lys Asn Lys Asp
305                 310                 315                 320
Leu Thr Glu Lys Val Arg Val Glu Leu Glu Arg Glu Met Lys Ile Lys
                325                 330                 335
Glu Asn Ala Ile Asp Glu Ser Gln Ile Ser Gln Phe Gln Phe Leu Gln
            340                 345                 350
Gln Cys Val Lys Glu Thr Leu Arg Leu Tyr Pro Pro Val Pro Phe Leu
        355                 360                 365
Leu Pro Arg Leu Ala Pro Glu Pro Cys Glu Val Met Gly Tyr Ser Ile
    370                 375                 380
Pro Lys Asp Thr Ser Ile Phe Val Asn Ala Trp Gly Ile Gly Arg Asp
385                 390                 395                 400
Pro Ser Ile Trp Glu Glu Pro Ser Ala Phe Lys Pro Glu Arg Phe Val
                405                 410                 415
Asn Ser Asp Leu Asp Phe Lys Ala Tyr Asp Tyr Arg Phe Leu Pro Phe
            420                 425                 430
Gly Gly Gly Arg Arg Ser Cys Pro Gly Leu Leu Met Thr Thr Val Gln
        435                 440                 445
Val Pro Leu Ile Ile Ala Thr Leu Ile His Asn Phe Asp Trp Ser Leu
    450                 455                 460
Pro Asn Gly Gly Asp Leu Ala Gln Leu Asp Leu Ser Gly Gln Met Gly
465                 470                 475                 480
Val Ser Leu Gln Lys Glu Lys Pro Leu Leu Leu Ile Pro Arg Lys Arg
                485                 490                 495
Thr
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<210> 883
<211> 1530
<212> DNA
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequence M CYP92A127 (codon optimized)

<400> 883
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atggaagctc cctcgtgggt gtcttatgcc gcagcttggg ttgcaacatt ggctctattg 60
ttacttagta ggcgtttgag aagaagaaaa ttgaatttgc cacctggacc taaaccctgg 120
ccattaattg gcaatttaaa cctaataggt tctttaccgc atcaatccat ccatcaattg 180
tcccaaaagt atggcccaat aatgcacttg agatttggat catttcctgt tgtagttggc 240
agttctgtgg atatggccaa gatcttcttg aaaactcagg atctaacctt cgtttcacgt 300
ccaaagacag cagctggcaa atacaccact tacaattata gcaatataac gtggtcacaa 360
tatggtcctt attggagaca agcgaggaaa atgtgtttga tggaattgtt ctctgctaga 420
agattggaca gttatgaata cattaggaaa gaagagatga atgccttgct taaggaaatt 480
tgcaaaagtt cgggaaaagt catcaaacta aaggactacc tatctacagt ttccttgaac 540
gtgataagca ggatggtctt agggaagaaa tacactgacg agtcagaaga tgcaatcgtt 600
agtccagacg aatttaagaa aatgcttgac gaattgtttc ttctatctgg tgtattgaac 660
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atcggtgatt cgataccgtg gattgatttc ttagatctac agggttacgt gaaacgtatg 720
aaagctttgt ccaagaaatt cgacagattt ctggagcatg ttttagacga gcataatgag 780
agaagaaaag gtgtcaaaga ttatgtagct aaagacatgg tcgatgtact gttacaactg 840
gcagatgatc cggatcttga ggtgaaattg gaacgtcacg gtgttaaggc gttcacacaa 900
gacttaatag ccggtggtac agaatcttcc gctgtcactg tagaatgggc aatgagcgaa 960
cttctaaaga aaccagagat gttcgaaaag gcctctgaag agttagatag agtgattggt 1020
agggaaagat gggttgagga aaaggatatc gcgaatttac cctatattga cgcaattgct 1080
aaagaaacca tgaggttaca tcctgtggca ccaatgttgg tacctagatt atgcagagaa 1140
gattgtcaga ttgctggcta cgatatagca aagggcacta gagttcttgt caacgtttgg 1200
acaattggaa gagatccaac tgtttgggaa aatccggatg aatttaaccc agaaagattt 1260
cttgggaaat caattgatgt caaagggcaa gactttgagt tgttaccctt tggaagtggt 1320
agaagaatgt gtcctggata ttcactgggt ttaaaagtta ttcagtcatc actagccaac 1380
ttattgcatg ggttttcctg gaagctggct ggtgatacca agaaagaaga tttgaatatg 1440
gaagaagtat tcggtttaag cacgccaaag aagtttcctt tggatgctgt tgccgaacca 1500
agactgcctc cacacctgta ttctatgtag 1530

<210> 884
<211> 509
<212> PRT
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequence N CYP92A127 Protein

<400> 884
Met Glu Ala Pro Ser Trp Val Ser Tyr Ala Ala Ala Trp Val Ala Thr
 1               5                  10                  15
Leu Ala Leu Leu Leu Leu Ser Arg Arg Leu Arg Arg Arg Lys Leu Asn
            20                  25                  30
Leu Pro Pro Gly Pro Lys Pro Trp Pro Leu Ile Gly Asn Leu Asn Leu
        35                  40                  45
Ile Gly Ser Leu Pro His Gln Ser Ile His Gln Leu Ser Gln Lys Tyr
    50                  55                  60
Gly Pro Ile Met His Leu Arg Phe Gly Ser Phe Pro Val Val Val Gly
65                  70                  75                  80
Ser Ser Val Asp Met Ala Lys Ile Phe Leu Lys Thr Gln Asp Leu Thr
                85                  90                  95
Phe Val Ser Arg Pro Lys Thr Ala Ala Gly Lys Tyr Thr Thr Tyr Asn
            100                 105                 110
Tyr Ser Asn Ile Thr Trp Ser Gln Tyr Gly Pro Tyr Trp Arg Gln Ala
        115                 120                 125
Arg Lys Met Cys Leu Met Glu Leu Phe Ser Ala Arg Arg Leu Asp Ser
    130                 135                 140
Tyr Glu Tyr Ile Arg Lys Glu Glu Met Asn Ala Leu Leu Lys Glu Ile
145                 150                 155                 160
Cys Lys Ser Ser Gly Lys Val Ile Lys Leu Lys Asp Tyr Leu Ser Thr
                165                 170                 175
Val Ser Leu Asn Val Ile Ser Arg Met Val Leu Gly Lys Lys Tyr Thr
            180                 185                 190
Asp Glu Ser Glu Asp Ala Ile Val Ser Pro Asp Glu Phe Lys Lys Met
        195                 200                 205
Leu Asp Glu Leu Phe Leu Leu Ser Gly Val Leu Asn Ile Gly Asp Ser
    210                 215                 220
Ile Pro Trp Ile Asp Phe Leu Asp Leu Gln Gly Tyr Val Lys Arg Met

225 230 235 240
Lys Ala Leu Ser Lys Lys Phe Asp Arg Phe Leu Glu His Val Leu Asp
245 250 255
Glu His Asn Glu Arg Arg Lys Gly Val Lys Asp Tyr Val Ala Lys Asp
260 265 270
Met Val Asp Val Leu Leu Gln Leu Ala Asp Asp Pro Asp Leu Glu Val
275 280 285
Lys Leu Glu Arg His Gly Val Lys Ala Phe Thr Gln Asp Leu Ile Ala
290 295 300
Gly Gly Thr Glu Ser Ser Ala Val Thr Val Glu Trp Ala Met Ser Glu
305 310 315 320
Leu Leu Lys Lys Pro Glu Met Phe Glu Lys Ala Ser Glu Glu Leu Asp
325 330 335
Arg Val Ile Gly Arg Glu Arg Trp Val Glu Glu Lys Asp Ile Ala Asn
340 345 350
Leu Pro Tyr Ile Asp Ala Ile Ala Lys Glu Thr Met Arg Leu His Pro
355 360 365
Val Ala Pro Met Leu Val Pro Arg Leu Cys Arg Glu Asp Cys Gln Ile
370 375 380
Ala Gly Tyr Asp Ile Ala Lys Gly Thr Arg Val Leu Val Asn Val Trp
385 390 395 400
Thr Ile Gly Arg Asp Pro Thr Val Trp Glu Asn Pro Asp Glu Phe Asn
405 410 415
Pro Glu Arg Phe Leu Gly Lys Ser Ile Asp Val Lys Gly Gln Asp Phe
420 425 430
Glu Leu Leu Pro Phe Gly Ser Gly Arg Arg Met Cys Pro Gly Tyr Ser
435 440 445
Leu Gly Leu Lys Val Ile Gln Ser Ser Leu Ala Asn Leu Leu His Gly
450 455 460
Phe Ser Trp Lys Leu Ala Gly Asp Thr Lys Lys Glu Asp Leu Asn Met
465 470 475 480
Glu Glu Val Phe Gly Leu Ser Thr Pro Lys Lys Phe Pro Leu Asp Ala
485 490 495
Val Ala Glu Pro Arg Leu Pro Pro His Leu Tyr Ser Met
500 505

<210> 885
<211> 1530
<212> DNA
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequence O CYP92A129 (codon
optimized)

<400> 885
atggaggcac caccgtgggt ttcatatgca gctgcgtggg tagcaacatt ggctctgtta 60
cttctgtcta gacatttgcg tagaagaaaa ttgaatttac cacctggtcc aaagccttgg 120
cctctaattg gcaatctgaa cttgatagga tcgctaccac atcaatccat acatcaattg 180
agtcagaaat atggcccaat tatgcagtta agatttggtt cttttcccgt tgttgttggt 240
tcaagcgtag atatggccaa aattttcctg aaaacacacg atcttacgtt tgtgagcaga 300
ccgaaaactg ctgcaggcaa atacaccacg tataactgtt ccaatataac ttggtcgcaa 360
tatggtccgt attggagaca agccaggaaa atgtgtttga tggagctgtt tagcgctaga 420

cgtctggatt catacgaata catcagaaaa gaggaaatga atgcactatt gaaggagatt 480
tgcaaaagta gtgggaaagt aatcaaactt aaagactatt tgtctactgt ctcgcttaat 540
gtcatcagta gaatggtgct aggaaagaag tacaccgatg agtctgaaga tgccattgtt 600
tctcccgatg aatttaagaa aatgttggat gaattgtttc tactgggcgg tgttttgaac 660
atcggtgatt ccataccttg gatcgacttc ttagatcttc aaggatatgt caagagaatg 720
aaggctttat caaagaaatt tgatcgtttt ctagaacacg tactagatga acacaacgag 780
cgtagaaaag gtgtgaagga ttatgttgct aaggacatgg tcgatgtgtt attgcaattg 840
gctgacgatc cagacttgga agtcaggtta gagaggcatg gtgttaaggc gtttacccaa 900
gacttgattg caggaggaac agaatcatcc gcagtaacag tagaatgggc catgtctgaa 960
ttgttaaaga agcccgaaat gttcgagaaa gcctcagaag agctagacag agtgattggt 1020
agggaaagat gggttgaaga gaaagacata gccaatttac cgtatataga cgccatcgct 1080
aaagaaacca tgagattgca tccagtcgca cctatgctag ttccacgttt atgcagagaa 1140
gattgtcaga ttgctggata cgatattgct aagggtacta gagtcttggt gaacgtttgg 1200
acaattggta gggatcctac tgtatgggaa aatcctgatg aattcaatcc cgaaagattc 1260
ttagggaaat ccatcgatgt caaaggtcaa gacttcgaat tattgccatt cggatcaggc 1320
agaagaatgt gtccagggta ctccttaggc ttaaaggtta tacagagtag cttagcaaat 1380
cttttgcatg gtttctcttg gagacttgct ggggacgtta agaaagaaga tttaaacatg 1440
gaagaagtgt ttggtctttc tactcccaag aaatttccat tggatgcggt tgctgaacct 1500
aggttaccac ctcacttgta ctctatttag 1530

<210> 886
<211> 509
<212> PRT
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequence P) CYP92A129 Protein

<400> 886
Met Glu Ala Pro Pro Trp Val Ser Tyr Ala Ala Ala Trp Val Ala Thr
 1               5                  10                  15
Leu Ala Leu Leu Leu Leu Ser Arg His Leu Arg Arg Arg Lys Leu Asn
            20                  25                  30
Leu Pro Pro Gly Pro Lys Pro Trp Pro Leu Ile Gly Asn Leu Asn Leu
        35                  40                  45
Ile Gly Ser Leu Pro His Gln Ser Ile His Gln Leu Ser Gln Lys Tyr
    50                  55                  60
Gly Pro Ile Met Gln Leu Arg Phe Gly Ser Phe Pro Val Val Val Gly
65                  70                  75                  80
Ser Ser Val Asp Met Ala Lys Ile Phe Leu Lys Thr His Asp Leu Thr
                85                  90                  95
Phe Val Ser Arg Pro Lys Thr Ala Ala Gly Lys Tyr Thr Thr Tyr Asn
            100                 105                 110
Cys Ser Asn Ile Thr Trp Ser Gln Tyr Gly Pro Tyr Trp Arg Gln Ala
        115                 120                 125
Arg Lys Met Cys Leu Met Glu Leu Phe Ser Ala Arg Arg Leu Asp Ser
    130                 135                 140
Tyr Glu Tyr Ile Arg Lys Glu Glu Met Asn Ala Leu Leu Lys Glu Ile
145                 150                 155                 160
Cys Lys Ser Ser Gly Lys Val Ile Lys Leu Lys Asp Tyr Leu Ser Thr
                165                 170                 175
Val Ser Leu Asn Val Ile Ser Arg Met Val Leu Gly Lys Lys Tyr Thr
            180                 185                 190
Asp Glu Ser Glu Asp Ala Ile Val Ser Pro Asp Glu Phe Lys Lys Met

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        195                 200                 205
Leu Asp Glu Leu Phe Leu Leu Gly Gly Val Leu Asn Ile Gly Asp Ser
    210                 215                 220
Ile Pro Trp Ile Asp Phe Leu Asp Leu Gln Gly Tyr Val Lys Arg Met
225                 230                 235                 240
Lys Ala Leu Ser Lys Lys Phe Asp Arg Phe Leu Glu His Val Leu Asp
                245                 250                 255
Glu His Asn Glu Arg Arg Lys Gly Val Lys Asp Tyr Val Ala Lys Asp
            260                 265                 270
Met Val Asp Val Leu Leu Gln Leu Ala Asp Asp Pro Asp Leu Glu Val
        275                 280                 285
Arg Leu Glu Arg His Gly Val Lys Ala Phe Thr Gln Asp Leu Ile Ala
    290                 295                 300
Gly Gly Thr Glu Ser Ser Ala Val Thr Val Glu Trp Ala Met Ser Glu
305                 310                 315                 320
Leu Leu Lys Lys Pro Glu Met Phe Glu Lys Ala Ser Glu Glu Leu Asp
                325                 330                 335
Arg Val Ile Gly Arg Glu Arg Trp Val Glu Glu Lys Asp Ile Ala Asn
            340                 345                 350
Leu Pro Tyr Ile Asp Ala Ile Ala Lys Glu Thr Met Arg Leu His Pro
        355                 360                 365
Val Ala Pro Met Leu Val Pro Arg Leu Cys Arg Glu Asp Cys Gln Ile
    370                 375                 380
Ala Gly Tyr Asp Ile Ala Lys Gly Thr Arg Val Leu Val Asn Val Trp
385                 390                 395                 400
Thr Ile Gly Arg Asp Pro Thr Val Trp Glu Asn Pro Asp Glu Phe Asn
                405                 410                 415
Pro Glu Arg Phe Leu Gly Lys Ser Ile Asp Val Lys Gly Gln Asp Phe
            420                 425                 430
Glu Leu Leu Pro Phe Gly Ser Gly Arg Arg Met Cys Pro Gly Tyr Ser
        435                 440                 445
Leu Gly Leu Lys Val Ile Gln Ser Ser Leu Ala Asn Leu Leu His Gly
    450                 455                 460
Phe Ser Trp Arg Leu Ala Gly Asp Val Lys Lys Glu Asp Leu Asn Met
465                 470                 475                 480
Glu Glu Val Phe Gly Leu Ser Thr Pro Lys Lys Phe Pro Leu Asp Ala
                485                 490                 495
Val Ala Glu Pro Arg Leu Pro Pro His Leu Tyr Ser Ile
            500                 505
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<210> 887
<211> 1155
<212> DNA
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequence Q CYP92A458 (codon optimized)

<400> 887
atggaaatgt catcatgtgt agccgctacg attagcatct ggatggtggt tgtttgtatt 60
gtgggtgttg gatggagagt ggtaaattgg gtttggctaa gacccaagaa attggagaaa 120
aggttaaggg aacaaggctt ggcagggaac tcttacagat tgttatttgg tgaccttaaa 180

gaacgtgcag caatggctga acaagccaat tcaaaaccga ttaattttag tcacgacatt 240
ggtccaagag ttttcccaag tatgtacaaa accattcaga attatgggaa gaattcctac 300
atgtggttag gtccctatcc aagagtgcat ataatggatc ctcaacagct gaaaaccgtc 360
tttacattgg tttatgacat tcaaaagccg aatctgaatc cactggtcaa attcttgtta 420
gatgggattg tcactcatga aggagaaaag tgggcaaagc atagaaagat cattaatcca 480
gcttttcacc ttgaaaagtt gaaggacatg attcctgcct tctttcactc ttgcaatgag 540
atagttaatg agtgggaaag actaatttcg aaggagggtt cctgtgaact tgatgttatg 600
ccttacttgc agaacttagc tgctgatgct atatccagaa cagcgtttgg ttctagctat 660
gaagagggta aaatgatatt ccaattactt aaggaattga ctgatttggt cgtaaaagta 720
gcgtttggtg tgtatatccc tggttggaga ttcttaccaa ccaaatcaaa caacaaaatg 780
aaagaaatca acaggaaaat caaatctctg ctattaggaa tcattaacaa acgtcagaaa 840
gcaatggaag aaggcgaagc tggtcaatct gatttgttag gcatactaat ggaatcgaat 900
tccaacgaaa ttcaaggaga aggaaacaat aaggaggacg gtatgtctat agaagatgta 960
atcgaggaat gcaaggtttt ctatataggt ggacaagaga ctacagccag actattaatt 1020
tggacaatga tacttttaag ttcacatacg gaatggcaag agagagcaag gactgaagtc 1080
ttgaaagtct ttggcaataa gaagcctgat tttgatggct tgaacagatt gaaaatcgtt 1140
agtgaaattc tatag 1155

<210> 888
<211> 384
<212> PRT
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequence R CYP92A458 Protein

<400> 888
Met Glu Met Ser Ser Cys Val Ala Ala Thr Ile Ser Ile Trp Met Val
 1               5                  10                  15
Val Val Cys Ile Val Gly Val Gly Trp Arg Val Val Asn Trp Val Trp
            20                  25                  30
Leu Arg Pro Lys Lys Leu Glu Lys Arg Leu Arg Glu Gln Gly Leu Ala
        35                  40                  45
Gly Asn Ser Tyr Arg Leu Leu Phe Gly Asp Leu Lys Glu Arg Ala Ala
    50                  55                  60
Met Ala Glu Gln Ala Asn Ser Lys Pro Ile Asn Phe Ser His Asp Ile
65                  70                  75                  80
Gly Pro Arg Val Phe Pro Ser Met Tyr Lys Thr Ile Gln Asn Tyr Gly
                85                  90                  95
Lys Asn Ser Tyr Met Trp Leu Gly Pro Tyr Pro Arg Val His Ile Met
            100                 105                 110
Asp Pro Gln Gln Leu Lys Thr Val Phe Thr Leu Val Tyr Asp Ile Gln
        115                 120                 125
Lys Pro Asn Leu Asn Pro Leu Val Lys Phe Leu Leu Asp Gly Ile Val
    130                 135                 140
Thr His Glu Gly Glu Lys Trp Ala Lys His Arg Lys Ile Ile Asn Pro
145                 150                 155                 160
Ala Phe His Leu Glu Lys Leu Lys Asp Met Ile Pro Ala Phe Phe His
                165                 170                 175
Ser Cys Asn Glu Ile Val Asn Glu Trp Glu Arg Leu Ile Ser Lys Glu
            180                 185                 190
Gly Ser Cys Glu Leu Asp Val Met Pro Tyr Leu Gln Asn Leu Ala Ala
        195                 200                 205
Asp Ala Ile Ser Arg Thr Ala Phe Gly Ser Ser Tyr Glu Glu Gly Lys

```
    210                 215                 220
Met Ile Phe Gln Leu Leu Lys Glu Leu Thr Asp Leu Val Val Lys Val
225                 230                 235                 240
Ala Phe Gly Val Tyr Ile Pro Gly Trp Arg Phe Leu Pro Thr Lys Ser
                245                 250                 255
Asn Asn Lys Met Lys Glu Ile Asn Arg Lys Ile Lys Ser Leu Leu Leu
            260                 265                 270
Gly Ile Ile Asn Lys Arg Gln Lys Ala Met Glu Glu Gly Glu Ala Gly
        275                 280                 285
Gln Ser Asp Leu Leu Gly Ile Leu Met Glu Ser Asn Ser Asn Glu Ile
    290                 295                 300
Gln Gly Glu Gly Asn Asn Lys Glu Asp Gly Met Ser Ile Glu Asp Val
305                 310                 315                 320
Ile Glu Glu Cys Lys Val Phe Tyr Ile Gly Gly Gln Glu Thr Thr Ala
                325                 330                 335
Arg Leu Leu Ile Trp Thr Met Ile Leu Leu Ser Ser His Thr Glu Trp
            340                 345                 350
Gln Glu Arg Ala Arg Thr Glu Val Leu Lys Val Phe Gly Asn Lys Lys
        355                 360                 365
Pro Asp Phe Asp Gly Leu Asn Arg Leu Lys Ile Val Ser Glu Ile Leu
    370                 375                 380


<210> 889
<211> 493
<212> PRT
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequence S CYP88D6 Protein

<400> 889
Met Glu Val His Trp Val Cys Met Cys Ala Ala Thr Leu Leu Val Cys
 1               5                  10                  15
Tyr Ile Phe Gly Ser Lys Phe Val Arg Asn Leu Asn Gly Trp Tyr Tyr
            20                  25                  30
Asp Val Lys Leu Arg Arg Lys Glu His Pro Leu Pro Pro Gly Asp Met
        35                  40                  45
Gly Trp Pro Leu Met Gly Asn Leu Leu Ser Phe Ile Lys Asp Phe Ser
    50                  55                  60
Ser Gly His Pro Asp Ser Phe Ile Asn Asn Leu Val Leu Lys Tyr Gly
65                  70                  75                  80
Arg Ser Gly Ile Tyr Lys Thr His Leu Phe Gly Asn Pro Ser Ile Ile
                85                  90                  95
Val Cys Glu Pro Gln Met Cys Arg Arg Val Leu Thr Asp Asp Val Asn
            100                 105                 110
Phe Lys Leu Gly Tyr Pro Lys Ser Ile Lys Glu Leu Ala Arg Cys Arg
        115                 120                 125
Pro Met Ile Asp Val Ser Asn Ala Glu His Arg Leu Phe Arg Arg Leu
    130                 135                 140
Ile Thr Ser Pro Ile Val Gly His Lys Ala Leu Ala Met Tyr Leu Glu
145                 150                 155                 160
Arg Leu Glu Glu Ile Val Ile Asn Ser Leu Glu Glu Leu Ser Ser Met
                165                 170                 175
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Lys His Pro Val Glu Leu Leu Lys Glu Met Lys Lys Val Ser Phe Lys
            180                 185                 190
Ala Ile Val His Val Phe Met Gly Ser Ser Asn Gln Asp Ile Ile Lys
        195                 200                 205
Lys Ile Gly Ser Ser Phe Thr Asp Leu Tyr Asn Gly Met Phe Ser Ile
    210                 215                 220
Pro Ile Asn Val Pro Gly Phe Thr Phe His Lys Ala Leu Glu Ala Arg
225                 230                 235                 240
Lys Lys Leu Ala Lys Ile Val Gln Pro Val Val Asp Glu Arg Arg Leu
                245                 250                 255
Met Ile Glu Asn Gly Gln Gln Glu Gly Asp Gln Arg Lys Asp Leu Ile
            260                 265                 270
Asp Ile Leu Leu Glu Val Lys Asp Glu Asn Gly Arg Lys Leu Glu Asp
        275                 280                 285
Glu Asp Ile Ser Asp Leu Leu Ile Gly Leu Leu Phe Ala Gly His Glu
    290                 295                 300
Ser Thr Ala Thr Ser Leu Met Trp Ser Ile Thr Tyr Leu Thr Gln His
305                 310                 315                 320
Pro His Ile Leu Lys Lys Ala Lys Glu Glu Gln Glu Glu Ile Met Arg
                325                 330                 335
Thr Arg Leu Ser Ser Gln Lys Gln Leu Ser Phe Lys Glu Ile Lys Gln
            340                 345                 350
Met Val Tyr Leu Ser Gln Val Ile Asp Glu Thr Leu Arg Cys Ala Asn
        355                 360                 365
Ile Ala Phe Ala Thr Phe Arg Glu Ala Thr Ala Asp Val Asn Ile Asn
    370                 375                 380
Gly Tyr Ile Ile Pro Lys Gly Trp Arg Val Leu Ile Trp Ala Arg Ala
385                 390                 395                 400
Ile His Met Asp Ser Glu Tyr Tyr Pro Asn Pro Glu Glu Phe Asn Pro
                405                 410                 415
Ser Arg Trp Asp Asp Tyr Asn Ala Lys Ala Gly Thr Phe Leu Pro Phe
            420                 425                 430
Gly Ala Gly Ser Arg Leu Cys Pro Gly Ala Asp Leu Ala Lys Leu Glu
        435                 440                 445
Ile Ser Ile Phe Leu His Tyr Phe Leu Leu Asn Tyr Arg Leu Glu Arg
    450                 455                 460
Val Asn Pro Glu Cys His Val Thr Ser Leu Pro Val Ser Lys Pro Thr
465                 470                 475                 480
Asp Asn Cys Leu Ala Lys Val Met Lys Val Ser Cys Ala
                485                 490
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<210> 890
<211> 1482
<212> DNA
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequence T CYP88D6 (codon optimized)

<400> 890
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agcaagtttg tgaggaattt gaatgggtgg tattatgatg taaaactaag aaggaaagaa 120

cacccactac ccccaggtga catgggatgg cctcttatgg gcaatctatt gtccttcatc 180
aaagatttct catcgggtca ccctgattca ttcatcaaca accttgttct caaatatgga 240
cgaagtggta tctacaagac tcacttgttt gggaatccaa gcatcattgt ttgcgagcct 300
cagatgtgta ggcgagttct cactgatgat gtgaacttta agcttggtta tccaaaatct 360
atcaaagagt tggcacgatg tagacccatg attgatgtct ctaatgcgga acataggctt 420
tttcgacgcc tcattacttc cccaatcgtg ggtcacaagg cgctagcaat gtacctagaa 480
cgtcttgagg aaattgtgat caattcgttg gaagaattgt ccagcatgaa gcaccccgtt 540
gagctcttga aagagatgaa gaaggtttcc tttaaagcca ttgtccacgt tttcatgggc 600
tcttccaatc aggacatcat taaaaaaatt ggaagttcgt ttactgattt gtacaatggc 660
atgttctcta tccccattaa cgtacctggt tttacattcc acaaagcact cgaggcacgt 720
aagaagctag ccaaaatagt tcaacccgtt gtggatgaaa ggcggttgat gatagaaaat 780
ggtcaacaag aaggggacca aagaaaagat cttattgata ttcttttgga agtcaaagat 840
gagaatggac gaaaattgga ggacgaggat attagcgatt tattaatagg gcttttgttt 900
gctggccatg aaagtacagc aaccagttta atgtggtcaa ttacatatct tacacagcat 960
ccccatatct tgaaaaaggc taaggaagag caggaagaaa taatgaggac aagattgtcc 1020
tcgcagaaac aattaagttt taaggaaatt aaacaaatgg tttatctttc tcaggtaatt 1080
gatgaaactt tacgatgtgc caatattgcc tttgcaactt ttcgagaggc aactgctgat 1140
gtgaacatca atggttatat cataccaaag ggatggagag tgctaatttg ggcaagagcc 1200
attcatatgg attctgaata ttacccaaat ccagaagaat ttaatccatc gagatgggat 1260
gattacaatg ccaaagcagg aaccttcctt ccttttggag caggaagtag actttgtcct 1320
ggagccgact tggcgaaact tgaaatttcc atatttcttc attatttcct ccttaattac 1380
aggttggagc gagtaaatcc agaatgtcat gttaccagct taccagtatc taagcccaca 1440
gacaattgcc tcgctaaggt gatgaaggtc tcatgtgctt ag 1482

<210> 891
<211> 1563
<212> DNA
<213> Artificial Sequence

<220>
<223> Pathway step 4 sequence U CYP1798 (codon
optimized)

<400> 891
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gttggtgttg gttggagagt tgttaattgg gtttggttaa gaccaaagaa gttggaaaag 120
agattgagag aacaaggttt ggctggtaac tcttacagat tgttgttcgg tgacttgaaa 180
gaaagagctg ctatggaaga acaagctaac tctaagccaa tcaacttctc ccatgatatt 240
ggtccaagag ttttcccatc tatgtacaag accattcaaa actacggtaa gaactcctat 300
atgtggttgg gtccataccc aagagttcat attatggatc cacaacaatt gaaaaccgtc 360
tttaccttgg tttacgacat ccaaaagcca aacttgaacc cattgatcaa gttcttgttg 420
gatggtattg tcacccatga aggtgaaaaa tgggctaaac atagaaagat tatcaaccca 480
gccttccact tggaaaagtt gaaagatatg attccagcct tcttccactc ttgcaacgaa 540
atagttaatg aatgggaaag attgatctcc aaagaaggtt cttgcgaatt ggatgttatg 600
ccatacttgc aaaatttggc tgctgatgct atttctagaa ctgcttttgg ttcctcttac 660
gaagaaggta agatgatctt ccaattattg aaagaattga ccgacttggt tgttaaggtt 720
gctttcggtg tttacattcc aggttggaga tttttgccaa ctaagtccaa caacaagatg 780
aaggaaatca acagaaagat caagtctttg ttgttaggta tcatcaacaa gagacaaaag 840
gccatggaag aaggtgaagc tggtcaatct gatttgttgg gtattttgat ggaatccaac 900
tccaacgaaa ttcaaggtga aggtaacaac aaagaagatg gtatgtccat cgaagatgtt 960
atcgaagaat gcaaggtttt ctacatcggt ggtcaagaaa ctaccgccag attattgatt 1020
tggaccatga tcttgttgag ttcccatact gaatggcaag aaagagcaag aactgaagtc 1080
ttgaaggttt tcggtaacaa aaagccagat ttcgacggtt tgtctagatt gaaggttgtc 1140
accatgattt tgaacgaagt tttgagatta tacccaccag cttctatgtt gaccagaatc 1200

attcaaaaag aaaccagagt cggtaagttg actttgccag ctggtgttat tttgatcatg 1260
ccaatcatct tgatccacag agatcatgat ttgtggggtg aagatgctaa tgaattcaag 1320
ccagaaagat tctccaaggg tgtttctaaa gctgctaaag ttcaaccagc tttctttcca 1380
tttggttggg gtccaagaat atgtatgggt caaaatttcg ctatgatcga agctaagatg 1440
gccttgtctt tgatcttgca aagattttcc ttcgaattgt cctcctcata tgttcatgct 1500
ccaactgttg ttttcaccac tcaaccacaa catggtgctc atatcgtttt gagaaagttg 1560
taa 1563

<210> 892
<211> 520
<212> PRT
<213> Artificial Sequence

<220>
<223> Pathway step 4 sequence V CYP1798 Protein

<400> 892
Met Glu Met Ser Ser Ser Val Ala Ala Thr Ile Ser Ile Trp Met Val
 1               5                  10                  15
Val Val Cys Ile Val Gly Val Gly Trp Arg Val Val Asn Trp Val Trp
            20                  25                  30
Leu Arg Pro Lys Lys Leu Glu Lys Arg Leu Arg Glu Gln Gly Leu Ala
        35                  40                  45
Gly Asn Ser Tyr Arg Leu Leu Phe Gly Asp Leu Lys Glu Arg Ala Ala
    50                  55                  60
Met Glu Glu Gln Ala Asn Ser Lys Pro Ile Asn Phe Ser His Asp Ile
65                  70                  75                  80
Gly Pro Arg Val Phe Pro Ser Met Tyr Lys Thr Ile Gln Asn Tyr Gly
                85                  90                  95
Lys Asn Ser Tyr Met Trp Leu Gly Pro Tyr Pro Arg Val His Ile Met
            100                 105                 110
Asp Pro Gln Gln Leu Lys Thr Val Phe Thr Leu Val Tyr Asp Ile Gln
        115                 120                 125
Lys Pro Asn Leu Asn Pro Leu Ile Lys Phe Leu Leu Asp Gly Ile Val
    130                 135                 140
Thr His Glu Gly Glu Lys Trp Ala Lys His Arg Lys Ile Ile Asn Pro
145                 150                 155                 160
Ala Phe His Leu Glu Lys Leu Lys Asp Met Ile Pro Ala Phe Phe His
                165                 170                 175
Ser Cys Asn Glu Ile Val Asn Glu Trp Glu Arg Leu Ile Ser Lys Glu
            180                 185                 190
Gly Ser Cys Glu Leu Asp Val Met Pro Tyr Leu Gln Asn Leu Ala Ala
        195                 200                 205
Asp Ala Ile Ser Arg Thr Ala Phe Gly Ser Ser Tyr Glu Glu Gly Lys
    210                 215                 220
Met Ile Phe Gln Leu Leu Lys Glu Leu Thr Asp Leu Val Val Lys Val
225                 230                 235                 240
Ala Phe Gly Val Tyr Ile Pro Gly Trp Arg Phe Leu Pro Thr Lys Ser
                245                 250                 255
Asn Asn Lys Met Lys Glu Ile Asn Arg Lys Ile Lys Ser Leu Leu Leu
            260                 265                 270
Gly Ile Ile Asn Lys Arg Gln Lys Ala Met Glu Glu Gly Glu Ala Gly
        275                 280                 285
Gln Ser Asp Leu Leu Gly Ile Leu Met Glu Ser Asn Ser Asn Glu Ile

```
    290                 295                 300
Gln Gly Glu Gly Asn Asn Lys Glu Asp Gly Met Ser Ile Glu Asp Val
305                 310                 315                 320
Ile Glu Glu Cys Lys Val Phe Tyr Ile Gly Gly Gln Glu Thr Thr Ala
                325                 330                 335
Arg Leu Leu Ile Trp Thr Met Ile Leu Leu Ser Ser His Thr Glu Trp
            340                 345                 350
Gln Glu Arg Ala Arg Thr Glu Val Leu Lys Val Phe Gly Asn Lys Lys
        355                 360                 365
Pro Asp Phe Asp Gly Leu Ser Arg Leu Lys Val Val Thr Met Ile Leu
    370                 375                 380
Asn Glu Val Leu Arg Leu Tyr Pro Pro Ala Ser Met Leu Thr Arg Ile
385                 390                 395                 400
Ile Gln Lys Glu Thr Arg Val Gly Lys Leu Thr Leu Pro Ala Gly Val
                405                 410                 415
Ile Leu Ile Met Pro Ile Ile Leu Ile His Arg Asp His Asp Leu Trp
            420                 425                 430
Gly Glu Asp Ala Asn Glu Phe Lys Pro Glu Arg Phe Ser Lys Gly Val
        435                 440                 445
Ser Lys Ala Ala Lys Val Gln Pro Ala Phe Phe Pro Phe Gly Trp Gly
    450                 455                 460
Pro Arg Ile Cys Met Gly Gln Asn Phe Ala Met Ile Glu Ala Lys Met
465                 470                 475                 480
Ala Leu Ser Leu Ile Leu Gln Arg Phe Ser Phe Glu Leu Ser Ser Ser
                485                 490                 495
Tyr Val His Ala Pro Thr Val Val Phe Thr Thr Gln Pro Gln His Gly
            500                 505                 510
Ala His Ile Val Leu Arg Lys Leu
        515                 520
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<210> 893
<211> 951
<212> DNA
<213> Artificial Sequence

<220>
<223> Pathway step 4 sequence W EPH2A (codon optimized)

<400> 893
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agacaccaac tactttacct gtcctccgtt gggtacagag caatagctcc agatttgaga 180
ggctatggcg atactgacag tccagctagt cctacctctt atactgctct tcatattgta 240
ggtgacctgg tcggcgcatt agacgaattg ggaatagaaa aggtcttttt agtgggtcat 300
gactggggtg ctattatcgc atggtacttt tgtttgttta gaccagatag aattaaagca 360
cttgtgaatt tgtctgtcca gtttatccca cgtaacccag caataccttt tatagaaggt 420
ttcagaacag cttttggtga tgacttctac atttgtagat ttcaagtacc tggggaagct 480
gaagaggatt tcgcgtctat cgatactgct caattgttta aaacttcatt atgcaataga 540
agctcagccc ctccttgttt gcctaaagag attggtttta gggctatccc accaccagaa 600
aatctgccat cttggctcac agaggaagat atcaacttct acgcagccaa gtttaaacaa 660
actggtttta ctggtgccct taactattat agagcattcg acttgacatg ggaattaaca 720
gccccatgga caggagccca gatccaagtt cctgtaaagt tcatagttgg tgattcagat 780
ctcacgtacc atttccctgg tgctaaggaa tacatccaca acggagggtt taaaagagat 840
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gtgccactat tagaggaagt tgttgtggta aaagatgcct gccacttcat taaccaagag 900
cgaccacaag agattaatgc tcatattcat gacttcatca ataagttcta a 951

<210> 894
<211> 316
<212> PRT
<213> Artificial Sequence

<220>
<223> Pathway step 3 sequenceID X step 44 EPH2A Protein

<400> 894
Met Asp Glu Ile Glu His Ile Thr Ile Asn Thr Asn Gly Ile Lys Met
1 5 10 15
His Ile Ala Ser Val Gly Thr Gly Pro Val Val Leu Leu Leu His Gly
20 25 30
Phe Pro Glu Leu Trp Tyr Ser Trp Arg His Gln Leu Leu Tyr Leu Ser
35 40 45
Ser Val Gly Tyr Arg Ala Ile Ala Pro Asp Leu Arg Gly Tyr Gly Asp
50 55 60
Thr Asp Ser Pro Ala Ser Pro Thr Ser Tyr Thr Ala Leu His Ile Val
65 70 75 80
Gly Asp Leu Val Gly Ala Leu Asp Glu Leu Gly Ile Glu Lys Val Phe
85 90 95
Leu Val Gly His Asp Trp Gly Ala Ile Ile Ala Trp Tyr Phe Cys Leu
100 105 110
Phe Arg Pro Asp Arg Ile Lys Ala Leu Val Asn Leu Ser Val Gln Phe
115 120 125
Ile Pro Arg Asn Pro Ala Ile Pro Phe Ile Glu Gly Phe Arg Thr Ala
130 135 140
Phe Gly Asp Asp Phe Tyr Ile Cys Arg Phe Gln Val Pro Gly Glu Ala
145 150 155 160
Glu Glu Asp Phe Ala Ser Ile Asp Thr Ala Gln Leu Phe Lys Thr Ser
165 170 175
Leu Cys Asn Arg Ser Ser Ala Pro Pro Cys Leu Pro Lys Glu Ile Gly
180 185 190
Phe Arg Ala Ile Pro Pro Pro Glu Asn Leu Pro Ser Trp Leu Thr Glu
195 200 205
Glu Asp Ile Asn Phe Tyr Ala Ala Lys Phe Lys Gln Thr Gly Phe Thr
210 215 220
Gly Ala Leu Asn Tyr Tyr Arg Ala Phe Asp Leu Thr Trp Glu Leu Thr
225 230 235 240
Ala Pro Trp Thr Gly Ala Gln Ile Gln Val Pro Val Lys Phe Ile Val
245 250 255
Gly Asp Ser Asp Leu Thr Tyr His Phe Pro Gly Ala Lys Glu Tyr Ile
260 265 270
His Asn Gly Gly Phe Lys Arg Asp Val Pro Leu Leu Glu Glu Val Val
275 280 285
Val Val Lys Asp Ala Cys His Phe Ile Asn Gln Glu Arg Pro Gln Glu
290 295 300
Ile Asn Ala His Ile His Asp Phe Ile Asn Lys Phe
305 310 315

<210> 895
<211> 4113
<212> DNA
<213> Artificial Sequence

<220>
<223> Pathway step 7 sequence Y tDexT DNA (native DNA sequence)

<400> 895
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catgatacgg accagcagga cgattcacta gaaaaacagc aagtattaga accgagcgta 120
aatagtaata taccaaaaaa gcagacaaat caacagttag cggttgttac agcaccagca 180
aattcagcac ctcaaaccaa aacaacagca gaaatttctg ctggtacaga gttagacacg 240
atgcctaatg ttaagcatgt agatggcaaa gtttattttt atggagatga tggccaacca 300
aaaaagaatt ttactactat tatagatggt aaaccttact actttgataa agatacaggg 360
gcactatcta ataacgataa gcaatatgta tcggaattat tcagtattgg caataaacat 420
aacgccgtct ataacacatc atcagataat tttacgcaat tagaaggaca tctgacggca 480
agtagttggt atcgtccaaa agatattttg aaaaatggta aacgttgggc accttcaaca 540
gtgactgatt tcagaccatt attgatggcc tggtggccgg ataagagtac gcaagtcact 600
tatctgaatt acatgaaaga tcagggcctc ttgtctggta ctcatcactt ttccgataat 660
gaaaatatgc ggaccttaac ggcagctgcc atgcaggcac aggtaaacat tgagaaaaaa 720
attgggcaac ttggcaatac ggattggttg aaaacggcga tgacgcaata cattgatgcc 780
cagcccaatt ggaatattga cagtgaggcg aaaggagatg atcatctaca aggtggtgca 840
ctactttata caaatagtga tatgtcgcca aaggccaatt ctgattatcg taagctgagc 900
cgtacgccta aaaatcaaaa aggtcaaatt gctgataaat ataagcaagg tgggtttgaa 960
ttattactag caaacgatgt cgataattct aatccagttg tgcaagcaga acaacttaat 1020
tggttacatt atatgatgaa tatcggtagt attttacaaa atgatgacca agctaatttt 1080
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gaatatgcta aggctgccta tggtgttgac aaaaatgacg cgagagcgaa tcaacattta 1200
tcaattttgg aagactgggg agatgaagat ccagactatg tcaaagcaca tggcaaccag 1260
caaattacaa tggatttccc cttgcattta gcgattaaat acgcgctcaa catgcctaat 1320
gataagcgga gtggccttga gccaacccgt gaacacagtt tagtcaaacg aattacagat 1380
gataaagaaa atgttgcaca accaaattat tcatttatcc gagctcatga cagtgaagta 1440
caaacgatta ttgctgatat tattaaagat aaaatcaacc cggcgtcaac agggctagat 1500
tcaacagtga ctttggatca aattaagcag gcttttgaca tctataatgc tgatgaattg 1560
aaagcagata aagtttacac accttacaat attccagcat catacgcttt gttattgact 1620
aataaagaca caattccacg tgtttattat ggggatatgt tcacggatga tggccaatac 1680
atggctaaac aatcacctta ctatcaagcg attgatgcgt tgttgaaagc tcgtatcaag 1740
tatgctgctg gtggtcaaac catgaaaatg aactattttc cagatgaaca atctgttatg 1800
acatcagttc gttatggtaa gggtgcaatg acggcaagtg actctggtaa ccaagagaca 1860
cgctatcaag gtattggact tgttgtcaac aatcgcccag atttgaaact atctgacaaa 1920
gatgaagtca aaatggatat gggtgcggca cataaaaacc aagattatcg cccagttttg 1980
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ttgtatgcat caaagacagt tggcgggggc atttatcagc aacaatatgg tggggccttc 2700
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tctgccttta tttgtgataa cggtaattgg tactactttg atgacaaagg gaaaatggtt 3060
gttggaaacc aagttatcaa tggcatcaat tattactttt taccgaatgg tatcgaatta 3120
caagatgcct atctagtaca tgatggtatg tactattatt ataataatat tggcaagcaa 3180
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cacatggcac agggtattgt caccatcatt caaagtgatg gcaccccagt cacacagtac 3300
tttgatgaga atggtaagca acaaaaaggc gtggcggtca aaggatcaga tggtcatttg 3360
cattactttg acggtgcgtc agggaatatg ctctttaaat catggggtag actagcagat 3420
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aatcaaacgg tttactttaa tgatgatggt cgtcaaatca aaaataactt taaagaatta 3540
gcagatggtt cttggcttta tcttaacaat aaaggtgttg cagtaacagg agagcaaata 3600
attaatgggc agacacttta ttttggtaac gatggtcgtc aatttaaagg gacaacacat 3660
ataaatgcta ctggtgaaag ccgttactat gacccagact caggtaatat gataactgat 3720
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ttagttcgta atcgatttgt attgctatct gatggttcat gggtttactt tggccaagat 3960
ggcgtacccg taactggcgt gcaagtgatt aatggccaaa cattatattt tgacgcagat 4020
ggtaggcaag tcaaagggca gcaacgtgta atcggcaatc aacgctattg gatggataaa 4080
gacaatggtg aaatgaaaaa aataacatac tag 4113

<210> 896
<211> 1370
<212> PRT
<213> Artificial Sequence

<220>
<223> Pathway step 7 sequence Z tDexT Protein

<400> 896
Met Pro Ala Asn Ala Pro Asp Lys Gln Ser Val Thr Asn Ala Pro Val
 1               5                  10                  15
Val Pro Pro Lys His Asp Thr Asp Gln Gln Asp Asp Ser Leu Glu Lys
            20                  25                  30
Gln Gln Val Leu Glu Pro Ser Val Asn Ser Asn Ile Pro Lys Lys Gln
        35                  40                  45
Thr Asn Gln Gln Leu Ala Val Val Thr Ala Pro Ala Asn Ser Ala Pro
    50                  55                  60
Gln Thr Lys Thr Thr Ala Glu Ile Ser Ala Gly Thr Glu Leu Asp Thr
65                  70                  75                  80
Met Pro Asn Val Lys His Val Asp Gly Lys Val Tyr Phe Tyr Gly Asp
                85                  90                  95
Asp Gly Gln Pro Lys Lys Asn Phe Thr Thr Ile Ile Asp Gly Lys Pro
            100                 105                 110
Tyr Tyr Phe Asp Lys Asp Thr Gly Ala Leu Ser Asn Asn Asp Lys Gln
        115                 120                 125
Tyr Val Ser Glu Leu Phe Ser Ile Gly Asn Lys His Asn Ala Val Tyr
    130                 135                 140
Asn Thr Ser Ser Asp Asn Phe Thr Gln Leu Glu Gly His Leu Thr Ala

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145                 150                 155                 160
Ser Ser Trp Tyr Arg Pro Lys Asp Ile Leu Lys Asn Gly Lys Arg Trp
                165                 170                 175
Ala Pro Ser Thr Val Thr Asp Phe Arg Pro Leu Leu Met Ala Trp Trp
            180                 185                 190
Pro Asp Lys Ser Thr Gln Val Thr Tyr Leu Asn Tyr Met Lys Asp Gln
        195                 200                 205
Gly Leu Leu Ser Gly Thr His His Phe Ser Asp Asn Glu Asn Met Arg
    210                 215                 220
Thr Leu Thr Ala Ala Ala Met Gln Ala Gln Val Asn Ile Glu Lys Lys
225                 230                 235                 240
Ile Gly Gln Leu Gly Asn Thr Asp Trp Leu Lys Thr Ala Met Thr Gln
                245                 250                 255
Tyr Ile Asp Ala Gln Pro Asn Trp Asn Ile Asp Ser Glu Ala Lys Gly
            260                 265                 270
Asp Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Thr Asn Ser Asp Met
        275                 280                 285
Ser Pro Lys Ala Asn Ser Asp Tyr Arg Lys Leu Ser Arg Thr Pro Lys
    290                 295                 300
Asn Gln Lys Gly Gln Ile Ala Asp Lys Tyr Lys Gln Gly Gly Phe Glu
305                 310                 315                 320
Leu Leu Leu Ala Asn Asp Val Asp Asn Ser Asn Pro Val Val Gln Ala
                325                 330                 335
Glu Gln Leu Asn Trp Leu His Tyr Met Met Asn Ile Gly Ser Ile Leu
            340                 345                 350
Gln Asn Asp Asp Gln Ala Asn Phe Asp Gly Tyr Arg Val Asp Ala Val
        355                 360                 365
Asp Asn Val Asp Ala Asp Leu Leu Gln Ile Ala Gly Glu Tyr Ala Lys
    370                 375                 380
Ala Ala Tyr Gly Val Asp Lys Asn Asp Ala Arg Ala Asn Gln His Leu
385                 390                 395                 400
Ser Ile Leu Glu Asp Trp Gly Asp Glu Asp Pro Asp Tyr Val Lys Ala
                405                 410                 415
His Gly Asn Gln Gln Ile Thr Met Asp Phe Pro Leu His Leu Ala Ile
            420                 425                 430
Lys Tyr Ala Leu Asn Met Pro Asn Asp Lys Arg Ser Gly Leu Glu Pro
        435                 440                 445
Thr Arg Glu His Ser Leu Val Lys Arg Ile Thr Asp Asp Lys Glu Asn
    450                 455                 460
Val Ala Gln Pro Asn Tyr Ser Phe Ile Arg Ala His Asp Ser Glu Val
465                 470                 475                 480
Gln Thr Ile Ile Ala Asp Ile Ile Lys Asp Lys Ile Asn Pro Ala Ser
                485                 490                 495
Thr Gly Leu Asp Ser Thr Val Thr Leu Asp Gln Ile Lys Gln Ala Phe
            500                 505                 510
Asp Ile Tyr Asn Ala Asp Glu Leu Lys Ala Asp Lys Val Tyr Thr Pro
        515                 520                 525
Tyr Asn Ile Pro Ala Ser Tyr Ala Leu Leu Leu Thr Asn Lys Asp Thr
    530                 535                 540
Ile Pro Arg Val Tyr Tyr Gly Asp Met Phe Thr Asp Asp Gly Gln Tyr
545                 550                 555                 560
Met Ala Lys Gln Ser Pro Tyr Tyr Gln Ala Ile Asp Ala Leu Leu Lys
                565                 570                 575
Ala Arg Ile Lys Tyr Ala Ala Gly Gly Gln Thr Met Lys Met Asn Tyr
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            580                 585                 590
Phe Pro Asp Glu Gln Ser Val Met Thr Ser Val Arg Tyr Gly Lys Gly
        595                 600                 605
Ala Met Thr Ala Ser Asp Ser Gly Asn Gln Glu Thr Arg Tyr Gln Gly
    610                 615                 620
Ile Gly Leu Val Val Asn Asn Arg Pro Asp Leu Lys Leu Ser Asp Lys
625                 630                 635                 640
Asp Glu Val Lys Met Asp Met Gly Ala Ala His Lys Asn Gln Asp Tyr
                645                 650                 655
Arg Pro Val Leu Leu Thr Thr Lys Ser Gly Leu Lys Val Tyr Ser Thr
            660                 665                 670
Asp Ala Asn Ala Pro Val Val Arg Thr Asp Ala Asn Gly Gln Leu Thr
        675                 680                 685
Phe Lys Ala Asp Met Val Tyr Gly Val Asn Asp Pro Gln Val Ser Gly
    690                 695                 700
Tyr Ile Ala Ala Trp Val Pro Val Gly Ala Ser Glu Asn Gln Asp Ala
705                 710                 715                 720
Arg Thr Lys Ser Glu Thr Thr Gln Ser Thr Asp Gly Ser Val Tyr His
                725                 730                 735
Ser Asn Ala Ala Leu Asp Ser Gln Val Ile Tyr Glu Gly Phe Ser Asn
            740                 745                 750
Phe Gln Asp Phe Pro Thr Thr Pro Asp Glu Phe Thr Asn Ile Lys Ile
        755                 760                 765
Ala Gln Asn Val Asn Leu Phe Lys Asp Trp Gly Ile Thr Ser Phe Glu
    770                 775                 780
Met Ala Pro Gln Tyr Arg Ala Ser Ser Asp Lys Ser Phe Leu Asp Ala
785                 790                 795                 800
Ile Val Gln Asn Gly Tyr Ala Phe Thr Asp Arg Tyr Asp Ile Gly Tyr
                805                 810                 815
Asn Thr Pro Thr Lys Tyr Gly Thr Ala Asp Asn Leu Leu Asp Ala Leu
            820                 825                 830
Arg Ala Leu His Gly Gln Gly Ile Gln Ala Ile Asn Asp Trp Val Pro
        835                 840                 845
Asp Gln Ile Tyr Asn Leu Pro Asp Glu Gln Leu Val Thr Ala Ile Arg
    850                 855                 860
Thr Asp Gly Ser Gly Asp His Thr Tyr Gly Ser Val Ile Asp His Thr
865                 870                 875                 880
Leu Tyr Ala Ser Lys Thr Val Gly Gly Gly Ile Tyr Gln Gln Gln Tyr
                885                 890                 895
Gly Gly Ala Phe Leu Glu Gln Leu Lys Thr Gln Tyr Pro Gln Leu Phe
            900                 905                 910
Gln Gln Lys Gln Ile Ser Thr Asp Gln Pro Met Asn Pro Asp Ile Gln
        915                 920                 925
Ile Lys Ser Trp Glu Ala Lys Tyr Phe Asn Gly Ser Asn Ile Gln Gly
    930                 935                 940
Arg Gly Ala Trp Tyr Val Leu Lys Asp Trp Gly Thr Gln Gln Tyr Phe
945                 950                 955                 960
Asn Val Ser Asp Ala Gln Thr Phe Leu Pro Lys Gln Leu Leu Gly Glu
                965                 970                 975
Lys Ala Lys Thr Gly Phe Val Thr Arg Gly Lys Glu Thr Ser Phe Tyr
            980                 985                 990
Ser Thr Ser Gly Tyr Gln Ala Lys Ser Ala Phe Ile Cys Asp Asn Gly
        995                 1000                1005
Asn Trp Tyr Tyr Phe Asp Asp Lys Gly Lys Met Val Val Gly Asn Gln
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    1010                1015                1020
Val Ile Asn Gly Ile Asn Tyr Tyr Phe Leu Pro Asn Gly Ile Glu Leu
1025                1030                1035                1040
Gln Asp Ala Tyr Leu Val His Asp Gly Met Tyr Tyr Tyr Tyr Asn Asn
                1045                1050                1055
Ile Gly Lys Gln Leu His Asn Thr Tyr Tyr Gln Asp Lys Gln Lys Asn
            1060                1065                1070
Phe His Tyr Phe Phe Glu Asp Gly His Met Ala Gln Gly Ile Val Thr
        1075                1080                1085
Ile Ile Gln Ser Asp Gly Thr Pro Val Thr Gln Tyr Phe Asp Glu Asn
    1090                1095                1100
Gly Lys Gln Gln Lys Gly Val Ala Val Lys Gly Ser Asp Gly His Leu
1105                1110                1115                1120
His Tyr Phe Asp Gly Ala Ser Gly Asn Met Leu Phe Lys Ser Trp Gly
                1125                1130                1135
Arg Leu Ala Asp Gly Ser Trp Leu Tyr Val Asp Glu Lys Gly Asn Ala
            1140                1145                1150
Val Thr Gly Lys Gln Thr Ile Asn Asn Gln Thr Val Tyr Phe Asn Asp
        1155                1160                1165
Asp Gly Arg Gln Ile Lys Asn Asn Phe Lys Glu Leu Ala Asp Gly Ser
    1170                1175                1180
Trp Leu Tyr Leu Asn Asn Lys Gly Val Ala Val Thr Gly Glu Gln Ile
1185                1190                1195                1200
Ile Asn Gly Gln Thr Leu Tyr Phe Gly Asn Asp Gly Arg Gln Phe Lys
                1205                1210                1215
Gly Thr Thr His Ile Asn Ala Thr Gly Glu Ser Arg Tyr Tyr Asp Pro
            1220                1225                1230
Asp Ser Gly Asn Met Ile Thr Asp Arg Phe Glu Arg Val Gly Asp Asn
        1235                1240                1245
Gln Trp Ala Tyr Phe Gly Tyr Asp Gly Val Ala Val Thr Gly Asp Arg
    1250                1255                1260
Ile Ile Lys Gly Gln Lys Leu Tyr Phe Asn Gln Asn Gly Ile Gln Met
1265                1270                1275                1280
Lys Gly His Leu Arg Leu Glu Asn Gly Ile Met Arg Tyr Tyr Asp Ala
                1285                1290                1295
Asp Thr Gly Glu Leu Val Arg Asn Arg Phe Val Leu Leu Ser Asp Gly
            1300                1305                1310
Ser Trp Val Tyr Phe Gly Gln Asp Gly Val Pro Val Thr Gly Val Gln
        1315                1320                1325
Val Ile Asn Gly Gln Thr Leu Tyr Phe Asp Ala Asp Gly Arg Gln Val
    1330                1335                1340
Lys Gly Gln Gln Arg Val Ile Gly Asn Gln Arg Tyr Trp Met Asp Lys
1345                1350                1355                1360
Asp Asn Gly Glu Met Lys Lys Ile Thr Tyr
                1365                1370
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<210> 897
<211> 1584
<212> DNA
<213> Artificial Sequence

<220>
<223> Step 1 sequence id A tHMG-CoA DNA

<400> 897
atggcagctg accaattggt gaaaactgaa gtcaccaaga agtcttttac tgctcctgta 60
caaaaggctt ctacaccagt tttaaccaat aaaacagtca tttctggatc gaaagtcaaa 120
agtttatcat ctgcgcaatc gagctcatca ggaccttcat catctagtga ggaagatgat 180
tcccgcgata ttgaaagctt ggataagaaa atacgtcctt tagaagaatt agaagcatta 240
ttaagtagtg gaaatacaaa acaattgaag aacaaagagg tcgctgcctt ggttattcac 300
ggtaagttac ctttgtacgc tttggagaaa aaattaggtg atactacgag agcggttgcg 360
gtacgtagga aggctctttc aattttggca gaagctcctg tattagcatc tgatcgttta 420
ccatataaaa attatgacta cgaccgcgta tttggcgctt gttgtgaaaa tgttataggt 480
tacatgcctt tgcccgttgg tgttataggc cccttggtta tcgatggtac atcttatcat 540
ataccaatgg caactacaga gggttgtttg gtagcttctg ccatgcgtgg ctgtaaggca 600
atcaatgctg gcggtggtgc aacaactgtt ttaactaagg atggtatgac aagaggccca 660
gtagtccgtt tcccaacttt gaaaagatct ggtgcctgta agatatggtt agactcagaa 720
gagggacaaa acgcaattaa aaaagctttt aactctacat caagatttgc acgtctgcaa 780
catattcaaa cttgtctagc aggagattta ctcttcatga gatttagaac aactactggt 840
gacgcaatgg gtatgaatat gatttctaaa ggtgtcgaat actcattaaa gcaaatggta 900
gaagagtatg gctgggaaga tatggaggtt gtctccgttt ctggtaacta ctgtaccgac 960
aaaaaaccag ctgccatcaa ctggatcgaa ggtcgtggta agagtgtcgt cgcagaagct 1020
actattcctg gtgatgttgt cagaaaagtg ttaaaaagtg atgtttccgc attggttgag 1080
ttgaacattg ctaagaattt ggttggatct gcaatggctg ggtctgttgg tggatttaac 1140
gcacatgcag ctaatttagt gacagctgtt ttcttggcat taggacaaga tcctgcacaa 1200
aatgttgaaa gttccaactg tataacattg atgaaagaag tggacggtga tttgagaatt 1260
tccgtatcca tgccatccat cgaagtaggt accatcggtg gtggtactgt tctagaacca 1320
caaggtgcca tgttggactt attaggtgta agaggcccgc atgctaccgc tcctggtacc 1380
aacgcacgtc aattagcaag aatagttgcc tgtgccgtct tggcaggtga attatcctta 1440
tgtgctgccc tagcagccgg ccatttggtt caaagtcata tgacccacaa caggaaacct 1500
gctgaaccaa caaaacctaa caatttggac gccactgata taaatcgttt gaaagatggg 1560
tccgtcacct gcattaaatc ctaa 1584

<210> 898
<211> 527
<212> PRT
<213> Artificial Sequence

<220>
<223> Step 1 sequence id B tHMG-CoA Protein

<400> 898
Met Ala Ala Asp Gln Leu Val Lys Thr Glu Val Thr Lys Lys Ser Phe
 1               5                  10                  15
Thr Ala Pro Val Gln Lys Ala Ser Thr Pro Val Leu Thr Asn Lys Thr
            20                  25                  30
Val Ile Ser Gly Ser Lys Val Lys Ser Leu Ser Ser Ala Gln Ser Ser
        35                  40                  45
Ser Ser Gly Pro Ser Ser Ser Ser Glu Glu Asp Asp Ser Arg Asp Ile
    50                  55                  60
Glu Ser Leu Asp Lys Lys Ile Arg Pro Leu Glu Glu Leu Glu Ala Leu
65                  70                  75                  80
Leu Ser Ser Gly Asn Thr Lys Gln Leu Lys Asn Lys Glu Val Ala Ala
                85                  90                  95
Leu Val Ile His Gly Lys Leu Pro Leu Tyr Ala Leu Glu Lys Lys Leu
            100                 105                 110
Gly Asp Thr Thr Arg Ala Val Ala Val Arg Arg Lys Ala Leu Ser Ile

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        115                 120                 125
Leu Ala Glu Ala Pro Val Leu Ala Ser Asp Arg Leu Pro Tyr Lys Asn
    130                 135                 140
Tyr Asp Tyr Asp Arg Val Phe Gly Ala Cys Cys Glu Asn Val Ile Gly
145                 150                 155                 160
Tyr Met Pro Leu Pro Val Gly Val Ile Gly Pro Leu Val Ile Asp Gly
                165                 170                 175
Thr Ser Tyr His Ile Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala
            180                 185                 190
Ser Ala Met Arg Gly Cys Lys Ala Ile Asn Ala Gly Gly Gly Ala Thr
        195                 200                 205
Thr Val Leu Thr Lys Asp Gly Met Thr Arg Gly Pro Val Val Arg Phe
    210                 215                 220
Pro Thr Leu Lys Arg Ser Gly Ala Cys Lys Ile Trp Leu Asp Ser Glu
225                 230                 235                 240
Glu Gly Gln Asn Ala Ile Lys Lys Ala Phe Asn Ser Thr Ser Arg Phe
                245                 250                 255
Ala Arg Leu Gln His Ile Gln Thr Cys Leu Ala Gly Asp Leu Leu Phe
            260                 265                 270
Met Arg Phe Arg Thr Thr Thr Gly Asp Ala Met Gly Met Asn Met Ile
        275                 280                 285
Ser Lys Gly Val Glu Tyr Ser Leu Lys Gln Met Val Glu Glu Tyr Gly
    290                 295                 300
Trp Glu Asp Met Glu Val Val Ser Val Ser Gly Asn Tyr Cys Thr Asp
305                 310                 315                 320
Lys Lys Pro Ala Ala Ile Asn Trp Ile Glu Gly Arg Gly Lys Ser Val
                325                 330                 335
Val Ala Glu Ala Thr Ile Pro Gly Asp Val Val Arg Lys Val Leu Lys
            340                 345                 350
Ser Asp Val Ser Ala Leu Val Glu Leu Asn Ile Ala Lys Asn Leu Val
        355                 360                 365
Gly Ser Ala Met Ala Gly Ser Val Gly Gly Phe Asn Ala His Ala Ala
    370                 375                 380
Asn Leu Val Thr Ala Val Phe Leu Ala Leu Gly Gln Asp Pro Ala Gln
385                 390                 395                 400
Asn Val Glu Ser Ser Asn Cys Ile Thr Leu Met Lys Glu Val Asp Gly
                405                 410                 415
Asp Leu Arg Ile Ser Val Ser Met Pro Ser Ile Glu Val Gly Thr Ile
            420                 425                 430
Gly Gly Gly Thr Val Leu Glu Pro Gln Gly Ala Met Leu Asp Leu Leu
        435                 440                 445
Gly Val Arg Gly Pro His Ala Thr Ala Pro Gly Thr Asn Ala Arg Gln
    450                 455                 460
Leu Ala Arg Ile Val Ala Cys Ala Val Leu Ala Gly Glu Leu Ser Leu
465                 470                 475                 480
Cys Ala Ala Leu Ala Ala Gly His Leu Val Gln Ser His Met Thr His
                485                 490                 495
Asn Arg Lys Pro Ala Glu Pro Thr Lys Pro Asn Asn Leu Asp Ala Thr
            500                 505                 510
Asp Ile Asn Arg Leu Lys Asp Gly Ser Val Thr Cys Ile Lys Ser
        515                 520                 525
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<210> 899

<211> 1491
<212> DNA
<213> Artificial Sequence

<220>
<223> Step 1 sequence id C erg1 DNA

<400> 899
atgtctgctg ttaacgttgc acctgaattg attaatgccg acaacacaat tacctacgat 60
gcgattgtca tcggtgctgg tgttatcggt ccatgtgttg ctactggtct agcaagaaag 120
ggtaagaaag ttcttatcgt agaacgtgac tgggctatgc ctgatagaat tgttggtgaa 180
ttgatgcaac caggtggtgt tagagcattg agaagtctgg gtatgattca atctatcaac 240
aacatcgaag catatcctgt taccggttat accgtctttt tcaacggcga acaagttgat 300
attccatacc cttacaaggc cgatatccct aaagttgaaa aattgaagga cttggtcaaa 360
gatggtaatg acaaggtctt ggaagacagc actattcaca tcaaggatta cgaagatgat 420
gaaagagaaa ggggtgttgc ttttgttcat ggtagattct tgaacaactt gagaaacatt 480
actgctcaag agccaaatgt tactagagtg caaggtaact gtattgagat attgaaggat 540
gaaaagaatg aggttgttgg tgccaaggtt gacattgatg gccgtggcaa ggtggaattc 600
aaagcccact tgacatttat ctgtgacggt atcttttcac gtttcagaaa ggaattgcac 660
ccagaccatg ttccaactgt cggttcttcg tttgtcggta tgtctttgtt caatgctaag 720
aatcctgctc ctatgcacgg tcacgttatt cttggtagtg atcatatgcc aatcttggtt 780
taccaaatca gtccagaaga aacaagaatc ctttgtgctt acaactctcc aaaggtccca 840
gctgatatca agagttggat gattaaggat gtccaacctt tcattccaaa gagtctacgt 900
ccttcatttg atgaagccgt cagccaaggt aaatttagag ctatgccaaa ctcctacttg 960
ccagctagac aaaacgacgt cactggtatg tgtgttatcg gtgacgctct aaatatgaga 1020
catccattga ctggtggtgg tatgactgtc ggtttgcatg atgttgtctt gttgattaag 1080
aaaataggtg acctagactt cagcgaccgt gaaaaggttt tggatgaatt actagactac 1140
catttcgaaa gaaagagtta cgattccgtt attaacgttt tgtcagtggc tttgtattct 1200
ttgttcgctg ctgacagcga taacttgaag gcattacaaa aaggttgttt caaatatttc 1260
caaagaggtg gcgattgtgt caacaaaccc gttgaatttc tgtctggtgt cttgccaaag 1320
cctttgcaat tgaccagggt tttcttcgct gtcgcttttt acaccattta cttgaacatg 1380
gaagaacgtg gtttcttggg attaccaatg gctttattgg aaggtattat gattttgatc 1440
acagctatta gagtattcac cccatttttg tttggtgagt tgattggtta a 1491

<210> 900
<211> 496
<212> PRT
<213> Artificial Sequence

<220>
<223> Step 1 sequence id D erg1 protein

<400> 900
Met Ser Ala Val Asn Val Ala Pro Glu Leu Ile Asn Ala Asp Asn Thr
 1               5                  10                  15
Ile Thr Tyr Asp Ala Ile Val Ile Gly Ala Gly Val Ile Gly Pro Cys
            20                  25                  30
Val Ala Thr Gly Leu Ala Arg Lys Gly Lys Lys Val Leu Ile Val Glu
        35                  40                  45
Arg Asp Trp Ala Met Pro Asp Arg Ile Val Gly Glu Leu Met Gln Pro
    50                  55                  60
Gly Gly Val Arg Ala Leu Arg Ser Leu Gly Met Ile Gln Ser Ile Asn
65                  70                  75                  80
Asn Ile Glu Ala Tyr Pro Val Thr Gly Tyr Thr Val Phe Phe Asn Gly

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                85                  90                  95
Glu Gln Val Asp Ile Pro Tyr Pro Tyr Lys Ala Asp Ile Pro Lys Val
            100                 105                 110
Glu Lys Leu Lys Asp Leu Val Lys Asp Gly Asn Asp Lys Val Leu Glu
        115                 120                 125
Asp Ser Thr Ile His Ile Lys Asp Tyr Glu Asp Asp Glu Arg Glu Arg
    130                 135                 140
Gly Val Ala Phe Val His Gly Arg Phe Leu Asn Asn Leu Arg Asn Ile
145                 150                 155                 160
Thr Ala Gln Glu Pro Asn Val Thr Arg Val Gln Gly Asn Cys Ile Glu
                165                 170                 175
Ile Leu Lys Asp Glu Lys Asn Glu Val Val Gly Ala Lys Val Asp Ile
            180                 185                 190
Asp Gly Arg Gly Lys Val Glu Phe Lys Ala His Leu Thr Phe Ile Cys
        195                 200                 205
Asp Gly Ile Phe Ser Arg Phe Arg Lys Glu Leu His Pro Asp His Val
    210                 215                 220
Pro Thr Val Gly Ser Ser Phe Val Gly Met Ser Leu Phe Asn Ala Lys
225                 230                 235                 240
Asn Pro Ala Pro Met His Gly His Val Ile Leu Gly Ser Asp His Met
                245                 250                 255
Pro Ile Leu Val Tyr Gln Ile Ser Pro Glu Glu Thr Arg Ile Leu Cys
            260                 265                 270
Ala Tyr Asn Ser Pro Lys Val Pro Ala Asp Ile Lys Ser Trp Met Ile
        275                 280                 285
Lys Asp Val Gln Pro Phe Ile Pro Lys Ser Leu Arg Pro Ser Phe Asp
    290                 295                 300
Glu Ala Val Ser Gln Gly Lys Phe Arg Ala Met Pro Asn Ser Tyr Leu
305                 310                 315                 320
Pro Ala Arg Gln Asn Asp Val Thr Gly Met Cys Val Ile Gly Asp Ala
                325                 330                 335
Leu Asn Met Arg His Pro Leu Thr Gly Gly Gly Met Thr Val Gly Leu
            340                 345                 350
His Asp Val Val Leu Leu Ile Lys Lys Ile Gly Asp Leu Asp Phe Ser
        355                 360                 365
Asp Arg Glu Lys Val Leu Asp Glu Leu Leu Asp Tyr His Phe Glu Arg
    370                 375                 380
Lys Ser Tyr Asp Ser Val Ile Asn Val Leu Ser Val Ala Leu Tyr Ser
385                 390                 395                 400
Leu Phe Ala Ala Asp Ser Asp Asn Leu Lys Ala Leu Gln Lys Gly Cys
                405                 410                 415
Phe Lys Tyr Phe Gln Arg Gly Gly Asp Cys Val Asn Lys Pro Val Glu
            420                 425                 430
Phe Leu Ser Gly Val Leu Pro Lys Pro Leu Gln Leu Thr Arg Val Phe
        435                 440                 445
Phe Ala Val Ala Phe Tyr Thr Ile Tyr Leu Asn Met Glu Glu Arg Gly
    450                 455                 460
Phe Leu Gly Leu Pro Met Ala Leu Leu Glu Gly Ile Met Ile Leu Ile
465                 470                 475                 480
Thr Ala Ile Arg Val Phe Thr Pro Phe Leu Phe Gly Glu Leu Ile Gly
                485                 490                 495
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<210> 901

<211> 2325
<212> DNA
<213> Artificial Sequence

<220>
<223> Pathway 2 sequence id E Cmelo DNA

<400> 901
atgtggagat taaaagtggg aaaagagagt gttggggaaa aagaagagaa atggattaag 60
agtataagca atcacttggg acgtcaagtt tgggaatttt gcagtggtga aaatgaaaat 120
gatgatgatg aagccattgc tgttgctaat aattctgctt caaagttcga gaatgccagg 180
aatcactttc gtaataatcg tttccatcgc aagcaatctt ccgacctctt tcttgccatt 240
cagtgtgaaa aggaaataat aagaaacggt gcaaaaaatg aaggaaccac caaagtaaaa 300
gaaggggaag atgtgaagaa agaagcagtg aagaatacat tagaaagagc attaagtttc 360
tattcggctg ttcaaacaag cgatgggaat tgggcttcgg atcttggcgg gcctatgttt 420
ttactaccgg gtttagtgat tgctctatat gtcactggag tcttgaattc tgttctgtcc 480
aagcaccatc gccaagaaat gtgtagatat atttacaatc atcagaatga agatggggga 540
tggggtttgc acattgaagg ttcgagcacg atgtttggtt cggcactgaa ttatgttgca 600
ctgagactgc ttggagaggc tgccgatggc ggagagcacg gcgcaatgac aaaagctcga 660
agttggatct tggagcgtgg tggagctacc gcaatcactt cttggggaaa attgtggctg 720
tcagtacttg gagtctatga atggagtggc aacaatcctc tcccacctga attttggtta 780
ctcccatata gcctaccatt tcatcctgga agaatgtggt gccattgtcg aatggtttat 840
ctaccaatgt cgtacttata tggaaagaga tttgttgggc caatcacacc catagtttta 900
tctctaagaa aagagcttta cacaattcca tatcatgaaa ttgattggaa tagatctcgc 960
aatacatgtg caaaggagga tttgtactat ccacatccga agatgcaaga tattttatgg 1020
ggatcgatat accacgtgta tgagccattg tttagtggtt ggccagggaa aaggttgagg 1080
gaaaaggcaa tgaaaattgc aatggaacat atacattatg aagatgaaaa tagtcgatat 1140
atatgtcttg gtcctgtcaa taaagtactt aatatgcttt gttgttgggt tgaagatcct 1200
tattcagatg ccttcaaatt tcatctacaa agaatccctg actatctttg gcttgctgaa 1260
gatggcatga gaatgcaggg ttacaatggg agtcaattgt gggacactgc tttctctatt 1320
caagcaatta tatccaccaa acttatagac acctttggcc caaccttaag aaaagcacat 1380
cattttgtta aacactctca gatccaggag gactgtcctg gtgatcctaa cgtttggttc 1440
cgtcacattc ataaaggtgc ttggcctttt tcaactcgag atcatggttg gctcatctct 1500
gactgtacgg ccgagggact aaaggcttct ttgatgttat ccaaacttcc atccaaaata 1560
gttggggagc cattagaaaa gaatcgcctt tgtgatgctg ttaatgttct cctttcttta 1620
caaaacgaaa atggtggatt tgcatcatac gagttgacaa gatcataccc ttggttggag 1680
ttgatcaacc ctgcagaaac atttggagat atcgtcatcg attattcgta tgtggagtgc 1740
acctcagcga caatggaagc attggcattg tttaagaagt tacatccagg gcataggacc 1800
aaagagattg atgctgctat tgccaaggcc gccaactttc ttgaaaatat gcaaaagact 1860
gatggctctt ggtatggatg ttgggggta tgcttcacat atgcagggtg gtttgggata 1920
aagggattgg ttgctgcagg aagaacatat aataactgtg ttgcaattcg taaggcttgt 1980
aattttcttt tatctaaaga gttacctggt ggtggatggg gggagagtta cctttcatgt 2040
cagaataagg tctacaccaa tcttgaagga aacaaaccac acttggttaa tactgcttgg 2100
gtaatgatgg ctctcattga agctggccag ggtgagagag acccagcccc attgcatcgt 2160
gcagcaagat tattaatcaa ttctcaattg gagagtggtg attttcccca acaggagatc 2220
atgggagtgt ttaataaaaa ctgtatgatt acatatgctg cataccgaaa catttttccc 2280
atttgggctc ttggagagta ttcccataga gttttggata tgtaa 2325

<210> 902
<211> 774
<212> PRT
<213> Artificial Sequence

<220>

<223> Pathway 2 sequence id F Cmelo Protein

<400> 902
Met Trp Arg Leu Lys Val Gly Lys Glu Ser Val Gly Glu Lys Glu Glu
 1               5                  10                  15
Lys Trp Ile Lys Ser Ile Ser Asn His Leu Gly Arg Gln Val Trp Glu
            20                  25                  30
Phe Cys Ser Gly Glu Asn Glu Asn Asp Asp Asp Glu Ala Ile Ala Val
        35                  40                  45
Ala Asn Asn Ser Ala Ser Lys Phe Glu Asn Ala Arg Asn His Phe Arg
    50                  55                  60
Asn Asn Arg Phe His Arg Lys Gln Ser Ser Asp Leu Phe Leu Ala Ile
65                  70                  75                  80
Gln Cys Glu Lys Glu Ile Ile Arg Asn Gly Ala Lys Asn Glu Gly Thr
                85                  90                  95
Thr Lys Val Lys Glu Gly Glu Asp Val Lys Lys Glu Ala Val Lys Asn
            100                 105                 110
Thr Leu Glu Arg Ala Leu Ser Phe Tyr Ser Ala Val Gln Thr Ser Asp
        115                 120                 125
Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro Met Phe Leu Leu Pro Gly
    130                 135                 140
Leu Val Ile Ala Leu Tyr Val Thr Gly Val Leu Asn Ser Val Leu Ser
145                 150                 155                 160
Lys His His Arg Gln Glu Met Cys Arg Tyr Ile Tyr Asn His Gln Asn
                165                 170                 175
Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly Ser Ser Thr Met Phe
            180                 185                 190
Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu Leu Gly Glu Ala Ala
        195                 200                 205
Asp Gly Gly Glu His Gly Ala Met Thr Lys Ala Arg Ser Trp Ile Leu
    210                 215                 220
Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser Trp Gly Lys Leu Trp Leu
225                 230                 235                 240
Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn Pro Leu Pro Pro
                245                 250                 255
Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro Phe His Pro Gly Arg Met
            260                 265                 270
Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly
        275                 280                 285
Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu Ser Leu Arg Lys
    290                 295                 300
Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile Asp Trp Asn Arg Ser Arg
305                 310                 315                 320
Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met Gln
                325                 330                 335
Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu Pro Leu Phe Ser
            340                 345                 350
Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met Lys Ile Ala Met
        355                 360                 365
Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile Cys Leu Gly
    370                 375                 380
Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro
385                 390                 395                 400
Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile Pro Asp Tyr Leu

```
                405                 410                 415
Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn Gly Ser Gln
            420                 425                 430
Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile Ser Thr Lys Leu
        435                 440                 445
Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His His Phe Val Lys
    450                 455                 460
His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro Asn Val Trp Phe
465                 470                 475                 480
Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His Gly
                485                 490                 495
Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ser Leu Met
            500                 505                 510
Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro Leu Glu Lys Asn
        515                 520                 525
Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Glu Asn
    530                 535                 540
Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu Glu
545                 550                 555                 560
Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr Ser
                565                 570                 575
Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Ala Leu Phe Lys
            580                 585                 590
Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Ala Ala Ile Ala
        595                 600                 605
Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys Thr Asp Gly Ser Trp
    610                 615                 620
Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly Ile
625                 630                 635                 640
Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Val Ala Ile
                645                 650                 655
Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly Gly
            660                 665                 670
Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu
        675                 680                 685
Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp Val Met Met Ala
    690                 695                 700
Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala Pro Leu His Arg
705                 710                 715                 720
Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser Gly Asp Phe Pro
                725                 730                 735
Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr
            740                 745                 750
Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Ser
        755                 760                 765
His Arg Val Leu Asp Met
    770
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<210> 903
<211> 2271
<212> DNA
<213> Artificial Sequence

<220>
<223> Pathway 2 sequence id G PSXY118L DNA (codon
optimized)

<400> 903
atgtggaaac ttaaagttgc tgagggtggc actccatggt taagaaccct aaacaatcac 60
gtgggtagac aggtttggga gtttgaccca cattctggtt ctcctcaaga cttggacgat 120
attgagacag caagaagaaa tttccatgac aatcgtttca ctcataaaca ctcagacgac 180
ttacttatga gattgcagtt tgccaaagaa aaccccatga atgaagtact gcctaaggtt 240
aaggttaaag acgttgaaga tgtcacagaa gaagcagttg ctaccactct aagaagaggc 300
ttgaacttct acagcaccat acaatcccac gatggtcatt ggcccggtga tttgggtggt 360
cctatgttct tgatgcctgg tttagttatc actttgtccg ttactggggc tcttaacgct 420
gttttaaccg atgaacatag aaaagagatg agaagatact tatacaatca ccaaaacaaa 480
gatggaggct ggggcttgca tattgaaggt cctagtacga tgtttggttc agtgttatgc 540
tatgttacct tgagactatt gggtgaaggg ccaaatgatg gtgagggtga catggagaga 600
ggaagagatt ggatcctaga acatggtgga gcaacatata taacctcttg gggcaaaatg 660
tggttatctg tattgggcgt gtttgaatgg tcagggaaca atccaatgcc accagaaatt 720
tggttgttgc cttatgctct tccagttcat ccaggaagaa tgtggtgtca ttgtaggatg 780
gtttacttac cgatgtcgta cttatacgga aaacgttttg tcggtcctat tacaccgacc 840
gtgcttagtc ttaggaaaga gctatttaca gtaccgtatc atgatataga ctggaaccaa 900
gcaagaaatt tatgtgccaa agaagattta tattaccctc atccactagt gcaggatata 960
ttatgggcta cacttcacaa gtttgtcgaa cccgtcttta tgaattggcc tggtaagaag 1020
ctaagggaaa aggcgatcaa aacagcaatt gagcacattc attatgagga tgagaatact 1080
aggtatatct gcattgggcc cgtcaacaaa gtgttgaata tgctgtgttg ttgggtggaa 1140
gatcctaatt ccgaagcttt caaactgcat ttgccgagaa tttatgatta cctatgggta 1200
gctgaagatg gcatgaaaat gcaaggttat aacggatcgc aattgtggga tacagcattt 1260
gctgcacaag ccattattag cacaaatcta attgacgaat tcggacccac gttaaagaag 1320
gcgcacgcct tcattaagaa tagtcaagta tccgaagatt gtcctggtga tctgagcaaa 1380
tggtacagac acatctcaaa aggtgcttgg ccattttcta ctgccgatca tggctggcca 1440
attagcgact gtactgcgga agggcttaag gcagtattgt tattatcgaa gatagcacct 1500
gagattgttg gagaaccatt ggattccaag cgtttgtatg atgcagttaa tgtaattctg 1560
tcactgcaga acgaaaatgg aggtttggcg acttacgaat tgactagatc atatacgtgg 1620
ctggaaataa tcaaccctgc cgaaacgttt ggtgacatag tcatagattg tccatatgtt 1680
gaatgcacaa gtgctgccat tcaggctcta gcaacttttg gtaaattgta tccaggtcat 1740
cgtcgtgaag aaatacaatg ttgcatagag aaagccgttg ccttcatcga gaagattcaa 1800
gcttctgatg gttcttggta tggatcatgg ggcgtctgtt ttacctacgg gacgtggttt 1860
ggtatcaagg gtttgattgc tgcagggaag aatttctcca attgcttaag tataaggaaa 1920
gcgtgtgagt tcttactgtc taaacaattg ccaagtggtg gatgggccga atcttacttg 1980
tcttgtcaga acaaagtgta ctctaactta gaaggaaata ggtcgcacgt cgttaataca 2040
ggatgggcta tgcttgcatt gattgaagca gagcaagcta agagagatcc aactccacta 2100
catagagcag ccgtatgctt aatcaactca caacttgaaa atggcgactt tccgcaagaa 2160
gaaatcatgg gcgtattcaa taagaactgt atgataactt acgctgcgta taggtgcatc 2220
tttcccattt gggctttggg tgaatataga agagtcttac aagcttgcta g 2271

<210> 904
<211> 756
<212> PRT
<213> Artificial Sequence

<220>
<223> Pathway 2 sequence id H PSXY118L Protein

<400> 904
Met Trp Lys Leu Lys Val Ala Glu Gly Gly Thr Pro Trp Leu Arg Thr

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 1               5                  10                  15
Leu Asn Asn His Val Gly Arg Gln Val Trp Glu Phe Asp Pro His Ser
            20                  25                  30
Gly Ser Pro Gln Asp Leu Asp Asp Ile Glu Thr Ala Arg Arg Asn Phe
        35                  40                  45
His Asp Asn Arg Phe Thr His Lys His Ser Asp Asp Leu Leu Met Arg
    50                  55                  60
Leu Gln Phe Ala Lys Glu Asn Pro Met Asn Glu Val Leu Pro Lys Val
65                  70                  75                  80
Lys Val Lys Asp Val Glu Asp Val Thr Glu Glu Ala Val Ala Thr Thr
                85                  90                  95
Leu Arg Arg Gly Leu Asn Phe Tyr Ser Thr Ile Gln Ser His Asp Gly
            100                 105                 110
His Trp Pro Gly Asp Leu Gly Gly Pro Met Phe Leu Met Pro Gly Leu
        115                 120                 125
Val Ile Thr Leu Ser Val Thr Gly Ala Leu Asn Ala Val Leu Thr Asp
    130                 135                 140
Glu His Arg Lys Glu Met Arg Arg Tyr Leu Tyr Asn His Gln Asn Lys
145                 150                 155                 160
Asp Gly Gly Trp Gly Leu His Ile Glu Gly Pro Ser Thr Met Phe Gly
                165                 170                 175
Ser Val Leu Cys Tyr Val Thr Leu Arg Leu Leu Gly Glu Gly Pro Asn
            180                 185                 190
Asp Gly Glu Gly Asp Met Glu Arg Gly Arg Asp Trp Ile Leu Glu His
        195                 200                 205
Gly Gly Ala Thr Tyr Ile Thr Ser Trp Gly Lys Met Trp Leu Ser Val
    210                 215                 220
Leu Gly Val Phe Glu Trp Ser Gly Asn Asn Pro Met Pro Pro Glu Ile
225                 230                 235                 240
Trp Leu Leu Pro Tyr Ala Leu Pro Val His Pro Gly Arg Met Trp Cys
                245                 250                 255
His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly Lys Arg
            260                 265                 270
Phe Val Gly Pro Ile Thr Pro Thr Val Leu Ser Leu Arg Lys Glu Leu
        275                 280                 285
Phe Thr Val Pro Tyr His Asp Ile Asp Trp Asn Gln Ala Arg Asn Leu
    290                 295                 300
Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Leu Val Gln Asp Ile
305                 310                 315                 320
Leu Trp Ala Thr Leu His Lys Phe Val Glu Pro Val Phe Met Asn Trp
                325                 330                 335
Pro Gly Lys Lys Leu Arg Glu Lys Ala Ile Lys Thr Ala Ile Glu His
            340                 345                 350
Ile His Tyr Glu Asp Glu Asn Thr Arg Tyr Ile Cys Ile Gly Pro Val
        355                 360                 365
Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro Asn Ser
    370                 375                 380
Glu Ala Phe Lys Leu His Leu Pro Arg Ile Tyr Asp Tyr Leu Trp Val
385                 390                 395                 400
Ala Glu Asp Gly Met Lys Met Gln Gly Tyr Asn Gly Ser Gln Leu Trp
                405                 410                 415
Asp Thr Ala Phe Ala Ala Gln Ala Ile Ile Ser Thr Asn Leu Ile Asp
            420                 425                 430
Glu Phe Gly Pro Thr Leu Lys Lys Ala His Ala Phe Ile Lys Asn Ser
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        435                 440                 445
Gln Val Ser Glu Asp Cys Pro Gly Asp Leu Ser Lys Trp Tyr Arg His
    450                 455                 460
Ile Ser Lys Gly Ala Trp Pro Phe Ser Thr Ala Asp His Gly Trp Pro
465                 470                 475                 480
Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Val Leu Leu Leu Ser
                485                 490                 495
Lys Ile Ala Pro Glu Ile Val Gly Glu Pro Leu Asp Ser Lys Arg Leu
            500                 505                 510
Tyr Asp Ala Val Asn Val Ile Leu Ser Leu Gln Asn Glu Asn Gly Gly
        515                 520                 525
Leu Ala Thr Tyr Glu Leu Thr Arg Ser Tyr Thr Trp Leu Glu Ile Ile
    530                 535                 540
Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Cys Pro Tyr Val
545                 550                 555                 560
Glu Cys Thr Ser Ala Ala Ile Gln Ala Leu Ala Thr Phe Gly Lys Leu
                565                 570                 575
Tyr Pro Gly His Arg Arg Glu Glu Ile Gln Cys Cys Ile Glu Lys Ala
            580                 585                 590
Val Ala Phe Ile Glu Lys Ile Gln Ala Ser Asp Gly Ser Trp Tyr Gly
        595                 600                 605
Ser Trp Gly Val Cys Phe Thr Tyr Gly Thr Trp Phe Gly Ile Lys Gly
    610                 615                 620
Leu Ile Ala Ala Gly Lys Asn Phe Ser Asn Cys Leu Ser Ile Arg Lys
625                 630                 635                 640
Ala Cys Glu Phe Leu Leu Ser Lys Gln Leu Pro Ser Gly Gly Trp Ala
                645                 650                 655
Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Ser Asn Leu Glu Gly
            660                 665                 670
Asn Arg Ser His Val Val Asn Thr Gly Trp Ala Met Leu Ala Leu Ile
        675                 680                 685
Glu Ala Glu Gln Ala Lys Arg Asp Pro Thr Pro Leu His Arg Ala Ala
    690                 695                 700
Val Cys Leu Ile Asn Ser Gln Leu Glu Asn Gly Asp Phe Pro Gln Glu
705                 710                 715                 720
Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr Ala Ala
                725                 730                 735
Tyr Arg Cys Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Arg Arg Val
            740                 745                 750
Leu Gln Ala Cys
        755
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<210> 905
<211> 2112
<212> DNA
<213> Artificial Sequence

<220>
<223> Pathway 2 sequence id I DdCASY80L DNA (codon optimized)

<400> 905
atgaccacga caaactggtc cctaaaggta gacagagggc gtcaaacttg ggaatactct 60

caagaaaaga aggaggccac tgatgtggac atccatttgc tacgactgaa ggaacccggc 120
acacattgcc ctgaaggttg tgatctgaat cgcgctaaaa ctccccaaca agcgattaag 180
aaagcatttc agtacttctc caaagtccaa acagaagatg gtcattgggc tggagatttg 240
ggtgggccaa tgttcttgtt acccggtttg gtgataacat gctacgttac tggctatcaa 300
ttgccagaat ccactcaaag ggaaattata aggtatctgt tcaatagaca gaatccggtt 360
gatggtggct ggggtttgca tatagaggcc cactctgata tatttggaac tacgttacaa 420
tatgtatcat tgagattact tggagttcca gccgaccatc catctgttgt aaaggcaaga 480
accttcttat tacagaatgg tggagcaacc ggtattcctt catggggtaa attctggttg 540
gccacgttga atgcatacga ctggaacggg ttgaatccaa ttcctattga attttggctg 600
ttaccctaca acttacccat tgctcctggt aggtggtggt gtcactgtcg gatggtctat 660
ctcccaatgt cttatatcta cgctaagaaa acaactggtc cactaacaga tttggtcaag 720
gatctgagga gagaaatcta ttgtcaagag tacgaaaaga ttaactggtc tgaacaaaga 780
aacaatattt cgaaattaga catgtactac gagcatacat ctcttttaaa tgttataaac 840
ggatcattga atgcttacga gaaagttcat tccaaatggc ttagggataa agccattgac 900
tatacctttg accatatacg ctatgaagat gagcagacga aatacattga cataggtcca 960
gtcaataaga ccgtcaatat gttatgcgtt tgggatagag aaggcaaatc tcctgcgttt 1020
tacaaacatg ccgatcgact taaagattat ctatggttat ctttcgatgg gatgaaaatg 1080
caaggctata acggttctca attgtgggac actgctttta cgatccaagc attcatggaa 1140
tctgggattg ccaatcaatt ccaggattgt atgaaattag ctggtcacta tttggacatc 1200
tcccaggtac cagaagatgc cagagatatg aagcactacc acagacacta ttcgaagggt 1260
gcatggcctt ttagtaccgt tgaccatgga tggccaattt cagattgcac agcagaaggt 1320
atcaagtcag cgcttgctct cagatctttg ccttttatcg aaccaatatc cttagataga 1380
attgctgatg gcattaatgt tctattaacc ttgcaaaatg gggatggtgg atgggcatcg 1440
tacgagaaca caagaggacc gaaatggctg gaaaagttta acccttccga agttttccag 1500
aatataatga ttgactatag ctatgtggaa tgtagtgctg cttgtattca agctatgagt 1560
gcgtttcgta aacatgcacc taatcatcca agaattaagg aaatcaacag atctattgca 1620
cgtggagtga aatttatcaa gagcattcaa cgtcaggatg gttcatggct gggcagttgg 1680
ggaatttgtt ttacctacgg tacttggttt ggcatagagg gcttagtagc atctggtgag 1740
cctctaacat cgccatcgat cgtgaaggct tgcaagtttc ttgcgtcaaa acaacgtgca 1800
gatggtggtt ggggagaaag ctttaaaagc aatgtgacta aagaatatgt tcaacacgaa 1860
acttcacaag tagtcaatac tggttgggct ctactcagtc taatgagtgc taaatatccg 1920
gacagagagt gcatagagag aggtatcaaa ttcttaatac agaggcaata tccgaacggt 1980
gattttccac aggaatccat tattggcgtt ttcaatttta actgtatgat ctcatattca 2040
aactataaga acatattccc tctttgggcc ttgagtaggt ataatcaatt gtaccttaaa 2100
agcaaaatct ga 2112

<210> 906
<211> 703
<212> PRT
<213> Artificial Sequence

<220>
<223> Pathway 2 sequence id J DdCASY80L protein

<400> 906
Met Thr Thr Thr Asn Trp Ser Leu Lys Val Asp Arg Gly Arg Gln Thr
 1               5                  10                  15
Trp Glu Tyr Ser Gln Glu Lys Lys Glu Ala Thr Asp Val Asp Ile His
            20                  25                  30
Leu Leu Arg Leu Lys Glu Pro Gly Thr His Cys Pro Glu Gly Cys Asp
        35                  40                  45
Leu Asn Arg Ala Lys Thr Pro Gln Gln Ala Ile Lys Lys Ala Phe Gln
    50                  55                  60
Tyr Phe Ser Lys Val Gln Thr Glu Asp Gly His Trp Ala Gly Asp Leu

```
65                  70                  75                  80
Gly Gly Pro Met Phe Leu Leu Pro Gly Leu Val Ile Thr Cys Tyr Val
                85                  90                  95
Thr Gly Tyr Gln Leu Pro Glu Ser Thr Gln Arg Glu Ile Ile Arg Tyr
            100                 105                 110
Leu Phe Asn Arg Gln Asn Pro Val Asp Gly Gly Trp Gly Leu His Ile
        115                 120                 125
Glu Ala His Ser Asp Ile Phe Gly Thr Thr Leu Gln Tyr Val Ser Leu
    130                 135                 140
Arg Leu Leu Gly Val Pro Ala Asp His Pro Ser Val Val Lys Ala Arg
145                 150                 155                 160
Thr Phe Leu Leu Gln Asn Gly Gly Ala Thr Gly Ile Pro Ser Trp Gly
                165                 170                 175
Lys Phe Trp Leu Ala Thr Leu Asn Ala Tyr Asp Trp Asn Gly Leu Asn
            180                 185                 190
Pro Ile Pro Ile Glu Phe Trp Leu Leu Pro Tyr Asn Leu Pro Ile Ala
        195                 200                 205
Pro Gly Arg Trp Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser
    210                 215                 220
Tyr Ile Tyr Ala Lys Lys Thr Thr Gly Pro Leu Thr Asp Leu Val Lys
225                 230                 235                 240
Asp Leu Arg Arg Glu Ile Tyr Cys Gln Glu Tyr Glu Lys Ile Asn Trp
                245                 250                 255
Ser Glu Gln Arg Asn Asn Ile Ser Lys Leu Asp Met Tyr Tyr Glu His
            260                 265                 270
Thr Ser Leu Leu Asn Val Ile Asn Gly Ser Leu Asn Ala Tyr Glu Lys
        275                 280                 285
Val His Ser Lys Trp Leu Arg Asp Lys Ala Ile Asp Tyr Thr Phe Asp
    290                 295                 300
His Ile Arg Tyr Glu Asp Glu Gln Thr Lys Tyr Ile Asp Ile Gly Pro
305                 310                 315                 320
Val Asn Lys Thr Val Asn Met Leu Cys Val Trp Asp Arg Glu Gly Lys
                325                 330                 335
Ser Pro Ala Phe Tyr Lys His Ala Asp Arg Leu Lys Asp Tyr Leu Trp
            340                 345                 350
Leu Ser Phe Asp Gly Met Lys Met Gln Gly Tyr Asn Gly Ser Gln Leu
        355                 360                 365
Trp Asp Thr Ala Phe Thr Ile Gln Ala Phe Met Glu Ser Gly Ile Ala
    370                 375                 380
Asn Gln Phe Gln Asp Cys Met Lys Leu Ala Gly His Tyr Leu Asp Ile
385                 390                 395                 400
Ser Gln Val Pro Glu Asp Ala Arg Asp Met Lys His Tyr His Arg His
                405                 410                 415
Tyr Ser Lys Gly Ala Trp Pro Phe Ser Thr Val Asp His Gly Trp Pro
            420                 425                 430
Ile Ser Asp Cys Thr Ala Glu Gly Ile Lys Ser Ala Leu Ala Leu Arg
        435                 440                 445
Ser Leu Pro Phe Ile Glu Pro Ile Ser Leu Asp Arg Ile Ala Asp Gly
    450                 455                 460
Ile Asn Val Leu Leu Thr Leu Gln Asn Gly Asp Gly Gly Trp Ala Ser
465                 470                 475                 480
Tyr Glu Asn Thr Arg Gly Pro Lys Trp Leu Glu Lys Phe Asn Pro Ser
                485                 490                 495
Glu Val Phe Gln Asn Ile Met Ile Asp Tyr Ser Tyr Val Glu Cys Ser
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            500                 505                 510
Ala Ala Cys Ile Gln Ala Met Ser Ala Phe Arg Lys His Ala Pro Asn
        515                 520                 525
His Pro Arg Ile Lys Glu Ile Asn Arg Ser Ile Ala Arg Gly Val Lys
    530                 535                 540
Phe Ile Lys Ser Ile Gln Arg Gln Asp Gly Ser Trp Leu Gly Ser Trp
545                 550                 555                 560
Gly Ile Cys Phe Thr Tyr Gly Thr Trp Phe Gly Ile Glu Gly Leu Val
                565                 570                 575
Ala Ser Gly Glu Pro Leu Thr Ser Pro Ser Ile Val Lys Ala Cys Lys
            580                 585                 590
Phe Leu Ala Ser Lys Gln Arg Ala Asp Gly Gly Trp Gly Glu Ser Phe
        595                 600                 605
Lys Ser Asn Val Thr Lys Glu Tyr Val Gln His Glu Thr Ser Gln Val
    610                 615                 620
Val Asn Thr Gly Trp Ala Leu Leu Ser Leu Met Ser Ala Lys Tyr Pro
625                 630                 635                 640
Asp Arg Glu Cys Ile Glu Arg Gly Ile Lys Phe Leu Ile Gln Arg Gln
                645                 650                 655
Tyr Pro Asn Gly Asp Phe Pro Gln Glu Ser Ile Ile Gly Val Phe Asn
            660                 665                 670
Phe Asn Cys Met Ile Ser Tyr Ser Asn Tyr Lys Asn Ile Phe Pro Leu
        675                 680                 685
Trp Ala Leu Ser Arg Tyr Asn Gln Leu Tyr Leu Lys Ser Lys Ile
    690                 695                 700
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<210> 907
<211> 2325
<212> DNA
<213> Artificial Sequence

<220>
<223> Pathway 2 sequence id K Cmelo DNA (codon optimized)

<400> 907
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gacgacgatg aagcaattgc tgtagctaac aattcagcct caaaatttga aaatgcaaga 180
aatcacttcc gtaataacag attccatagg aagcaatctt ccgacttatt cttggctata 240
caatgcgaga aagagatcat taggaatggt gctaagaatg aaggtactac caaagtgaaa 300
gaaggtgaag atgttaagaa agaagccgta aaaaatacac tagaaagagc attgtcgttc 360
tattctgctg tacagacctc tgacggtaat tgggcatcag acttgggagg acctatgttc 420
cttttaccag ggctagttat tgcgctatac gttacaggcg ttcttaacag tgtgttgtca 480
aaacatcaca ggcaagaaat gtgtcgttac atctataatc accaaaacga agatggaggg 540
tggggtttac atatagaagg ctcttctact atgtttgggt ctgcactgaa ttacgttgcg 600
ttaaggttac taggagaagc ggcagatggc ggtgagcatg gtgcgatgac caaagcaagg 660
tcctggatat tggaaagagg aggtgccaca gcaataactt cctggggcaa actttggctt 720
tccgtattag gagtgtatga atggtcggga aacaatccat tgccacccga attttggtta 780
cttccatata gccttccctt tcatccaggg agaatgtggt gtcattgtag aatggtttat 840
ctgccaatgt cgtatcttta tggtaagaga tttgttggtc caatcactcc aatagtttta 900
tcgttgagaa aagagttata taccattccg taccacgaga ttgattggaa tagatccaga 960
aacacgtgtg ctaaggagga cttatattac cctcacccta agatgcaaga tatcctatgg 1020
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ggcagtatct accatgtcta cgaaccgcta ttttcaggtt ggccaggtaa gagattgagg 1080
gaaaaggcca tgaaaattgc aatggaacat atccattacg aagatgagaa ttccaggtac 1140
atatgccttg gacccgtgaa caaagttcta aatatgctgt gttgctgggt tgaggatcct 1200
tactctgatg ctttcaagtt tcacttgcag agaattcctg actatctatg gttagctgaa 1260
gatggaatga gaatgcaggg ttataatggt tcacagcttt gggacactgc attcagcata 1320
caagcgataa tctcaacgaa attgattgat acgtttggtc cgacattacg taaagcacac 1380
catttcgtca agcatagtca gattcaagag gattgtccag gtgatccaaa cgtatggttc 1440
agacacattc ataaaggagc ttggcctttt agcactagag atcatggttg gcttatatcg 1500
gattgcacag ctgagggatt gaaagcttca ctgatgttat ctaagttgcc ttctaaaatt 1560
gtgggtgaac ccttggagaa gaaccgttta tgtgatgcag tcaatgtttt gttatcattg 1620
caaaacgaaa atggtgggtt cgcttcttat gaattaacta ggtcctatcc ctggttagag 1680
ttgattaacc ctgccgaaac atttggtgat atcgtaattg actacagtta tgtggaatgc 1740
actagtgcga cgatggaagc cttagccttg tttaagaagt tgcaccctgg gcatagaacc 1800
aaagaaattg atgccgctat tgctaaagcc gcaaattttc tggagaatat gcagaaaaca 1860
gacgggtctt ggtatggttg ttggggtgtc tgttttactt atgctggttg gtttggcatc 1920
aaaggcttag tagctgctgg tagaacatac aataattgtg ttgccattag aaaggcttgt 1980
aacttcctgt tgtcaaaaga attgcctggc ggtggttggg gcgaaagcta cctaagttgc 2040
caaaacaaag tttataccaa tctggaggga aacaagccac acttagtcaa tactgcatgg 2100
gtcatgatgg ccttgattga agcaggacaa ggggaaagag atccagctcc gttgcataga 2160
gctgccagat tgctaatcaa tagtcaattg gagtcaggtg actttccaca acaagaaatc 2220
atgggtgtgt ttaataagaa ctgtatgata acatatgccg catacagaaa catattccct 2280
atatgggctc taggtgaata ctcccatcgt gtcttggata tgtga 2325

<210> 908
<211> 1587
<212> DNA
<213> Artificial Sequence

<220>
<223> Step 1 sequence id L SQE1 DNA (codon optimized)

<400> 908
atggtcgatc aatgtgcgtt aggctggata ttagctagtg cactaggatt ggttatcgct 60
ctatgcttct tcgttgcacc aagaagaaac cacagaggtg ttgatagcaa agaaagggat 120
gagtgtgtgc agtctgcagc cacaactaag ggcgaatgca gatttaacga tagagatgtg 180
gatgttattg tggttggtgc aggagtagct ggttcggcat tagcccatac acttggtaaa 240
gacggtagaa gagttcatgt cattgagagg gatttgactg aaccagacag gattgttggt 300
gaacttctac aaccaggagg ctatttgaag ttgattgagt taggcttaca agactgtgtg 360
gaagaaatag atgcacaaag agtttacggg tatgctttgt ttaaagatgg taagaacacc 420
agactatctt atccacttga aaattttcac tcagatgtct ccggtagaag ctttcacaac 480
ggtagattca ttcagaggat gagagaaaag gctgcttcgc tgccaaatgt aagattggaa 540
caagggacgg ttactagtct actggaagag aaagggacga tcaaaggagt tcagtataag 600
tccaagaatg gagaggagaa aaccgcgtat gcgcctttaa cgatagtgtg tgatggctgt 660
ttctctaact tacgtagatc attatgtaat cccatggttg acgttccgag ctactttgtt 720
ggtcttgtgt tagaaaattg cgaactgcca tttgccaatc atggacatgt tatccttggt 780
gatccatccc caatcttatt ctatcagatc tcaagaaccg aaattaggtg tttggtcgat 840
gtacccggtc aaaaggtccc ttcaattgcc aatggcgaaa tggagaaata tttaaagact 900
gttgtagctc cacaagtacc acctcagatt tacgacagtt ttatagccgc cattgacaaa 960
gggaatatca gaactatgcc taataggtct atgcctgcag ctccccatcc aactccaggt 1020
gcgttactga tgggcgatgc attcaacatg agacatcctc taacaggagg tggcatgaca 1080
gtagcactgt ctgacattgt ggtcttgaga aacttgttaa aaccgttaaa agacttgtct 1140
gacgcctcta ctttgtgcaa atacttggaa tccttttata cccttcgtaa accagtagct 1200
agcacaatca acaccttagc tggagccttg tacaaagtct tttgcgcatc accggatcaa 1260
gcgagaaagg aaatgagaca agcttgtttt gattacctaa gtctgggagg tattttctcg 1320

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ttcttcgctg tcgcaattta tggtgttggt cgtttgcttc tacctttcc aagtgttaag 1440
ggtatatgga ttggtgcaag gttgatctac tctgcctctg gtataatatt tcccataatt 1500
agagctgaag gcgttcgtca aatgttcttt cctgctacag tgcccgctta ctatcgttcc 1560
ccacctgtat ttaaaccgat agtgtag 1587

<210> 909
<211> 528
<212> PRT
<213> Artificial Sequence

<220>
<223> Step 1 sequence id M  SQE1 Protein

<400> 909
Met Val Asp Gln Cys Ala Leu Gly Trp Ile Leu Ala Ser Ala Leu Gly
 1               5                  10                  15
Leu Val Ile Ala Leu Cys Phe Phe Val Ala Pro Arg Arg Asn His Arg
            20                  25                  30
Gly Val Asp Ser Lys Glu Arg Asp Glu Cys Val Gln Ser Ala Ala Thr
        35                  40                  45
Thr Lys Gly Glu Cys Arg Phe Asn Asp Arg Asp Val Asp Val Ile Val
    50                  55                  60
Val Gly Ala Gly Val Ala Gly Ser Ala Leu Ala His Thr Leu Gly Lys
65                  70                  75                  80
Asp Gly Arg Arg Val His Val Ile Glu Arg Asp Leu Thr Glu Pro Asp
                85                  90                  95
Arg Ile Val Gly Glu Leu Leu Gln Pro Gly Gly Tyr Leu Lys Leu Ile
            100                 105                 110
Glu Leu Gly Leu Gln Asp Cys Val Glu Glu Ile Asp Ala Gln Arg Val
        115                 120                 125
Tyr Gly Tyr Ala Leu Phe Lys Asp Gly Lys Asn Thr Arg Leu Ser Tyr
    130                 135                 140
Pro Leu Glu Asn Phe His Ser Asp Val Ser Gly Arg Ser Phe His Asn
145                 150                 155                 160
Gly Arg Phe Ile Gln Arg Met Arg Glu Lys Ala Ala Ser Leu Pro Asn
                165                 170                 175
Val Arg Leu Glu Gln Gly Thr Val Thr Ser Leu Leu Glu Glu Lys Gly
            180                 185                 190
Thr Ile Lys Gly Val Gln Tyr Lys Ser Lys Asn Gly Glu Glu Lys Thr
        195                 200                 205
Ala Tyr Ala Pro Leu Thr Ile Val Cys Asp Gly Cys Phe Ser Asn Leu
    210                 215                 220
Arg Arg Ser Leu Cys Asn Pro Met Val Asp Val Pro Ser Tyr Phe Val
225                 230                 235                 240
Gly Leu Val Leu Glu Asn Cys Glu Leu Pro Phe Ala Asn His Gly His
                245                 250                 255
Val Ile Leu Gly Asp Pro Ser Pro Ile Leu Phe Tyr Gln Ile Ser Arg
            260                 265                 270
Thr Glu Ile Arg Cys Leu Val Asp Val Pro Gly Gln Lys Val Pro Ser
        275                 280                 285
Ile Ala Asn Gly Glu Met Glu Lys Tyr Leu Lys Thr Val Val Ala Pro
    290                 295                 300
Gln Val Pro Pro Gln Ile Tyr Asp Ser Phe Ile Ala Ala Ile Asp Lys

305 310 315 320
Gly Asn Ile Arg Thr Met Pro Asn Arg Ser Met Pro Ala Ala Pro His
325 330 335
Pro Thr Pro Gly Ala Leu Leu Met Gly Asp Ala Phe Asn Met Arg His
340 345 350
Pro Leu Thr Gly Gly Gly Met Thr Val Ala Leu Ser Asp Ile Val Val
355 360 365
Leu Arg Asn Leu Leu Lys Pro Leu Lys Asp Leu Ser Asp Ala Ser Thr
370 375 380
Leu Cys Lys Tyr Leu Glu Ser Phe Tyr Thr Leu Arg Lys Pro Val Ala
385 390 395 400
Ser Thr Ile Asn Thr Leu Ala Gly Ala Leu Tyr Lys Val Phe Cys Ala
405 410 415
Ser Pro Asp Gln Ala Arg Lys Glu Met Arg Gln Ala Cys Phe Asp Tyr
420 425 430
Leu Ser Leu Gly Gly Ile Phe Ser Asn Gly Pro Val Ser Leu Leu Ser
435 440 445
Gly Leu Asn Pro Arg Pro Leu Ser Leu Val Leu His Phe Phe Ala Val
450 455 460
Ala Ile Tyr Gly Val Gly Arg Leu Leu Leu Pro Phe Pro Ser Val Lys
465 470 475 480
Gly Ile Trp Ile Gly Ala Arg Leu Ile Tyr Ser Ala Ser Gly Ile Ile
485 490 495
Phe Pro Ile Ile Arg Ala Glu Gly Val Arg Gln Met Phe Phe Pro Ala
500 505 510
Thr Val Pro Ala Tyr Tyr Arg Ser Pro Pro Val Phe Lys Pro Ile Val
515 520 525

<210> 910
<211> 1575
<212> DNA
<213> Artificial Sequence

<220>
<223> Step 1 sequence id N SQE2 DNA (codon optimized)

<400> 910
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tatttcttgt ttggtagaaa gaatggtggt gtgtctaatg aaagaaggca tgaaagtatt 120
aagaacattg caactaccaa tggtgagtat aagtcaagta actccgatgg tgacatcatc 180
attgttggtg ctggcgttgc tggatctgct ttggcctata cgctaggtaa agatgggaga 240
agagtgcatg tcattgaaag ggatttgaca gaaccagacc gtatagtagg tgaattgtta 300
caaccaggag ggtatctaaa actgacagag ttgggtttag aagattgtgt ggatgatata 360
gatgctcaac gtgtttatgg gtatgcatta ttcaaagacg gtaaagatac cagattgtcc 420
tatcccttgg aaaagtttca ctctgacgtc gcaggcagat cctttcataa tggcagattc 480
attcagcgta tgagagagaa agctgcttca ttgcctaaag tgagcctaga gcaagggact 540
gtaacgtcac tgttggagga aaacggaata atcaaagggg tacagtataa aactaagact 600
ggtcaagaga tgactgcata tgctccttta acaatcgtct gtgacggctg cttttcgaac 660
cttcgtagaa gcttgtgcaa cccaaaagtc gatgttccct catgttttgt gggattagtt 720
ctagaaaatt gcgatttgcc ttacgccaat cacggacatg tgatcttggc tgatccgtca 780
cctattctgt tctacagaat atctagtacc gaaatcaggt gtttggttga tgttccaggt 840
cagaaagtgc cttctatcag taatggcgaa atggccaact acttgaagaa tgttgttgca 900
cctcagattc caagccaact ttacgactct tttgttgcag ccattgacaa gggaaacata 960

agaacaatgc cgaatagatc tatgccagca gatccatatc caacacccgg tgcgctgcta 1020
atgggtgatg cctttaacat gagacatcct ctaacaggtg gtggtatgac agtcgcttta 1080
tcggatgttg tcgtattaag agacttactg aaaccactta gagacttgaa tgatgcacct 1140
accttgagca agtatttaga agccttttac actctgcgta agcctgttgc ttctaccata 1200
aacacgttag caggagcatt gtacaaggta ttctgtgctt ctcctgatca agcgagaaag 1260
gaaatgagac aagcctgttt tgactacctt tcacttggtg gcatattcag taatggacca 1320
gtatccttat tgtcaggtct taatccaagg cccatttccc ttgttttaca cttctttgca 1380
gtggctatct atggtgttgg aaggctatta ataccgtttc catcaccgaa aagggtatgg 1440
attggtgcta gaattatttc gggcgcgagt gcaattattt tccccattat caaagctgaa 1500
ggcgtcagac aaatgttctt tccagccact gtagctgcct actacagagc cccaagagtt 1560
gttaaaggta ggtag 1575

<210> 911
<211> 524
<212> PRT
<213> Artificial Sequence

<220>
<223> Step 1 sequence id O SQE2 Protein

<400> 911
Met Val Asp Gln Cys Ala Leu Gly Trp Ile Leu Ala Ser Val Leu Gly
 1               5                  10                  15
Ala Ala Ala Leu Tyr Phe Leu Phe Gly Arg Lys Asn Gly Gly Val Ser
            20                  25                  30
Asn Glu Arg Arg His Glu Ser Ile Lys Asn Ile Ala Thr Thr Asn Gly
        35                  40                  45
Glu Tyr Lys Ser Ser Asn Ser Asp Gly Asp Ile Ile Ile Val Gly Ala
    50                  55                  60
Gly Val Ala Gly Ser Ala Leu Ala Tyr Thr Leu Gly Lys Asp Gly Arg
65                  70                  75                  80
Arg Val His Val Ile Glu Arg Asp Leu Thr Glu Pro Asp Arg Ile Val
                85                  90                  95
Gly Glu Leu Leu Gln Pro Gly Gly Tyr Leu Lys Leu Thr Glu Leu Gly
            100                 105                 110
Leu Glu Asp Cys Val Asp Asp Ile Asp Ala Gln Arg Val Tyr Gly Tyr
        115                 120                 125
Ala Leu Phe Lys Asp Gly Lys Asp Thr Arg Leu Ser Tyr Pro Leu Glu
    130                 135                 140
Lys Phe His Ser Asp Val Ala Gly Arg Ser Phe His Asn Gly Arg Phe
145                 150                 155                 160
Ile Gln Arg Met Arg Glu Lys Ala Ala Ser Leu Pro Lys Val Ser Leu
                165                 170                 175
Glu Gln Gly Thr Val Thr Ser Leu Leu Glu Glu Asn Gly Ile Ile Lys
            180                 185                 190
Gly Val Gln Tyr Lys Thr Lys Thr Gly Gln Glu Met Thr Ala Tyr Ala
        195                 200                 205
Pro Leu Thr Ile Val Cys Asp Gly Cys Phe Ser Asn Leu Arg Arg Ser
    210                 215                 220
Leu Cys Asn Pro Lys Val Asp Val Pro Ser Cys Phe Val Gly Leu Val
225                 230                 235                 240
Leu Glu Asn Cys Asp Leu Pro Tyr Ala Asn His Gly His Val Ile Leu
                245                 250                 255
Ala Asp Pro Ser Pro Ile Leu Phe Tyr Arg Ile Ser Ser Thr Glu Ile

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            260                 265                 270
Arg Cys Leu Val Asp Val Pro Gly Gln Lys Val Pro Ser Ile Ser Asn
        275                 280                 285
Gly Glu Met Ala Asn Tyr Leu Lys Asn Val Val Ala Pro Gln Ile Pro
    290                 295                 300
Ser Gln Leu Tyr Asp Ser Phe Val Ala Ala Ile Asp Lys Gly Asn Ile
305                 310                 315                 320
Arg Thr Met Pro Asn Arg Ser Met Pro Ala Asp Pro Tyr Pro Thr Pro
                325                 330                 335
Gly Ala Leu Leu Met Gly Asp Ala Phe Asn Met Arg His Pro Leu Thr
            340                 345                 350
Gly Gly Gly Met Thr Val Ala Leu Ser Asp Val Val Val Leu Arg Asp
        355                 360                 365
Leu Leu Lys Pro Leu Arg Asp Leu Asn Asp Ala Pro Thr Leu Ser Lys
    370                 375                 380
Tyr Leu Glu Ala Phe Tyr Thr Leu Arg Lys Pro Val Ala Ser Thr Ile
385                 390                 395                 400
Asn Thr Leu Ala Gly Ala Leu Tyr Lys Val Phe Cys Ala Ser Pro Asp
                405                 410                 415
Gln Ala Arg Lys Glu Met Arg Gln Ala Cys Phe Asp Tyr Leu Ser Leu
            420                 425                 430
Gly Gly Ile Phe Ser Asn Gly Pro Val Ser Leu Leu Ser Gly Leu Asn
        435                 440                 445
Pro Arg Pro Ile Ser Leu Val Leu His Phe Phe Ala Val Ala Ile Tyr
    450                 455                 460
Gly Val Gly Arg Leu Leu Ile Pro Phe Pro Ser Pro Lys Arg Val Trp
465                 470                 475                 480
Ile Gly Ala Arg Ile Ile Ser Gly Ala Ser Ala Ile Ile Phe Pro Ile
                485                 490                 495
Ile Lys Ala Glu Gly Val Arg Gln Met Phe Phe Pro Ala Thr Val Ala
            500                 505                 510
Ala Tyr Tyr Arg Ala Pro Arg Val Val Lys Gly Arg
        515                 520
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<210> 912
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Step 1 sequence id P SQE3 DNA (codon optimized)

<400> 912
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ttcttcttta ctttgagaga tggtaccaag aacaagaaaa ccacaactgg gtcatctgtg 120
gatctgaaac gtactgacgc tgtcctacaa atgtctcccg aaaacgatgc tagaaggcag 180
gaaatcatag gggattcaga cgtgattgta gtaggtgcag gagttgcagg agctgcatta 240
gcctatacgt tgggcaaaga tggtagaaaa gttcacgtaa ttgaaagaga cttgacagag 300
ccagatagaa ttgtaggtga actattacaa cctggtggct acttgaagct agtggagttg 360
ggtcttgaag atagtgttaa aggtattgac gctcaacaag tctttggata tgcgttgtat 420
aaggacggta aacacacaag acttacgtat cctttggaaa agttcgactc aactgtatca 480
ggcagatcct tccataatgg cagattcatc caaagattaa gggaatctgt gagactagaa 540
caaggaactg ttaccagcat cttagaagag gatggaacag ttaaaggtgt tcagtataag 600
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acgaaaattg gagaggagtt tacagcttat gcaccattga caatcgtctg tgatggcggg 660
tttagtaact tgagaagaaa tttatgcaaa ccacaaatcg acattccctc gtgttttgtg 720
ggattagttt tggaaaactg caaacttccc ttcgagaatc atggccatgt agtactggca 780
gatccgtcac ctattctgtt atacccgatt agttcaacgg aaattcgttg tttggttgac 840
attccaggtc agaaagtgcc ctcagtagcc aatggcgaaa tggccagata cttaaagact 900
gttgtcgctc cgcaagttcc acctgaacta catgctgcct ttatagcggc tatagagaaa 960
ggtaatatca agagcacaac taacagatct atgccagcag cacctcaccc aacacctggc 1020
gccctgttgc taggtgatgc attcaatatg agacatccct taaccggtgg tggtatgact 1080
gttgccttag cggacattgt tgtgcttaga gatttgttgc gtcctcttgc taatctaaag 1140
gatgctgatg ccttgtgtca ctatctagag tccttttaca cccttcgtaa acctgtcgca 1200
tccaccataa acacattagc tggcgcatta tacaaggtct tttgtgcctc tccagattct 1260
gctagaaagg aaatgaggga agcatgtttt gattacctga gtttaggtgg tgtcttttcg 1320
tctggacctg tagctttgtt atccggtttg aatccaagac ctttgtcctt attttgccat 1380
ttctttgcag tggccatata tggagtttct aggttgctta taccattccc aagcccaatg 1440
aggatttgga ttggtgttag attaatcact gttgcggccg gtataatatt tccgattatc 1500
aaagctgaag gggtcagaca gatgttcttt cctgctactg tcccagctta ttacagggca 1560
ccaccaatgt ag 1572

<210> 913
<211> 523
<212> PRT
<213> Artificial Sequence

<220>
<223> Step 1 sequence id Q SQE3 Protein

<400> 913
Met Glu Phe Gln Ser Glu Pro Leu Phe Gly Val Leu Leu Ala Ser Leu
 1               5                  10                  15
Leu Ala Leu Val Phe Phe Phe Thr Leu Arg Asp Gly Thr Lys Asn Lys
            20                  25                  30
Lys Thr Thr Thr Gly Ser Ser Val Asp Leu Lys Arg Thr Asp Ala Val
        35                  40                  45
Leu Gln Met Ser Pro Glu Asn Asp Ala Arg Arg Gln Glu Ile Ile Gly
    50                  55                  60
Asp Ser Asp Val Ile Val Val Gly Ala Gly Val Ala Gly Ala Ala Leu
65                  70                  75                  80
Ala Tyr Thr Leu Gly Lys Asp Gly Arg Lys Val His Val Ile Glu Arg
                85                  90                  95
Asp Leu Thr Glu Pro Asp Arg Ile Val Gly Glu Leu Leu Gln Pro Gly
            100                 105                 110
Gly Tyr Leu Lys Leu Val Glu Leu Gly Leu Glu Asp Ser Val Lys Gly
        115                 120                 125
Ile Asp Ala Gln Gln Val Phe Gly Tyr Ala Leu Tyr Lys Asp Gly Lys
    130                 135                 140
His Thr Arg Leu Thr Tyr Pro Leu Glu Lys Phe Asp Ser Thr Val Ser
145                 150                 155                 160
Gly Arg Ser Phe His Asn Gly Arg Phe Ile Gln Arg Leu Arg Glu Ser
                165                 170                 175
Val Arg Leu Glu Gln Gly Thr Val Thr Ser Ile Leu Glu Glu Asp Gly
            180                 185                 190
Thr Val Lys Gly Val Gln Tyr Lys Thr Lys Ile Gly Glu Glu Phe Thr
        195                 200                 205
Ala Tyr Ala Pro Leu Thr Ile Val Cys Asp Gly Gly Phe Ser Asn Leu

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    210                 215                 220
Arg Arg Asn Leu Cys Lys Pro Gln Ile Asp Ile Pro Ser Cys Phe Val
225                 230                 235                 240
Gly Leu Val Leu Glu Asn Cys Lys Leu Pro Phe Glu Asn His Gly His
                245                 250                 255
Val Val Leu Ala Asp Pro Ser Pro Ile Leu Leu Tyr Pro Ile Ser Ser
            260                 265                 270
Thr Glu Ile Arg Cys Leu Val Asp Ile Pro Gly Gln Lys Val Pro Ser
        275                 280                 285
Val Ala Asn Gly Glu Met Ala Arg Tyr Leu Lys Thr Val Val Ala Pro
    290                 295                 300
Gln Val Pro Pro Glu Leu His Ala Ala Phe Ile Ala Ala Ile Glu Lys
305                 310                 315                 320
Gly Asn Ile Lys Ser Thr Thr Asn Arg Ser Met Pro Ala Ala Pro His
                325                 330                 335
Pro Thr Pro Gly Ala Leu Leu Leu Gly Asp Ala Phe Asn Met Arg His
            340                 345                 350
Pro Leu Thr Gly Gly Gly Met Thr Val Ala Leu Ala Asp Ile Val Val
        355                 360                 365
Leu Arg Asp Leu Leu Arg Pro Leu Ala Asn Leu Lys Asp Ala Asp Ala
    370                 375                 380
Leu Cys His Tyr Leu Glu Ser Phe Tyr Thr Leu Arg Lys Pro Val Ala
385                 390                 395                 400
Ser Thr Ile Asn Thr Leu Ala Gly Ala Leu Tyr Lys Val Phe Cys Ala
                405                 410                 415
Ser Pro Asp Ser Ala Arg Lys Glu Met Arg Glu Ala Cys Phe Asp Tyr
            420                 425                 430
Leu Ser Leu Gly Gly Val Phe Ser Ser Gly Pro Val Ala Leu Leu Ser
        435                 440                 445
Gly Leu Asn Pro Arg Pro Leu Ser Leu Phe Cys His Phe Phe Ala Val
    450                 455                 460
Ala Ile Tyr Gly Val Ser Arg Leu Leu Ile Pro Phe Pro Ser Pro Met
465                 470                 475                 480
Arg Ile Trp Ile Gly Val Arg Leu Ile Thr Val Ala Ala Gly Ile Ile
                485                 490                 495
Phe Pro Ile Ile Lys Ala Glu Gly Val Arg Gln Met Phe Phe Pro Ala
            500                 505                 510
Thr Val Pro Ala Tyr Tyr Arg Ala Pro Pro Met
        515                 520


<210> 914

<400> 914
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<210> 915
<211> 2400
<212> DNA
<213> Artificial Sequence

<220>
<223> SS3e-E7 Full gene NT Seq Full gene NT Seq
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<400> 915
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gaaaagtgga ttaaaagcat tagtaaccat ttgggcagac aagtctggga gttttgctct 180
ggtgaaaatg aaaacgacga cgatgaagca attgctgtag ctaacaattc agcctcaaaa 240
tttgaaaatg caagaaatca cttccgtaat aacagattcc ataggaagca atcttccgac 300
ttattcttgg ctatacaatg cgagaaagag atcattagga atggtgctaa gaatgaaggt 360
actaccaaag tgaaagaagg tgaagatgtt aagaaagaag ccgtaaaaaa tacactagaa 420
agagcattgt cgttctattc tgctgtacag acctctgacg gtaattgggc atcagacttg 480
ggaggaccta tgttcctttt accagggcta gttattgcgc tatacgttac aggcgttctt 540
aacagtgtgt tgtcaaaaca tcacaggcaa gaaatgtgtc gttacatcta taatcaccaa 600
aacgaagatg gagggtgggg tttacatata gaaggctctt ctactatgtt tgggtctgca 660
ctgaattacg ttgcgttaag gttactagga gaagcggcag atggcggtga gcatggtgcg 720
atgaccaaag caaggtcctg gatattggaa agaggaggtg ccacagcaat aacttcctgg 780
ggcaaacttt ggctttccgt attaggagtg tatgaatggt cgggaaacaa tccattgcca 840
cccgaatttt ggttacttcc atatagcctt ccctttcatc cagggagaat gtggtgtcat 900
tgtagaatgg tttatctgcc aatgtcgtat ctttatggta agagatttgt tggtccaatc 960
actccaatag ttttatcgtt gagaaaagag ttatatacca ttccgtacca cgagattgat 1020
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caagatatcc tatggggcag tatctaccat gtctacgaac cgctattttc aggttggcca 1140
ggtaagagat tgagggaaaa ggccatgaaa attgcaatgg aacatatcca ttacgaagat 1200
gagaattcca ggtacatatg ccttggaccc gtgaacaaag ttctaaatat gctgtgttgc 1260
tgggttgagg atccttactc tgatgctttc aagtttcact tgcagagaat tcctgactat 1320
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actgcattca gcatacaagc gataatctca acgaaattga ttgatacgtt tggtccgaca 1440
ttacgtaaag cacaccattt cgtcaagcat agtcagattc aagaggattg tccaggtgat 1500
ccaaacgtat ggttcagaca cattcataaa ggagcttggc cttttagcac tagagatcat 1560
ggttggctta tatcggattg cacagctgag ggattgaaag cttcactgat gttatctaag 1620
ttgccttcta aaattgtggg tgaacccttg gagaagaacc gtttatgtga tgcagtcaat 1680
gttttgttat cattgcaaaa cgaaaatggt gggttcgctt cttatgaatt aactaggtcc 1740
tatccctggt tagagttgat taaccctgcc gaaacatttg gtgatatcgt aattgactac 1800
agttatgtgg aatgcactag tgcgacgatg gaagccttag ccttgtttaa gaagttgcac 1860
cctgggcata gaaccaaaga aattgatgcc gctattgcta aagccgcaaa ttttctggag 1920
aatatgcaga aaacagacgg gtcttggtat ggttgttggg gtgtctgttt tacttatgct 1980
ggttggtttg gcatcaaagg cttagtagct gctggtagaa catacaataa ttgtgttgcc 2040
attagaaagg cttgtaactt cctgttgtca aaagaattgc ctggcggtgg ttggggcgaa 2100
agctacctaa gttgccaaaa caaagtttat accaatctgg agggaaacaa gccacactta 2160
gtcaatactg catgggtcat gatggccttg attgaagcag gacaaggggа aagagatcca 2220
gctccgttgc atagagctgc cagattgcta atcaatagtc aattggagtc aggtgacttt 2280
ccacaacaag aaatcatggg tgtgtttaat aagaactgta tgataacata tgccgcatac 2340
agaaacatat tccctatatg ggctctaggt gaatactccc atcgtgtctt ggatatgtga 2400

<210> 916
<211> 799
<212> PRT
<213> Artificial Sequence

<220>
<223> SS3e-E7 Full Gene AA seq

<400> 916
Met Ser Glu Asn His Val Pro Ala Val Val Lys Thr Arg Gly Ser Ala
 1               5                  10                  15

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Ala Pro Gly Ser Gly Ser Gly Ser Gly Met Trp Arg Leu Lys Val Gly
            20                  25                  30
Lys Glu Ser Val Gly Glu Lys Glu Glu Lys Trp Ile Lys Ser Ile Ser
        35                  40                  45
Asn His Leu Gly Arg Gln Val Trp Glu Phe Cys Ser Gly Glu Asn Glu
    50                  55                  60
Asn Asp Asp Asp Glu Ala Ile Ala Val Ala Asn Asn Ser Ala Ser Lys
65                  70                  75                  80
Phe Glu Asn Ala Arg Asn His Phe Arg Asn Asn Arg Phe His Arg Lys
                85                  90                  95
Gln Ser Ser Asp Leu Phe Leu Ala Ile Gln Cys Glu Lys Glu Ile Ile
            100                 105                 110
Arg Asn Gly Ala Lys Asn Glu Gly Thr Thr Lys Val Lys Glu Gly Glu
        115                 120                 125
Asp Val Lys Lys Glu Ala Val Lys Asn Thr Leu Glu Arg Ala Leu Ser
    130                 135                 140
Phe Tyr Ser Ala Val Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu
145                 150                 155                 160
Gly Gly Pro Met Phe Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val
                165                 170                 175
Thr Gly Val Leu Asn Ser Val Leu Ser Lys His His Arg Gln Glu Met
            180                 185                 190
Cys Arg Tyr Ile Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu
        195                 200                 205
His Ile Glu Gly Ser Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val
    210                 215                 220
Ala Leu Arg Leu Leu Gly Glu Ala Ala Asp Gly Gly Glu His Gly Ala
225                 230                 235                 240
Met Thr Lys Ala Arg Ser Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala
                245                 250                 255
Ile Thr Ser Trp Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu
            260                 265                 270
Trp Ser Gly Asn Asn Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr
        275                 280                 285
Ser Leu Pro Phe His Pro Gly Arg Met Trp Cys His Cys Arg Met Val
    290                 295                 300
Tyr Leu Pro Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile
305                 310                 315                 320
Thr Pro Ile Val Leu Ser Leu Arg Lys Glu Leu Tyr Thr Ile Pro Tyr
                325                 330                 335
His Glu Ile Asp Trp Asn Arg Ser Arg Asn Thr Cys Ala Lys Glu Asp
            340                 345                 350
Leu Tyr Tyr Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile
        355                 360                 365
Tyr His Val Tyr Glu Pro Leu Phe Ser Gly Trp Pro Gly Lys Arg Leu
    370                 375                 380
Arg Glu Lys Ala Met Lys Ile Ala Met Glu His Ile His Tyr Glu Asp
385                 390                 395                 400
Glu Asn Ser Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn
                405                 410                 415
Met Leu Cys Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Phe
            420                 425                 430
His Leu Gln Arg Ile Pro Asp Tyr Leu Trp Leu Ala Glu Asp Gly Met
        435                 440                 445
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Arg Met Gln Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser
    450                 455                 460
Ile Gln Ala Ile Ile Ser Thr Lys Leu Ile Asp Thr Phe Gly Pro Thr
465                 470                 475                 480
Leu Arg Lys Ala His His Phe Val Lys His Ser Gln Ile Gln Glu Asp
                485                 490                 495
Cys Pro Gly Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala
            500                 505                 510
Trp Pro Phe Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr
        515                 520                 525
Ala Glu Gly Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Lys
    530                 535                 540
Ile Val Gly Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn
545                 550                 555                 560
Val Leu Leu Ser Leu Gln Asn Glu Asn Gly Gly Phe Ala Ser Tyr Glu
                565                 570                 575
Leu Thr Arg Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr
            580                 585                 590
Phe Gly Asp Ile Val Ile Asp Tyr Ser Tyr Val Glu Cys Thr Ser Ala
        595                 600                 605
Thr Met Glu Ala Leu Ala Leu Phe Lys Lys Leu His Pro Gly His Arg
    610                 615                 620
Thr Lys Glu Ile Asp Ala Ala Ile Ala Lys Ala Ala Asn Phe Leu Glu
625                 630                 635                 640
Asn Met Gln Lys Thr Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys
                645                 650                 655
Phe Thr Tyr Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly
            660                 665                 670
Arg Thr Tyr Asn Asn Cys Val Ala Ile Arg Lys Ala Cys Asn Phe Leu
        675                 680                 685
Leu Ser Lys Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser
    690                 695                 700
Cys Gln Asn Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu
705                 710                 715                 720
Val Asn Thr Ala Trp Val Met Met Ala Leu Ile Glu Ala Gly Gln Gly
                725                 730                 735
Glu Arg Asp Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu Ile Asn
            740                 745                 750
Ser Gln Leu Glu Ser Gly Asp Phe Pro Gln Gln Glu Ile Met Gly Val
        755                 760                 765
Phe Asn Lys Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe
    770                 775                 780
Pro Ile Trp Ala Leu Gly Glu Tyr Ser His Arg Val Leu Asp Met
785                 790                 795
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<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> SS3e-E7 Fusion AA seq

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 1               5                  10


<210> 918

<400> 918
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<210> 919
<211> 2403
<212> DNA
<213> Artificial Sequence

<220>
<223> SS3d-G5 Full gene NT Seq

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gaagaaaagt ggattaaaag cattagtaac catttgggca gacaagtctg ggagttttgc 180
tctggtgaaa atgaaaacga cgacgatgaa gcaattgctg tagctaacaa ttcagcctca 240
aaatttgaaa atgcaagaaa tcacttccgt aataacagat tccataggaa gcaatcttcc 300
gacttattct tggctataca atgcgagaaa gagatcatta ggaatggtgc taagaatgaa 360
ggtactacca aagtgaaaga aggtgaagat gttaagaaag aagccgtaaa aaatacacta 420
gaaagagcat tgtcgttcta ttctgctgta cagacctctg acggtaattg ggcatcagac 480
ttgggaggac ctatgttcct tttaccaggg ctagttattg cgctatacgt tacaggcgtt 540
cttaacagtg tgttgtcaaa acatcacagg caagaaatgt gtcgttacat ctataatcac 600
caaaacgaag atggagggtg gggtttacat atagaaggct cttctactat gtttgggtct 660
gcactgaatt acgttgcgtt aaggttacta ggagaagcgg cagatggcgg tgagcatggt 720
gcgatgacca aagcaaggtc ctggatattg gaaagaggag gtgccacagc aataacttcc 780
tggggcaaac tttggctttc cgtattagga gtgtatgaat ggtcgggaaa caatccattg 840
ccacccgaat tttggttact tccatatagc cttccctttc atccagggag aatgtggtgt 900
cattgtagaa tggtttatct gccaatgtcg tatctttatg gtaagagatt tgttggtcca 960
atcactccaa tagttttatc gttgagaaaa gagttatata ccattccgta ccacgagatt 1020
gattggaata gatccagaaa cacgtgtgct aaggaggact tatattaccc tcaccctaag 1080
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gacactgcat tcagcataca agcgataatc tcaacgaaat tgattgatac gtttggtccg 1440
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ccagctccgt tgcatagagc tgccagattg ctaatcaata gtcaattgga gtcaggtgac 2280
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tga 2403

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<211> 800
<212> PRT
<213> Artificial Sequence

<220>
<223> SS3d-G5 Full Gene AA seq

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

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    290                 295                 300
Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro
305                 310                 315                 320
Ile Thr Pro Ile Val Leu Ser Leu Arg Lys Glu Leu Tyr Thr Ile Pro
                325                 330                 335
Tyr His Glu Ile Asp Trp Asn Arg Ser Arg Asn Thr Cys Ala Lys Glu
            340                 345                 350
Asp Leu Tyr Tyr Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser
        355                 360                 365
Ile Tyr His Val Tyr Glu Pro Leu Phe Ser Gly Trp Pro Gly Lys Arg
    370                 375                 380
Leu Arg Glu Lys Ala Met Lys Ile Ala Met Glu His Ile His Tyr Glu
385                 390                 395                 400
Asp Glu Asn Ser Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu
                405                 410                 415
Asn Met Leu Cys Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys
            420                 425                 430
Phe His Leu Gln Arg Ile Pro Asp Tyr Leu Trp Leu Ala Glu Asp Gly
        435                 440                 445
Met Arg Met Gln Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe
    450                 455                 460
Ser Ile Gln Ala Ile Ile Ser Thr Lys Leu Ile Asp Thr Phe Gly Pro
465                 470                 475                 480
Thr Leu Arg Lys Ala His His Phe Val Lys His Ser Gln Ile Gln Glu
                485                 490                 495
Asp Cys Pro Gly Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly
            500                 505                 510
Ala Trp Pro Phe Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys
        515                 520                 525
Thr Ala Glu Gly Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser
    530                 535                 540
Lys Ile Val Gly Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val
545                 550                 555                 560
Asn Val Leu Leu Ser Leu Gln Asn Glu Asn Gly Gly Phe Ala Ser Tyr
                565                 570                 575
Glu Leu Thr Arg Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu
            580                 585                 590
Thr Phe Gly Asp Ile Val Ile Asp Tyr Ser Tyr Val Glu Cys Thr Ser
        595                 600                 605
Ala Thr Met Glu Ala Leu Ala Leu Phe Lys Lys Leu His Pro Gly His
    610                 615                 620
Arg Thr Lys Glu Ile Asp Ala Ala Ile Ala Lys Ala Ala Asn Phe Leu
625                 630                 635                 640
Glu Asn Met Gln Lys Thr Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val
                645                 650                 655
Cys Phe Thr Tyr Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala
            660                 665                 670
Gly Arg Thr Tyr Asn Asn Cys Val Ala Ile Arg Lys Ala Cys Asn Phe
        675                 680                 685
Leu Leu Ser Lys Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu
    690                 695                 700
Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His
705                 710                 715                 720
Leu Val Asn Thr Ala Trp Val Met Met Ala Leu Ile Glu Ala Gly Gln
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                725                 730                 735
Gly Glu Arg Asp Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu Ile
            740                 745                 750
Asn Ser Gln Leu Glu Ser Gly Asp Phe Pro Gln Gln Glu Ile Met Gly
        755                 760                 765
Val Phe Asn Lys Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile
    770                 775                 780
Phe Pro Ile Trp Ala Leu Gly Glu Tyr Ser His Arg Val Leu Asp Met
785                 790                 795                 800
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<212> PRT
<213> Artificial Sequence

<220>
<223> SS3d-G5 Fusion AA seq

<400> 921
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<210> 922

<400> 922
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<210> 923
<211> 2391
<212> DNA
<213> Artificial Sequence

<220>
<223> SS3c-G8 Full gene NT Seq

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attaaaagca ttagtaacca tttgggcaga caagtctggg agttttgctc tggtgaaaat 180
gaaaacgacg acgatgaagc aattgctgta gctaacaatt cagcctcaaa atttgaaaat 240
gcaagaaatc acttccgtaa taacagattc cataggaagc aatcttccga cttattcttg 300
gctatacaat gcgagaaaga gatcattagg aatggtgcta agaatgaagg tactaccaaa 360
gtgaaagaag gtgaagatgt taagaaagaa gccgtaaaaa atacactaga aagagcattg 420
tcgttctatt ctgctgtaca gacctctgac ggtaattggg catcagactt gggaggacct 480
atgttccttt taccagggct agttattgcg ctatacgtta caggcgttct taacagtgtg 540
ttgtcaaaac atcacaggca agaaatgtgt cgttacatct ataatcacca aaacgaagat 600
ggagggtggg gtttacatat agaaggctct tctactatgt ttgggtctgc actgaattac 660
gttgcgttaa ggttactagg agaagcggca gatggcggtg agcatggtgc gatgaccaaa 720
gcaaggtcct ggatattgga aagaggaggt gccacagcaa taacttcctg gggcaaactt 780
tggctttccg tattaggagt gtatgaatgg tcgggaaaca atccattgcc acccgaattt 840
tggttacttc catatagcct tccctttcat ccagggagaa tgtggtgtca ttgtagaatg 900
gtttatctgc caatgtcgta tctttatggt aagagatttg ttggtccaat cactccaata 960
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gttttatcgt tgagaaaaga gttatatacc attccgtacc acgagattga ttggaataga 1020
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aggtacatat gccttggacc cgtgaacaaa gttctaaata tgctgtgttg ctgggttgag 1260
gatccttact ctgatgcttt caagtttcac ttgcagagaa ttcctgacta tctatggtta 1320
gctgaagatg gaatgagaat gcagggttat aatggttcac agctttggga cactgcattc 1380
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gcacaccatt tcgtcaagca tagtcagatt caagaggatt gtccaggtga tccaaacgta 1500
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gcatgggtca tgatggcctt gattgaagca ggacaagggg aaagagatcc agctccgttg 2220
catagagctg ccagattgct aatcaatagt caattggagt caggtgactt tccacaacaa 2280
gaaatcatgg gtgtgtttaa taagaactgt atgataacat atgccgcata cagaaacata 2340
ttccctatat gggctctagg tgaatactcc catcgtgtct tggatatgtg a 2391

<210> 924
<211> 796
<212> PRT
<213> Artificial Sequence

<220>
<223> SS3c-G8 Full Gene AA seq

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

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Met Phe Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val Thr Gly Val
                165                 170                 175
Leu Asn Ser Val Leu Ser Lys His His Arg Gln Glu Met Cys Arg Tyr
            180                 185                 190
Ile Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile Glu
        195                 200                 205
Gly Ser Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg
    210                 215                 220
Leu Leu Gly Glu Ala Ala Asp Gly Gly Glu His Gly Ala Met Thr Lys
225                 230                 235                 240
Ala Arg Ser Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser
                245                 250                 255
Trp Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp Ser Gly
            260                 265                 270
Asn Asn Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro
        275                 280                 285
Phe His Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr Leu Pro
    290                 295                 300
Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr Pro Ile
305                 310                 315                 320
Val Leu Ser Leu Arg Lys Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile
                325                 330                 335
Asp Trp Asn Arg Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr
            340                 345                 350
Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His Val
        355                 360                 365
Tyr Glu Pro Leu Phe Ser Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys
    370                 375                 380
Ala Met Lys Ile Ala Met Glu His Ile His Tyr Glu Asp Glu Asn Ser
385                 390                 395                 400
Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu Cys
                405                 410                 415
Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Phe His Leu Gln
            420                 425                 430
Arg Ile Pro Asp Tyr Leu Trp Leu Ala Glu Asp Gly Met Arg Met Gln
        435                 440                 445
Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala
    450                 455                 460
Ile Ile Ser Thr Lys Leu Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys
465                 470                 475                 480
Ala His His Phe Val Lys His Ser Gln Ile Gln Glu Asp Cys Pro Gly
                485                 490                 495
Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp Pro Phe
            500                 505                 510
Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly
        515                 520                 525
Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Lys Ile Val Gly
    530                 535                 540
Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val Leu Leu
545                 550                 555                 560
Ser Leu Gln Asn Glu Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg
                565                 570                 575
Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp
            580                 585                 590
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Ile Val Ile Asp Tyr Ser Tyr Val Glu Cys Thr Ser Ala Thr Met Glu
595 600 605
Ala Leu Ala Leu Phe Lys Lys Leu His Pro Gly His Arg Thr Lys Glu
610 615 620
Ile Asp Ala Ala Ile Ala Lys Ala Ala Asn Phe Leu Glu Asn Met Gln
625 630 635 640
Lys Thr Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr
645 650 655
Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr
660 665 670
Asn Asn Cys Val Ala Ile Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys
675 680 685
Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn
690 695 700
Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val Asn Thr
705 710 715 720
Ala Trp Val Met Met Ala Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp
725 730 735
Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu
740 745 750
Glu Ser Gly Asp Phe Pro Gln Gln Glu Ile Met Gly Val Phe Asn Lys
755 760 765
Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp
770 775 780
Ala Leu Gly Glu Tyr Ser His Arg Val Leu Asp Met
785 790 795

<210> 925
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> SS3c-G8 Fusion AA seq

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<210> 926

<400> 926
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<210> 927
<211> 2394
<212> DNA
<213> Artificial Sequence

<220>
<223> SS3c-E5 Full gene NT Seq

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tggattaaaa gcattagtaa ccatttgggc agacaagtct gggagttttg ctctggtgaa 180
aatgaaaacg acgacgatga agcaattgct gtagctaaca attcagcctc aaaatttgaa 240
aatgcaagaa atcacttccg taataacaga ttccatagga agcaatcttc cgacttattc 300
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atagttttat cgttgagaaa agagttatat accattccgt accacgagat tgattggaat 1020
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caagaaatca tgggtgtgtt taataagaac tgtatgataa catatgccgc atacagaaac 2340
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<211> 797
<212> PRT
<213> Artificial Sequence

<220>
<223> SS3c-E5Full Gene AA seq

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Ser Val Gly Glu Lys Glu Glu Lys Trp Ile Lys Ser Ile Ser Asn His
        35                  40                  45
Leu Gly Arg Gln Val Trp Glu Phe Cys Ser Gly Glu Asn Glu Asn Asp
    50                  55                  60
Asp Asp Glu Ala Ile Ala Val Ala Asn Asn Ser Ala Ser Lys Phe Glu
65                  70                  75                  80
Asn Ala Arg Asn His Phe Arg Asn Asn Arg Phe His Arg Lys Gln Ser
                85                  90                  95
Ser Asp Leu Phe Leu Ala Ile Gln Cys Glu Lys Glu Ile Ile Arg Asn
            100                 105                 110
Gly Ala Lys Asn Glu Gly Thr Thr Lys Val Lys Glu Gly Glu Asp Val
        115                 120                 125
Lys Lys Glu Ala Val Lys Asn Thr Leu Glu Arg Ala Leu Ser Phe Tyr
    130                 135                 140
Ser Ala Val Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu Gly Gly
145                 150                 155                 160
Pro Met Phe Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val Thr Gly
                165                 170                 175
Val Leu Asn Ser Val Leu Ser Lys His His Arg Gln Glu Met Cys Arg
            180                 185                 190
Tyr Ile Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile
        195                 200                 205
Glu Gly Ser Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu
    210                 215                 220
Arg Leu Leu Gly Glu Ala Ala Asp Gly Gly Glu His Gly Ala Met Thr
225                 230                 235                 240
Lys Ala Arg Ser Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile Thr
                245                 250                 255
Ser Trp Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp Ser
            260                 265                 270
Gly Asn Asn Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr Ser Leu
        275                 280                 285
Pro Phe His Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr Leu
    290                 295                 300
Pro Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr Pro
305                 310                 315                 320
Ile Val Leu Ser Leu Arg Lys Glu Leu Tyr Thr Ile Pro Tyr His Glu
                325                 330                 335
Ile Asp Trp Asn Arg Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr
            340                 345                 350
Tyr Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His
        355                 360                 365
Val Tyr Glu Pro Leu Phe Ser Gly Trp Pro Gly Lys Arg Leu Arg Glu
    370                 375                 380
Lys Ala Met Lys Ile Ala Met Glu His Ile His Tyr Glu Asp Glu Asn
385                 390                 395                 400
Ser Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu
                405                 410                 415
Cys Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Phe His Leu
            420                 425                 430
Gln Arg Ile Pro Asp Tyr Leu Trp Leu Ala Glu Asp Gly Met Arg Met
        435                 440                 445
Gln Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln
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    450                 455                 460
Ala Ile Ile Ser Thr Lys Leu Ile Asp Thr Phe Gly Pro Thr Leu Arg
465                 470                 475                 480
Lys Ala His His Phe Val Lys His Ser Gln Ile Gln Glu Asp Cys Pro
                485                 490                 495
Gly Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp Pro
            500                 505                 510
Phe Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu
        515                 520                 525
Gly Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Lys Ile Val
    530                 535                 540
Gly Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val Leu
545                 550                 555                 560
Leu Ser Leu Gln Asn Glu Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr
                565                 570                 575
Arg Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly
            580                 585                 590
Asp Ile Val Ile Asp Tyr Ser Tyr Val Glu Cys Thr Ser Ala Thr Met
        595                 600                 605
Glu Ala Leu Ala Leu Phe Lys Lys Leu His Pro Gly His Arg Thr Lys
    610                 615                 620
Glu Ile Asp Ala Ala Ile Ala Lys Ala Ala Asn Phe Leu Glu Asn Met
625                 630                 635                 640
Gln Lys Thr Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr
                645                 650                 655
Tyr Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr
            660                 665                 670
Tyr Asn Asn Cys Val Ala Ile Arg Lys Ala Cys Asn Phe Leu Leu Ser
        675                 680                 685
Lys Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln
    690                 695                 700
Asn Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val Asn
705                 710                 715                 720
Thr Ala Trp Val Met Met Ala Leu Ile Glu Ala Gly Gln Gly Glu Arg
                725                 730                 735
Asp Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu Ile Asn Ser Gln
            740                 745                 750
Leu Glu Ser Gly Asp Phe Pro Gln Gln Glu Ile Met Gly Val Phe Asn
        755                 760                 765
Lys Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile
    770                 775                 780
Trp Ala Leu Gly Glu Tyr Ser His Arg Val Leu Asp Met
785                 790                 795
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<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> SS3c-E5 Fusion AA seq

<400> 929

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 1               5                  10


<210> 930

<400> 930
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<210> 931
<211> 2382
<212> DNA
<213> Artificial Sequence

<220>
<223> SS2c-E2Full gene NT Seq

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gacgacgatg aagcaattgc tgtagctaac aattcagcct caaaatttga aaatgcaaga 180
aatcacttcc gtaataacag attccatagg aagcaatctt ccgacttatt cttggctata 240
caatgcgaga aagagatcat taggaatggt gctaagaatg aaggtactac caaagtgaaa 300
gaaggtgaag atgttaagaa agaagccgta aaaaatacac tagaaagagc attgtcgttc 360
tattctgctg tacagacctc tgacggtaat tgggcatcag acttgggagg acctatgttc 420
cttttaccag ggctagttat tgcgctatac gttacaggcg ttcttaacag tgtgttgtca 480
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ttaaggttac taggagaagc ggcagatggc ggtgagcatg gtgcgatgac caaagcaagg 660
tcctggatat tggaaagagg aggtgccaca gcaataactt cctggggcaa actttggctt 720
tccgtattag gagtgtatga atggtcggga aacaatccat tgccacccga attttggtta 780
cttccatata gccttccctt tcatccaggg agaatgtggt gtcattgtag aatggtttat 840
ctgccaatgt cgtatcttta tggtaagaga tttgttggtc caatcactcc aatagtttta 900
tcgttgagaa aagagttata taccattccg taccacgaga ttgattggaa tagatccaga 960
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gatggaatga gaatgcaggg ttataatggt tcacagcttt gggacactgc attcagcata 1320
caagcgataa tctcaacgaa attgattgat acgtttggtc cgacattacg taaagcacac 1380
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gctgccagat tgctaatcaa tagtcaattg gagtcaggtg actttccaca acaagaaatc 2220
atgggtgtgt ttaataagaa ctgtatgata acatatgccg catacagaaa catattccct 2280
atatgggctc taggtgaata ctcccatcgt gtcttggata tgggaagtgc agctcctgga 2340
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<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> SS2c-E2 Full Gene AA seq

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

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305                 310                 315                 320
Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met Gln
                325                 330                 335
Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu Pro Leu Phe Ser
            340                 345                 350
Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met Lys Ile Ala Met
        355                 360                 365
Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile Cys Leu Gly
    370                 375                 380
Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro
385                 390                 395                 400
Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile Pro Asp Tyr Leu
                405                 410                 415
Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn Gly Ser Gln
            420                 425                 430
Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile Ser Thr Lys Leu
        435                 440                 445
Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His His Phe Val Lys
    450                 455                 460
His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro Asn Val Trp Phe
465                 470                 475                 480
Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His Gly
                485                 490                 495
Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ser Leu Met
            500                 505                 510
Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro Leu Glu Lys Asn
        515                 520                 525
Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Glu Asn
    530                 535                 540
Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu Glu
545                 550                 555                 560
Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr Ser
                565                 570                 575
Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Ala Leu Phe Lys
            580                 585                 590
Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Ala Ala Ile Ala
        595                 600                 605
Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys Thr Asp Gly Ser Trp
    610                 615                 620
Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly Ile
625                 630                 635                 640
Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Val Ala Ile
                645                 650                 655
Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly Gly
            660                 665                 670
Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu
        675                 680                 685
Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp Val Met Met Ala
    690                 695                 700
Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala Pro Leu His Arg
705                 710                 715                 720
Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser Gly Asp Phe Pro
                725                 730                 735
Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr
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            740                 745                 750
Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Ser
        755                 760                 765
His Arg Val Leu Asp Met Gly Ser Ala Ala Pro Gly Ser Gly Ser Gly
    770                 775                 780
Ser Gly Met Met Leu Glu Pro Ser Pro
785                 790
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<212> PRT
<213> Artificial Sequence

<220>
<223> SS2c-E2 Fusion AA seq

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Met Met Leu Glu Pro Ser Pro
 1               5

<210> 934

<400> 934
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<210> 935
<211> 2394
<212> DNA
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<220>
<223> SS2c-A10b Full gene NT Seq

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gacgacgatg aagcaattgc tgtagctaac aattcagcct caaaatttga aaatgcaaga 180
aatcacttcc gtaataacag attccatagg aagcaatctt ccgacttatt cttggctata 240
caatgcgaga aagagatcat taggaatggt gctaagaatg aaggtactac caaagtgaaa 300
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gattgcacag ctgagggatt gaaagcttca ctgatgttat ctaagttgcc ttctaaaatt 1560
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atatgggctc taggtgaata ctcccatcgt gtcttggata tgggaagtgc agctcctgga 2340
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<211> 797
<212> PRT
<213> Artificial Sequence

<220>
<223> SS2c-A10b Full Gene AA seq

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

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Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly Ser Ser Thr Met Phe
            180                 185                 190
Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu Leu Gly Glu Ala Ala
        195                 200                 205
Asp Gly Gly Glu His Gly Ala Met Thr Lys Ala Arg Ser Trp Ile Leu
    210                 215                 220
Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser Trp Gly Lys Leu Trp Leu
225                 230                 235                 240
Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn Pro Leu Pro Pro
                245                 250                 255
Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro Phe His Pro Gly Arg Met
            260                 265                 270
Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly
        275                 280                 285
Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu Ser Leu Arg Lys
    290                 295                 300
Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile Asp Trp Asn Arg Ser Arg
305                 310                 315                 320
Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met Gln
                325                 330                 335
Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu Pro Leu Phe Ser
            340                 345                 350
Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met Lys Ile Ala Met
        355                 360                 365
Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile Cys Leu Gly
    370                 375                 380
Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro
385                 390                 395                 400
Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile Pro Asp Tyr Leu
                405                 410                 415
Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn Gly Ser Gln
            420                 425                 430
Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile Ser Thr Lys Leu
        435                 440                 445
Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His His Phe Val Lys
    450                 455                 460
His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro Asn Val Trp Phe
465                 470                 475                 480
Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His Gly
                485                 490                 495
Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ser Leu Met
            500                 505                 510
Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro Leu Glu Lys Asn
        515                 520                 525
Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Glu Asn
    530                 535                 540
Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu Glu
545                 550                 555                 560
Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr Ser
                565                 570                 575
Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Ala Leu Phe Lys
            580                 585                 590
Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Ala Ala Ile Ala
        595                 600                 605
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Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys Thr Asp Gly Ser Trp
    610                 615                 620
Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly Ile
625                 630                 635                 640
Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Val Ala Ile
                645                 650                 655
Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly Gly
            660                 665                 670
Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu
        675                 680                 685
Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp Val Met Met Ala
    690                 695                 700
Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala Pro Leu His Arg
705                 710                 715                 720
Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser Gly Asp Phe Pro
                725                 730                 735
Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr
            740                 745                 750
Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Ser
        755                 760                 765
His Arg Val Leu Asp Met Gly Ser Ala Ala Pro Gly Ser Gly Ser Gly
    770                 775                 780
Ser Gly Met Asn Ser Asn Glu Asp Ile Ile Pro Glu Leu
785                 790                 795
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<212> PRT
<213> Artificial Sequence

<220>
<223> SS2c-A10b Fusion AA seq

<400> 937
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<210> 938

<400> 938
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<210> 939
<211> 2388
<212> DNA
<213> Artificial Sequence

<220>
<223> SS3b-C1 Full gene NT Seq

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aaaagcatta gtaaccattt gggcagacaa gtctgggagt tttgctctgg tgaaaatgaa 180
aacgacgacg atgaagcaat tgctgtagct aacaattcag cctcaaaatt tgaaaatgca 240
agaaatcact tccgtaataa cagattccat aggaagcaat cttccgactt attcttggct 300
atacaatgcg agaaagagat cattaggaat ggtgctaaga atgaaggtac taccaaagtg 360
aaagaaggtg aagatgttaa gaaagaagcc gtaaaaaata cactagaaag agcattgtcg 420
ttctattctg ctgtacagac ctctgacggt aattgggcat cagacttggg aggacctatg 480
ttccttttac cagggctagt tattgcgcta tacgttacag gcgttcttaa cagtgtgttg 540
tcaaaacatc acaggcaaga aatgtgtcgt tacatctata atcaccaaaa cgaagatgga 600
gggtggggtt tacatataga aggctcttct actatgtttg ggtctgcact gaattacgtt 660
gcgttaaggt tactaggaga agcggcagat ggcggtgagc atggtgcgat gaccaaagca 720
aggtcctgga tattggaaag aggaggtgcc acagcaataa cttcctgggg caaactttgg 780
ctttccgtat taggagtgta tgaatggtcg ggaaacaatc cattgccacc cgaattttgg 840
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tatctgccaa tgtcgtatct ttatggtaag agatttgttg gtccaatcac tccaatagtt 960
ttatcgttga gaaaagagtt atataccatt ccgtaccacg agattgattg gaatagatcc 1020
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tacatatgcc ttggacccgt gaacaaagtt ctaaatatgc tgtgttgctg ggttgaggat 1260
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agagctgcca gattgctaat caatagtcaa ttggagtcag gtgactttcc acaacaagaa 2280
atcatgggtg tgtttaataa gaactgtatg ataacatatg ccgcatacag aaacatattc 2340
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<211> 795
<212> PRT
<213> Artificial Sequence

<220>
<223> SS3b-C1 Full Gene AA seq

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            20                  25                  30
Gly Glu Lys Glu Glu Lys Trp Ile Lys Ser Ile Ser Asn His Leu Gly

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        35                  40                  45
Arg Gln Val Trp Glu Phe Cys Ser Gly Glu Asn Glu Asn Asp Asp Asp
    50                  55                  60
Glu Ala Ile Ala Val Ala Asn Asn Ser Ala Ser Lys Phe Glu Asn Ala
65                  70                  75                  80
Arg Asn His Phe Arg Asn Asn Arg Phe His Arg Lys Gln Ser Ser Asp
                85                  90                  95
Leu Phe Leu Ala Ile Gln Cys Glu Lys Glu Ile Ile Arg Asn Gly Ala
            100                 105                 110
Lys Asn Glu Gly Thr Thr Lys Val Lys Glu Gly Glu Asp Val Lys Lys
        115                 120                 125
Glu Ala Val Lys Asn Thr Leu Glu Arg Ala Leu Ser Phe Tyr Ser Ala
    130                 135                 140
Val Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro Met
145                 150                 155                 160
Phe Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val Thr Gly Val Leu
                165                 170                 175
Asn Ser Val Leu Ser Lys His His Arg Gln Glu Met Cys Arg Tyr Ile
            180                 185                 190
Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly
        195                 200                 205
Ser Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu
    210                 215                 220
Leu Gly Glu Ala Ala Asp Gly Gly Glu His Gly Ala Met Thr Lys Ala
225                 230                 235                 240
Arg Ser Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser Trp
                245                 250                 255
Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn
            260                 265                 270
Asn Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro Phe
        275                 280                 285
His Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr Leu Pro Met
    290                 295                 300
Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val
305                 310                 315                 320
Leu Ser Leu Arg Lys Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile Asp
                325                 330                 335
Trp Asn Arg Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro
            340                 345                 350
His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr
        355                 360                 365
Glu Pro Leu Phe Ser Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala
    370                 375                 380
Met Lys Ile Ala Met Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg
385                 390                 395                 400
Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys
                405                 410                 415
Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg
            420                 425                 430
Ile Pro Asp Tyr Leu Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly
        435                 440                 445
Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile
    450                 455                 460
Ile Ser Thr Lys Leu Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala
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465                 470                 475                 480
His His Phe Val Lys His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp
                485                 490                 495
Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp Pro Phe Ser
            500                 505                 510
Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu
        515                 520                 525
Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu
    530                 535                 540
Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser
545                 550                 555                 560
Leu Gln Asn Glu Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser
                565                 570                 575
Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile
            580                 585                 590
Val Ile Asp Tyr Ser Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala
        595                 600                 605
Leu Ala Leu Phe Lys Lys Leu His Pro Gly His Arg Thr Lys Glu Ile
    610                 615                 620
Asp Ala Ala Ile Ala Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys
625                 630                 635                 640
Thr Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala
                645                 650                 655
Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn
            660                 665                 670
Asn Cys Val Ala Ile Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu
        675                 680                 685
Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys
    690                 695                 700
Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala
705                 710                 715                 720
Trp Val Met Met Ala Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro
                725                 730                 735
Ala Pro Leu His Arg Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu
            740                 745                 750
Ser Gly Asp Phe Pro Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn
        755                 760                 765
Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala
    770                 775                 780
Leu Gly Glu Tyr Ser His Arg Val Leu Asp Met
785                 790                 795
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<210> 941
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> SS3b-C1 Fusion AA seq

<400> 941
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Met Trp Asn Lys Thr Lys Lys Thr Gln
 1               5
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<210> 942

<400> 942
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<210> 943
<211> 2394
<212> DNA
<213> Artificial Sequence

<220>
<223> SS3b-B10 Full gene NT Seq

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tggattaaaa gcattagtaa ccatttgggc agacaagtct gggagttttg ctctggtgaa 180
aatgaaaacg acgacgatga agcaattgct gtagctaaca attcagcctc aaaatttgaa 240
aatgcaagaa atcacttccg taataacaga ttccatagga agcaatcttc cgacttattc 300
ttggctatac aatgcgagaa agagatcatt aggaatggtg ctaagaatga aggtactacc 360
aaagtgaaag aaggtgaaga tgttaagaaa gaagccgtaa aaaatacact agaaagagca 420
ttgtcgttct attctgctgt acagacctct gacggtaatt gggcatcaga cttgggagga 480
cctatgttcc ttttaccagg gctagttatt gcgctatacg ttacaggcgt tcttaacagt 540
gtgttgtcaa aacatcacag gcaagaaatg tgtcgttaca tctataatca ccaaaacgaa 600
gatggagggt ggggtttaca tatagaaggc tcttctacta tgtttgggtc tgcactgaat 660
tacgttgcgt taaggttact aggagaagcg gcagatggcg gtgagcatgg tgcgatgacc 720
aaagcaaggt cctggatatt ggaaagagga ggtgccacag caataacttc ctggggcaaa 780
ctttggcttt ccgtattagg agtgtatgaa tggtcgggaa acaatccatt gccacccgaa 840
ttttggttac ttccatatag ccttcccttt catccaggga gaatgtggtg tcattgtaga 900
atggtttatc tgccaatgtc gtatctttat ggtaagagat ttgttggtcc aatcactcca 960
atagttttat cgttgagaaa agagttatat accattccgt accacgagat tgattggaat 1020
agatccagaa acacgtgtgc taaggaggac ttatattacc ctcaccctaa gatgcaagat 1080
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tccaggtaca tatgccttgg acccgtgaac aaagttctaa atatgctgtg ttgctgggtt 1260
gaggatcctt actctgatgc tttcaagttt cacttgcaga gaattcctga ctatctatgg 1320
ttagctgaag atggaatgag aatgcagggt tataatggtt cacagctttg ggacactgca 1380
ttcagcatac aagcgataat ctcaacgaaa ttgattgata cgtttggtcc gacattacgt 1440
aaagcacacc atttcgtcaa gcatagtcag attcaagagg attgtccagg tgatccaaac 1500
gtatggttca gacacattca taaaggagct tggcctttta gcactagaga tcatggttgg 1560
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cagaaaacag acgggtcttg gtatggttgt tggggtgtct gttttactta tgctggttgg 1980
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ttgcatagag ctgccagatt gctaatcaat agtcaattgg agtcaggtga ctttccacaa 2280

caagaaatca tgggtgtgtt taataagaac tgtatgataa catatgccgc atacagaaac 2340
atattcccta tatgggctct aggtgaatac tcccatcgtg tcttggatat gtga 2394

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<211> 797
<212> PRT
<213> Artificial Sequence

<220>
<223> SS3b-B10 Full Gene AA seq

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

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Ile Asp Trp Asn Arg Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr
            340                 345                 350
Tyr Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His
        355                 360                 365
Val Tyr Glu Pro Leu Phe Ser Gly Trp Pro Gly Lys Arg Leu Arg Glu
    370                 375                 380
Lys Ala Met Lys Ile Ala Met Glu His Ile His Tyr Glu Asp Glu Asn
385                 390                 395                 400
Ser Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu
                405                 410                 415
Cys Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Phe His Leu
            420                 425                 430
Gln Arg Ile Pro Asp Tyr Leu Trp Leu Ala Glu Asp Gly Met Arg Met
        435                 440                 445
Gln Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln
    450                 455                 460
Ala Ile Ile Ser Thr Lys Leu Ile Asp Thr Phe Gly Pro Thr Leu Arg
465                 470                 475                 480
Lys Ala His His Phe Val Lys His Ser Gln Ile Gln Glu Asp Cys Pro
                485                 490                 495
Gly Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp Pro
            500                 505                 510
Phe Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu
        515                 520                 525
Gly Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Lys Ile Val
    530                 535                 540
Gly Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val Leu
545                 550                 555                 560
Leu Ser Leu Gln Asn Glu Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr
                565                 570                 575
Arg Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly
            580                 585                 590
Asp Ile Val Ile Asp Tyr Ser Tyr Val Glu Cys Thr Ser Ala Thr Met
        595                 600                 605
Glu Ala Leu Ala Leu Phe Lys Lys Leu His Pro Gly His Arg Thr Lys
    610                 615                 620
Glu Ile Asp Ala Ala Ile Ala Lys Ala Ala Asn Phe Leu Glu Asn Met
625                 630                 635                 640
Gln Lys Thr Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr
                645                 650                 655
Tyr Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr
            660                 665                 670
Tyr Asn Asn Cys Val Ala Ile Arg Lys Ala Cys Asn Phe Leu Leu Ser
        675                 680                 685
Lys Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln
    690                 695                 700
Asn Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val Asn
705                 710                 715                 720
Thr Ala Trp Val Met Met Ala Leu Ile Glu Ala Gly Gln Gly Glu Arg
                725                 730                 735
Asp Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu Ile Asn Ser Gln
            740                 745                 750
Leu Glu Ser Gly Asp Phe Pro Gln Gln Glu Ile Met Gly Val Phe Asn
        755                 760                 765
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Lys Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile
    770                 775                 780
Trp Ala Leu Gly Glu Tyr Ser His Arg Val Leu Asp Met
785                 790                 795

<210> 945
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<212> PRT
<213> Artificial Sequence

<220>
<223> SS3b-B10 Fusion AA seq

<400> 945
Met Ala Lys Glu Asp Thr Val Lys Leu Lys Arg
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<210> 946

<400> 946
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<210> 947
<211> 2391
<212> DNA
<213> Artificial Sequence

<220>
<223> SS3a-D8 Full gene NT Seq

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attaaaagca ttagtaacca tttgggcaga caagtctggg agttttgctc tggtgaaaat 180
gaaaacgacg acgatgaagc aattgctgta gctaacaatt cagcctcaaa atttgaaaat 240
gcaagaaatc acttccgtaa taacagattc cataggaagc aatcttccga cttattcttg 300
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gtgaaagaag gtgaagatgt taagaaagaa gccgtaaaaa atacactaga aagagcattg 420
tcgttctatt ctgctgtaca gacctctgac ggtaattggg catcagactt gggaggacct 480
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aggtacatat gccttggacc cgtgaacaaa gttctaaata tgctgtgttg ctgggttgag 1260

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gctgaagatg gaatgagaat gcagggttat aatggttcac agctttggga cactgcattc 1380
agcatacaag cgataatctc aacgaaattg attgatacgt ttggtccgac attacgtaaa 1440
gcacaccatt tcgtcaagca tagtcagatt caagaggatt gtccaggtga tccaaacgta 1500
tggttcagac acattcataa aggagcttgg ccttttagca ctagagatca tggttggctt 1560
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gcttgtaact tcctgttgtc aaaagaattg cctggcggtg gttggggcga aagctaccta 2100
agttgccaaa acaaagttta taccaatctg gagggaaaca agccacactt agtcaatact 2160
gcatgggtca tgatggcctt gattgaagca ggacaagggg aaagagatcc agctccgttg 2220
catagagctg ccagattgct aatcaatagt caattggagt caggtgactt tccacaacaa 2280
gaaatcatgg gtgtgtttaa taagaactgt atgataacat atgccgcata cagaaacata 2340
ttccctatat gggctctagg tgaatactcc catcgtgtct tggatatgtg a 2391

<210> 948
<211> 796
<212> PRT
<213> Artificial Sequence

<220>
<223> SS3a-D8Full Gene AA seq

<400> 948
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Ser Gly Ser Gly Ser Gly Met Trp Arg Leu Lys Val Gly Lys Glu Ser
            20                  25                  30
Val Gly Glu Lys Glu Glu Lys Trp Ile Lys Ser Ile Ser Asn His Leu
        35                  40                  45
Gly Arg Gln Val Trp Glu Phe Cys Ser Gly Glu Asn Glu Asn Asp Asp
    50                  55                  60
Asp Glu Ala Ile Ala Val Ala Asn Asn Ser Ala Ser Lys Phe Glu Asn
65                  70                  75                  80
Ala Arg Asn His Phe Arg Asn Asn Arg Phe His Arg Lys Gln Ser Ser
                85                  90                  95
Asp Leu Phe Leu Ala Ile Gln Cys Glu Lys Glu Ile Ile Arg Asn Gly
            100                 105                 110
Ala Lys Asn Glu Gly Thr Thr Lys Val Lys Glu Gly Glu Asp Val Lys
        115                 120                 125
Lys Glu Ala Val Lys Asn Thr Leu Glu Arg Ala Leu Ser Phe Tyr Ser
    130                 135                 140
Ala Val Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro
145                 150                 155                 160
Met Phe Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val Thr Gly Val
                165                 170                 175
Leu Asn Ser Val Leu Ser Lys His His Arg Gln Glu Met Cys Arg Tyr
            180                 185                 190
Ile Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile Glu

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        195                 200                 205
Gly Ser Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg
    210                 215                 220
Leu Leu Gly Glu Ala Ala Asp Gly Gly Glu His Gly Ala Met Thr Lys
225                 230                 235                 240
Ala Arg Ser Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser
                245                 250                 255
Trp Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp Ser Gly
            260                 265                 270
Asn Asn Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro
        275                 280                 285
Phe His Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr Leu Pro
    290                 295                 300
Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr Pro Ile
305                 310                 315                 320
Val Leu Ser Leu Arg Lys Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile
                325                 330                 335
Asp Trp Asn Arg Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr
            340                 345                 350
Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His Val
        355                 360                 365
Tyr Glu Pro Leu Phe Ser Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys
    370                 375                 380
Ala Met Lys Ile Ala Met Glu His Ile His Tyr Glu Asp Glu Asn Ser
385                 390                 395                 400
Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu Cys
                405                 410                 415
Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Phe His Leu Gln
            420                 425                 430
Arg Ile Pro Asp Tyr Leu Trp Leu Ala Glu Asp Gly Met Arg Met Gln
        435                 440                 445
Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala
    450                 455                 460
Ile Ile Ser Thr Lys Leu Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys
465                 470                 475                 480
Ala His His Phe Val Lys His Ser Gln Ile Gln Glu Asp Cys Pro Gly
                485                 490                 495
Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp Pro Phe
            500                 505                 510
Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly
        515                 520                 525
Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Lys Ile Val Gly
    530                 535                 540
Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val Leu Leu
545                 550                 555                 560
Ser Leu Gln Asn Glu Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg
                565                 570                 575
Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp
            580                 585                 590
Ile Val Ile Asp Tyr Ser Tyr Val Glu Cys Thr Ser Ala Thr Met Glu
        595                 600                 605
Ala Leu Ala Leu Phe Lys Lys Leu His Pro Gly His Arg Thr Lys Glu
    610                 615                 620
Ile Asp Ala Ala Ile Ala Lys Ala Ala Asn Phe Leu Glu Asn Met Gln
```

625 630 635 640
Lys Thr Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr
645 650 655
Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr
660 665 670
Asn Asn Cys Val Ala Ile Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys
675 680 685
Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn
690 695 700
Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val Asn Thr
705 710 715 720
Ala Trp Val Met Met Ala Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp
725 730 735
Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu
740 745 750
Glu Ser Gly Asp Phe Pro Gln Gln Glu Ile Met Gly Val Phe Asn Lys
755 760 765
Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp
770 775 780
Ala Leu Gly Glu Tyr Ser His Arg Val Leu Asp Met
785 790 795

<210> 949
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> SS3a-D8 Fusion AA seq

<400> 949
Met Ser Phe Gln Ile Glu Thr Val Arg Thr
1 5 10

<210> 950

<400> 950
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<210> 951
<211> 2400
<212> DNA
<213> Artificial Sequence

<220>
<223> SS3a-A2 Full gene NT Seq

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ggaagtggtt caggaatgtg gagactgaaa gtaggcaaag aatctgttgg cgaaaaggaa 120
gaaaagtgga ttaaaagcat tagtaaccat ttgggcagac aagtctggga gttttgctct 180
ggtgaaaatg aaaacgacga cgatgaagca attgctgtag ctaacaattc agcctcaaaa 240

tttgaaaatg caagaaatca cttccgtaat aacagattcc ataggaagca atcttccgac 300
ttattcttgg ctatacaatg cgagaaagag atcattagga atggtgctaa gaatgaaggt 360
actaccaaag tgaaagaagg tgaagatgtt aagaaagaag ccgtaaaaaa tacactagaa 420
agagcattgt cgttctattc tgctgtacag acctctgacg gtaattgggc atcagacttg 480
ggaggaccta tgttcctttt accagggcta gttattgcgc tatacgttac aggcgttctt 540
aacagtgtgt tgtcaaaaca tcacaggcaa gaaatgtgtc gttacatcta taatcaccaa 600
aacgaagatg gagggtgggg tttacatata gaaggctctt ctactatgtt tgggtctgca 660
ctgaattacg ttgcgttaag gttactagga gaagcggcag atggcggtga gcatggtgcg 720
atgaccaaag caaggtcctg gatattggaa agaggaggtg ccacagcaat aacttcctgg 780
ggcaaacttt ggctttccgt attaggagtg tatgaatggt cgggaaacaa tccattgcca 840
cccgaatttt ggttacttcc atatagcctt ccctttcatc cagggagaat gtggtgtcat 900
tgtagaatgg tttatctgcc aatgtcgtat ctttatggta agagatttgt tggtccaatc 960
actccaatag ttttatcgtt gagaaaagag ttatatacca ttccgtacca cgagattgat 1020
tggaatagat ccagaaacac gtgtgctaag gaggacttat attaccctca ccctaagatg 1080
caagatatcc tatggggcag tatctaccat gtctacgaac cgctattttc aggttggcca 1140
ggtaagagat tgagggaaaa ggccatgaaa attgcaatgg aacatatcca ttacgaagat 1200
gagaattcca ggtacatatg ccttggaccc gtgaacaaag ttctaaatat gctgtgttgc 1260
tgggttgagg atccttactc tgatgctttc aagtttcact tgcagagaat tcctgactat 1320
ctatggttag ctgaagatgg aatgagaatg cagggttata atggttcaca gctttgggac 1380
actgcattca gcatacaagc gataatctca acgaaattga ttgatacgtt tggtccgaca 1440
ttacgtaaag cacaccattt cgtcaagcat agtcagattc aagaggattg tccaggtgat 1500
ccaaacgtat ggttcagaca cattcataaa ggagcttggc cttttagcac tagagatcat 1560
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ttgccttcta aaattgtggg tgaacccttg gagaagaacc gtttatgtga tgcagtcaat 1680
gttttgttat cattgcaaaa cgaaaatggt gggttcgctt cttatgaatt aactaggtcc 1740
tatccctggt tagagttgat taaccctgcc gaaacatttg gtgatatcgt aattgactac 1800
agttatgtgg aatgcactag tgcgacgatg gaagccttag ccttgtttaa gaagttgcac 1860
cctgggcata gaaccaaaga aattgatgcc gctattgcta aagccgcaaa ttttctggag 1920
aatatgcaga aaacagacgg gtcttggtat ggttgttggg gtgtctgttt tacttatgct 1980
ggttggtttg gcatcaaagg cttagtagct gctggtagaa catacaataa ttgtgttgcc 2040
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agctacctaa gttgccaaaa caaagtttat accaatctgg agggaaacaa gccacactta 2160
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gctccgttgc atagagctgc cagattgcta atcaatagtc aattggagtc aggtgacttt 2280
ccacaacaag aaatcatggg tgtgtttaat aagaactgta tgataacata tgccgcatac 2340
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<211> 799
<212> PRT
<213> Artificial Sequence

<220>
<223> SS3a-A2 Full Gene AA seq

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Ala Pro Gly Ser Gly Ser Gly Ser Gly Met Trp Arg Leu Lys Val Gly
            20                  25                  30
Lys Glu Ser Val Gly Glu Lys Glu Glu Lys Trp Ile Lys Ser Ile Ser
        35                  40                  45
Asn His Leu Gly Arg Gln Val Trp Glu Phe Cys Ser Gly Glu Asn Glu

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    50                  55                  60
Asn Asp Asp Asp Glu Ala Ile Ala Val Ala Asn Asn Ser Ala Ser Lys
65                  70                  75                  80
Phe Glu Asn Ala Arg Asn His Phe Arg Asn Asn Arg Phe His Arg Lys
                85                  90                  95
Gln Ser Ser Asp Leu Phe Leu Ala Ile Gln Cys Glu Lys Glu Ile Ile
            100                 105                 110
Arg Asn Gly Ala Lys Asn Glu Gly Thr Thr Lys Val Lys Glu Gly Glu
        115                 120                 125
Asp Val Lys Lys Glu Ala Val Lys Asn Thr Leu Glu Arg Ala Leu Ser
    130                 135                 140
Phe Tyr Ser Ala Val Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu
145                 150                 155                 160
Gly Gly Pro Met Phe Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val
                165                 170                 175
Thr Gly Val Leu Asn Ser Val Leu Ser Lys His His Arg Gln Glu Met
            180                 185                 190
Cys Arg Tyr Ile Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu
        195                 200                 205
His Ile Glu Gly Ser Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val
    210                 215                 220
Ala Leu Arg Leu Leu Gly Glu Ala Ala Asp Gly Gly Glu His Gly Ala
225                 230                 235                 240
Met Thr Lys Ala Arg Ser Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala
                245                 250                 255
Ile Thr Ser Trp Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu
            260                 265                 270
Trp Ser Gly Asn Asn Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr
        275                 280                 285
Ser Leu Pro Phe His Pro Gly Arg Met Trp Cys His Cys Arg Met Val
    290                 295                 300
Tyr Leu Pro Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile
305                 310                 315                 320
Thr Pro Ile Val Leu Ser Leu Arg Lys Glu Leu Tyr Thr Ile Pro Tyr
                325                 330                 335
His Glu Ile Asp Trp Asn Arg Ser Arg Asn Thr Cys Ala Lys Glu Asp
            340                 345                 350
Leu Tyr Tyr Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile
        355                 360                 365
Tyr His Val Tyr Glu Pro Leu Phe Ser Gly Trp Pro Gly Lys Arg Leu
    370                 375                 380
Arg Glu Lys Ala Met Lys Ile Ala Met Glu His Ile His Tyr Glu Asp
385                 390                 395                 400
Glu Asn Ser Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn
                405                 410                 415
Met Leu Cys Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Phe
            420                 425                 430
His Leu Gln Arg Ile Pro Asp Tyr Leu Trp Leu Ala Glu Asp Gly Met
        435                 440                 445
Arg Met Gln Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser
    450                 455                 460
Ile Gln Ala Ile Ile Ser Thr Lys Leu Ile Asp Thr Phe Gly Pro Thr
465                 470                 475                 480
Leu Arg Lys Ala His His Phe Val Lys His Ser Gln Ile Gln Glu Asp
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                485                 490                 495
Cys Pro Gly Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala
            500                 505                 510
Trp Pro Phe Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr
        515                 520                 525
Ala Glu Gly Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Lys
    530                 535                 540
Ile Val Gly Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn
545                 550                 555                 560
Val Leu Leu Ser Leu Gln Asn Glu Asn Gly Gly Phe Ala Ser Tyr Glu
                565                 570                 575
Leu Thr Arg Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr
            580                 585                 590
Phe Gly Asp Ile Val Ile Asp Tyr Ser Tyr Val Glu Cys Thr Ser Ala
        595                 600                 605
Thr Met Glu Ala Leu Ala Leu Phe Lys Lys Leu His Pro Gly His Arg
    610                 615                 620
Thr Lys Glu Ile Asp Ala Ala Ile Ala Lys Ala Ala Asn Phe Leu Glu
625                 630                 635                 640
Asn Met Gln Lys Thr Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys
                645                 650                 655
Phe Thr Tyr Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly
            660                 665                 670
Arg Thr Tyr Asn Asn Cys Val Ala Ile Arg Lys Ala Cys Asn Phe Leu
        675                 680                 685
Leu Ser Lys Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser
    690                 695                 700
Cys Gln Asn Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu
705                 710                 715                 720
Val Asn Thr Ala Trp Val Met Met Ala Leu Ile Glu Ala Gly Gln Gly
                725                 730                 735
Glu Arg Asp Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu Ile Asn
            740                 745                 750
Ser Gln Leu Glu Ser Gly Asp Phe Pro Gln Gln Glu Ile Met Gly Val
        755                 760                 765
Phe Asn Lys Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe
    770                 775                 780
Pro Ile Trp Ala Leu Gly Glu Tyr Ser His Arg Val Leu Asp Met
785                 790                 795
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<210> 953
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> SS3a-A2 Fusion AA seq

<400> 953

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Met Thr Gly Leu Asn Gly Asp Ala Asp Ser Asp Leu Leu
 1               5                  10
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<210> 954

<400> 954
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<210> 955
<211> 2394
<212> DNA
<213> Artificial Sequence

<220>
<223> SS3f-A8 Full gene NT Seq

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tggattaaaa gcattagtaa ccatttgggc agacaagtct gggagttttg ctctggtgaa 180
aatgaaaacg acgacgatga agcaattgct gtagctaaca attcagcctc aaaatttgaa 240
aatgcaagaa atcacttccg taataacaga ttccatagga agcaatcttc cgacttattc 300
ttggctatac aatgcgagaa agagatcatt aggaatggtg ctaagaatga aggtactacc 360
aaagtgaaag aaggtgaaga tgttaagaaa gaagccgtaa aaaatacact agaaagagca 420
ttgtcgttct attctgctgt acagacctct gacggtaatt gggcatcaga cttgggagga 480
cctatgttcc ttttaccagg gctagttatt gcgctatacg ttacaggcgt tcttaacagt 540
gtgttgtcaa aacatcacag gcaagaaatg tgtcgttaca tctataatca ccaaaacgaa 600
gatggagggt ggggtttaca tatagaaggc tcttctacta tgtttgggtc tgcactgaat 660
tacgttgcgt taaggttact aggagaagcg gcagatggcg gtgagcatgg tgcgatgacc 720
aaagcaaggt cctggatatt ggaaagagga ggtgccacag caataacttc ctggggcaaa 780
ctttggcttt ccgtattagg agtgtatgaa tggtcgggaa acaatccatt gccacccgaa 840
ttttggttac ttccatatag ccttcccttt catccaggga gaatgtggtg tcattgtaga 900
atggtttatc tgccaatgtc gtatctttat ggtaagagat ttgttggtcc aatcactcca 960
atagttttat cgttgagaaa agagttatat accattccgt accacgagat tgattggaat 1020
agatccagaa acacgtgtgc taaggaggac ttatattacc ctcaccctaa gatgcaagat 1080
atcctatggg gcagtatcta ccatgtctac gaaccgctat tttcaggttg gccaggtaag 1140
agattgaggg aaaaggccat gaaaattgca atggaacata tccattacga agatgagaat 1200
tccaggtaca tatgccttgg acccgtgaac aaagttctaa atatgctgtg ttgctgggtt 1260
gaggatcctt actctgatgc tttcaagttt cacttgcaga gaattcctga ctatctatgg 1320
ttagctgaag atggaatgag aatgcagggt tataatggtt cacagctttg ggacactgca 1380
ttcagcatac aagcgataat ctcaacgaaa ttgattgata cgtttggtcc gacattacgt 1440
aaagcacacc atttcgtcaa gcatagtcag attcaagagg attgtccagg tgatccaaac 1500
gtatggttca gacacattca taaaggagct tggcctttta gcactagaga tcatggttgg 1560
cttatatcgg attgcacagc tgagggattg aaagcttcac tgatgttatc taagttgcct 1620
tctaaaattg tgggtgaacc cttggagaag aaccgtttat gtgatgcagt caatgttttg 1680
ttatcattgc aaaacgaaaa tggtgggttc gcttcttatg aattaactag gtcctatccc 1740
tggttagagt tgattaaccc tgccgaaaca tttggtgata tcgtaattga ctacagttat 1800
gtggaatgca ctagtgcgac gatggaagcc ttagccttgt ttaagaagtt gcaccctggg 1860
catagaacca aagaaattga tgccgctatt gctaaagccg caaattttct ggagaatatg 1920
cagaaaacag acgggtcttg gtatggttgt tggggtgtct gttttactta tgctggttgg 1980
tttggcatca aaggcttagt agctgctggt agaacataca ataattgtgt tgccattaga 2040
aaggcttgta acttcctgtt gtcaaaagaa ttgcctggcg gtggttgggg cgaaagctac 2100
ctaagttgcc aaaacaaagt ttataccaat ctggagggaa acaagccaca cttagtcaat 2160
actgcatggg tcatgatggc cttgattgaa gcaggacaag gggaaagaga tccagctccg 2220
ttgcatagag ctgccagatt gctaatcaat agtcaattgg agtcaggtga ctttccacaa 2280
caagaaatca tgggtgtgtt taataagaac tgtatgataa catatgccgc atacagaaac 2340

atattcccta tatgggctct aggtgaatac tcccatcgtg tcttggatat gtga 2394

<210> 956
<211> 797
<212> PRT
<213> Artificial Sequence

<220>
<223> SS3f-A8 Full Gene AA seq

<400> 956
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20 25 30
Ser Val Gly Glu Lys Glu Glu Lys Trp Ile Lys Ser Ile Ser Asn His
35 40 45
Leu Gly Arg Gln Val Trp Glu Phe Cys Ser Gly Glu Asn Glu Asn Asp
50 55 60
Asp Asp Glu Ala Ile Ala Val Ala Asn Asn Ser Ala Ser Lys Phe Glu
65 70 75 80
Asn Ala Arg Asn His Phe Arg Asn Asn Arg Phe His Arg Lys Gln Ser
85 90 95
Ser Asp Leu Phe Leu Ala Ile Gln Cys Glu Lys Glu Ile Ile Arg Asn
100 105 110
Gly Ala Lys Asn Glu Gly Thr Thr Lys Val Lys Glu Gly Glu Asp Val
115 120 125
Lys Lys Glu Ala Val Lys Asn Thr Leu Glu Arg Ala Leu Ser Phe Tyr
130 135 140
Ser Ala Val Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu Gly Gly
145 150 155 160
Pro Met Phe Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val Thr Gly
165 170 175
Val Leu Asn Ser Val Leu Ser Lys His His Arg Gln Glu Met Cys Arg
180 185 190
Tyr Ile Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile
195 200 205
Glu Gly Ser Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu
210 215 220
Arg Leu Leu Gly Glu Ala Ala Asp Gly Gly Glu His Gly Ala Met Thr
225 230 235 240
Lys Ala Arg Ser Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile Thr
245 250 255
Ser Trp Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp Ser
260 265 270
Gly Asn Asn Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr Ser Leu
275 280 285
Pro Phe His Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr Leu
290 295 300
Pro Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr Pro
305 310 315 320
Ile Val Leu Ser Leu Arg Lys Glu Leu Tyr Thr Ile Pro Tyr His Glu
325 330 335
Ile Asp Trp Asn Arg Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr

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            340                 345                 350
Tyr Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His
        355                 360                 365
Val Tyr Glu Pro Leu Phe Ser Gly Trp Pro Gly Lys Arg Leu Arg Glu
    370                 375                 380
Lys Ala Met Lys Ile Ala Met Glu His Ile His Tyr Glu Asp Glu Asn
385                 390                 395                 400
Ser Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu
                405                 410                 415
Cys Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Phe His Leu
            420                 425                 430
Gln Arg Ile Pro Asp Tyr Leu Trp Leu Ala Glu Asp Gly Met Arg Met
        435                 440                 445
Gln Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln
    450                 455                 460
Ala Ile Ile Ser Thr Lys Leu Ile Asp Thr Phe Gly Pro Thr Leu Arg
465                 470                 475                 480
Lys Ala His His Phe Val Lys His Ser Gln Ile Gln Glu Asp Cys Pro
                485                 490                 495
Gly Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp Pro
            500                 505                 510
Phe Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu
        515                 520                 525
Gly Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Lys Ile Val
    530                 535                 540
Gly Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val Leu
545                 550                 555                 560
Leu Ser Leu Gln Asn Glu Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr
                565                 570                 575
Arg Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly
            580                 585                 590
Asp Ile Val Ile Asp Tyr Ser Tyr Val Glu Cys Thr Ser Ala Thr Met
        595                 600                 605
Glu Ala Leu Ala Leu Phe Lys Lys Leu His Pro Gly His Arg Thr Lys
    610                 615                 620
Glu Ile Asp Ala Ala Ile Ala Lys Ala Ala Asn Phe Leu Glu Asn Met
625                 630                 635                 640
Gln Lys Thr Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr
                645                 650                 655
Tyr Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr
            660                 665                 670
Tyr Asn Asn Cys Val Ala Ile Arg Lys Ala Cys Asn Phe Leu Leu Ser
        675                 680                 685
Lys Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln
    690                 695                 700
Asn Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val Asn
705                 710                 715                 720
Thr Ala Trp Val Met Met Ala Leu Ile Glu Ala Gly Gln Gly Glu Arg
                725                 730                 735
Asp Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu Ile Asn Ser Gln
            740                 745                 750
Leu Glu Ser Gly Asp Phe Pro Gln Gln Glu Ile Met Gly Val Phe Asn
        755                 760                 765
Lys Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile
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    770                 775                 780
Trp Ala Leu Gly Glu Tyr Ser His Arg Val Leu Asp Met
785                 790                 795


<210> 957
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> SS3f-A8 Fusion AA seq

<400> 957
Met Ala Ser Asn Gln Leu Glu Pro Leu Gln Thr
 1               5                  10


<210> 958

<400> 958
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<210> 959
<211> 2391
<212> PRT
<213> Artificial Sequence

<220>
<223> SS4b-B8a Full gene NT Seq

<400> 959
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 1               5                  10                  15
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            20                  25                  30
Thr Gly Gly Cys Gly Ala Ala Ala Ala Gly Gly Ala Ala Gly Ala Ala
        35                  40                  45
Ala Ala Gly Thr Gly Gly Ala Thr Thr Ala Ala Ala Ala Gly Cys Ala
    50                  55                  60
Thr Thr Ala Gly Thr Ala Ala Cys Cys Ala Thr Thr Thr Gly Gly Gly
65                  70                  75                  80
Cys Ala Gly Ala Cys Ala Ala Gly Thr Cys Thr Gly Gly Gly Ala Gly
                85                  90                  95
Thr Thr Thr Thr Gly Cys Thr Cys Thr Gly Gly Thr Gly Ala Ala Ala
            100                 105                 110
Ala Thr Gly Ala Ala Ala Ala Cys Gly Ala Cys Gly Ala Cys Gly Ala
        115                 120                 125
Thr Gly Ala Ala Gly Cys Ala Ala Thr Thr Gly Cys Thr Gly Thr Ala
    130                 135                 140
Gly Cys Thr Ala Ala Cys Ala Ala Thr Thr Cys Ala Gly Cys Cys Thr
145                 150                 155                 160
Cys Ala Ala Ala Ala Thr Thr Thr Gly Ala Ala Ala Ala Thr Gly Cys
                165                 170                 175
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Ala Ala Gly Ala Ala Ala Thr Cys Ala Cys Thr Thr Cys Cys Gly Thr
            180                 185                 190
Ala Ala Thr Ala Ala Cys Ala Gly Ala Thr Thr Cys Cys Ala Thr Ala
        195                 200                 205
Gly Gly Ala Ala Gly Cys Ala Ala Thr Cys Thr Thr Cys Cys Gly Ala
    210                 215                 220
Cys Thr Thr Ala Thr Thr Cys Thr Thr Gly Gly Cys Thr Ala Thr Ala
225                 230                 235                 240
Cys Ala Ala Thr Gly Cys Gly Ala Gly Ala Ala Ala Gly Ala Gly Ala
                245                 250                 255
Thr Cys Ala Thr Thr Ala Gly Gly Ala Ala Thr Gly Gly Thr Gly Cys
            260                 265                 270
Thr Ala Ala Gly Ala Ala Thr Gly Ala Ala Gly Gly Thr Ala Cys Thr
        275                 280                 285
Ala Cys Cys Ala Ala Ala Gly Thr Gly Ala Ala Ala Gly Ala Ala Gly
    290                 295                 300
Gly Thr Gly Ala Ala Gly Ala Thr Gly Thr Thr Ala Ala Gly Ala Ala
305                 310                 315                 320
Ala Gly Ala Ala Gly Cys Cys Gly Thr Ala Ala Ala Ala Ala Ala Thr
                325                 330                 335
Ala Cys Ala Cys Thr Ala Gly Ala Ala Ala Gly Ala Gly Cys Ala Thr
            340                 345                 350
Thr Gly Thr Cys Gly Thr Thr Cys Thr Ala Thr Thr Cys Thr Gly Cys
        355                 360                 365
Thr Gly Thr Ala Cys Ala Gly Ala Cys Cys Thr Cys Thr Gly Ala Cys
    370                 375                 380
Gly Gly Thr Ala Ala Thr Thr Gly Gly Gly Cys Ala Thr Cys Ala Gly
385                 390                 395                 400
Ala Cys Thr Thr Gly Gly Gly Ala Gly Gly Ala Cys Cys Thr Ala Thr
                405                 410                 415
Gly Thr Thr Cys Cys Thr Thr Thr Thr Ala Cys Cys Ala Gly Gly Gly
            420                 425                 430
Cys Thr Ala Gly Thr Thr Ala Thr Thr Gly Cys Gly Cys Thr Ala Thr
        435                 440                 445
Ala Cys Gly Thr Thr Ala Cys Ala Gly Gly Cys Gly Thr Thr Cys Thr
    450                 455                 460
Thr Ala Ala Cys Ala Gly Thr Gly Thr Gly Thr Thr Gly Thr Cys Ala
465                 470                 475                 480
Ala Ala Ala Cys Ala Thr Cys Ala Cys Ala Gly Gly Cys Ala Ala Gly
                485                 490                 495
Ala Ala Ala Thr Gly Thr Gly Thr Cys Gly Thr Thr Ala Cys Ala Thr
            500                 505                 510
Cys Thr Ala Thr Ala Ala Thr Cys Ala Cys Cys Ala Ala Ala Ala Cys
        515                 520                 525
Gly Ala Ala Gly Ala Thr Gly Gly Ala Gly Gly Gly Thr Gly Gly Gly
    530                 535                 540
Gly Thr Thr Thr Ala Cys Ala Thr Ala Thr Ala Gly Ala Ala Gly Gly
545                 550                 555                 560
Cys Thr Cys Thr Thr Cys Thr Ala Cys Thr Ala Thr Gly Thr Thr Thr
                565                 570                 575
Gly Gly Gly Thr Cys Thr Gly Cys Ala Cys Thr Gly Ala Ala Thr Thr
            580                 585                 590
Ala Cys Gly Thr Thr Gly Cys Gly Thr Thr Ala Ala Gly Gly Thr Thr
        595                 600                 605
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Ala Cys Thr Ala Gly Gly Ala Gly Ala Ala Gly Cys Gly Gly Cys Ala
    610                 615                 620
Gly Ala Thr Gly Gly Cys Gly Gly Thr Gly Ala Gly Cys Ala Thr Gly
625                 630                 635                 640
Gly Thr Gly Cys Gly Ala Thr Gly Ala Cys Cys Ala Ala Ala Gly Cys
                645                 650                 655
Ala Ala Gly Gly Thr Cys Cys Thr Gly Gly Ala Thr Ala Thr Thr Gly
            660                 665                 670
Gly Ala Ala Ala Gly Ala Gly Gly Ala Gly Gly Thr Gly Cys Cys Ala
        675                 680                 685
Cys Ala Gly Cys Ala Ala Thr Ala Ala Cys Thr Thr Cys Cys Thr Gly
    690                 695                 700
Gly Gly Gly Cys Ala Ala Ala Cys Thr Thr Thr Gly Gly Cys Thr Thr
705                 710                 715                 720
Thr Cys Cys Gly Thr Ala Thr Thr Ala Gly Gly Ala Gly Thr Gly Thr
                725                 730                 735
Ala Thr Gly Ala Ala Thr Gly Gly Thr Cys Gly Gly Gly Ala Ala Ala
            740                 745                 750
Cys Ala Ala Thr Cys Cys Ala Thr Thr Gly Cys Cys Ala Cys Cys Cys
        755                 760                 765
Gly Ala Ala Thr Thr Thr Thr Gly Gly Thr Thr Ala Cys Thr Thr Cys
    770                 775                 780
Cys Ala Thr Ala Thr Ala Gly Cys Cys Thr Thr Cys Cys Cys Thr Thr
785                 790                 795                 800
Thr Cys Ala Thr Cys Cys Ala Gly Gly Gly Ala Gly Ala Ala Thr Gly
                805                 810                 815
Thr Gly Gly Thr Gly Thr Cys Ala Thr Thr Gly Thr Ala Gly Ala Ala
            820                 825                 830
Thr Gly Gly Thr Thr Thr Ala Thr Cys Thr Gly Cys Cys Ala Ala Thr
        835                 840                 845
Gly Thr Cys Gly Thr Ala Thr Cys Thr Thr Thr Ala Thr Gly Gly Thr
    850                 855                 860
Ala Ala Gly Ala Gly Ala Thr Thr Thr Gly Thr Thr Gly Gly Thr Cys
865                 870                 875                 880
Cys Ala Ala Thr Cys Ala Cys Thr Cys Cys Ala Ala Thr Ala Gly Thr
                885                 890                 895
Thr Thr Thr Ala Thr Cys Gly Thr Thr Gly Ala Gly Ala Ala Ala Ala
            900                 905                 910
Gly Ala Gly Thr Thr Ala Thr Ala Thr Ala Cys Cys Ala Thr Thr Cys
        915                 920                 925
Cys Gly Thr Ala Cys Cys Ala Cys Gly Ala Gly Ala Thr Thr Gly Ala
    930                 935                 940
Thr Thr Gly Gly Ala Ala Thr Ala Gly Ala Thr Cys Cys Ala Gly Ala
945                 950                 955                 960
Ala Ala Cys Ala Cys Gly Thr Gly Thr Gly Cys Thr Ala Ala Gly Gly
                965                 970                 975
Ala Gly Gly Ala Cys Thr Thr Ala Thr Ala Thr Thr Ala Cys Cys Cys
            980                 985                 990
Thr Cys Ala Cys Cys Cys Thr Ala Ala Gly Ala Thr Gly Cys Ala Ala
        995                 1000                1005
Gly Ala Thr Ala Thr Cys Cys Thr Ala Thr Gly Gly Gly Gly Cys Ala
    1010                1015                1020
Gly Thr Ala Thr Cys Thr Ala Cys Cys Ala Thr Gly Thr Cys Thr Ala
1025                1030                1035                1040
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Cys Gly Ala Ala Cys Cys Gly Cys Thr Ala Thr Thr Thr Thr Cys Ala
                1045                1050                1055
Gly Gly Thr Thr Gly Gly Cys Cys Ala Gly Gly Thr Ala Ala Gly Ala
            1060                1065                1070
Gly Ala Thr Thr Gly Ala Gly Gly Gly Ala Ala Ala Ala Gly Gly Cys
        1075                1080                1085
Cys Ala Thr Gly Ala Ala Ala Ala Thr Thr Gly Cys Ala Ala Thr Gly
    1090                1095                1100
Gly Ala Ala Cys Ala Thr Ala Thr Cys Cys Ala Thr Thr Ala Cys Gly
1105                1110                1115                1120
Ala Ala Gly Ala Thr Gly Ala Gly Ala Ala Thr Thr Cys Cys Ala Gly
                1125                1130                1135
Gly Thr Ala Cys Ala Thr Ala Thr Gly Cys Cys Thr Thr Gly Gly Ala
            1140                1145                1150
Cys Cys Cys Gly Thr Gly Ala Ala Cys Ala Ala Ala Gly Thr Thr Cys
        1155                1160                1165
Thr Ala Ala Ala Thr Ala Thr Gly Cys Thr Gly Thr Gly Thr Thr Gly
    1170                1175                1180
Cys Thr Gly Gly Gly Thr Thr Gly Ala Gly Gly Ala Thr Cys Cys Thr
1185                1190                1195                1200
Thr Ala Cys Thr Cys Thr Gly Ala Thr Gly Cys Thr Thr Thr Cys Ala
                1205                1210                1215
Ala Gly Thr Thr Thr Cys Ala Cys Thr Thr Gly Cys Ala Gly Ala Gly
            1220                1225                1230
Ala Ala Thr Thr Cys Cys Thr Gly Ala Cys Thr Ala Thr Cys Thr Ala
        1235                1240                1245
Thr Gly Gly Thr Thr Ala Gly Cys Thr Gly Ala Ala Gly Ala Thr Gly
    1250                1255                1260
Gly Ala Ala Thr Gly Ala Gly Ala Ala Thr Gly Cys Ala Gly Gly Gly
1265                1270                1275                1280
Thr Thr Ala Thr Ala Ala Thr Gly Gly Thr Thr Cys Ala Cys Ala Gly
                1285                1290                1295
Cys Thr Thr Thr Gly Gly Gly Ala Cys Ala Cys Thr Gly Cys Ala Thr
            1300                1305                1310
Thr Cys Ala Gly Cys Ala Thr Ala Cys Ala Ala Gly Cys Gly Ala Thr
        1315                1320                1325
Ala Ala Thr Cys Thr Cys Ala Ala Cys Gly Ala Ala Ala Thr Thr Gly
    1330                1335                1340
Ala Thr Thr Gly Ala Thr Ala Cys Gly Thr Thr Thr Gly Gly Thr Cys
1345                1350                1355                1360
Cys Gly Ala Cys Ala Thr Thr Ala Cys Gly Thr Ala Ala Ala Gly Cys
                1365                1370                1375
Ala Cys Ala Cys Cys Ala Thr Thr Thr Cys Gly Thr Cys Ala Ala Gly
            1380                1385                1390
Cys Ala Thr Ala Gly Thr Cys Ala Gly Ala Thr Thr Cys Ala Ala Gly
        1395                1400                1405
Ala Gly Gly Ala Thr Thr Gly Thr Cys Cys Ala Gly Gly Thr Gly Ala
    1410                1415                1420
Thr Cys Cys Ala Ala Ala Cys Gly Thr Ala Thr Gly Gly Thr Thr Cys
1425                1430                1435                1440
Ala Gly Ala Cys Ala Cys Ala Thr Thr Cys Ala Thr Ala Ala Ala Gly
                1445                1450                1455
Gly Ala Gly Cys Thr Thr Gly Gly Cys Cys Thr Thr Thr Thr Ala Gly
            1460                1465                1470
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Cys Ala Cys Thr Ala Gly Ala Gly Ala Thr Cys Ala Thr Gly Gly Thr
        1475                1480                1485
Thr Gly Gly Cys Thr Thr Ala Thr Ala Thr Cys Gly Gly Ala Thr Thr
    1490                1495                1500
Gly Cys Ala Cys Ala Gly Cys Thr Gly Ala Gly Gly Gly Ala Thr Thr
1505                1510                1515                1520
Gly Ala Ala Ala Gly Cys Thr Thr Cys Ala Cys Thr Gly Ala Thr Gly
                1525                1530                1535
Thr Thr Ala Thr Cys Thr Ala Ala Gly Thr Thr Gly Cys Cys Thr Thr
            1540                1545                1550
Cys Thr Ala Ala Ala Ala Thr Thr Gly Thr Gly Gly Gly Thr Gly Ala
        1555                1560                1565
Ala Cys Cys Cys Thr Thr Gly Gly Ala Gly Ala Ala Gly Ala Ala Cys
    1570                1575                1580
Cys Gly Thr Thr Thr Ala Thr Gly Thr Gly Ala Thr Gly Cys Ala Gly
1585                1590                1595                1600
Thr Cys Ala Ala Thr Gly Thr Thr Thr Thr Gly Thr Thr Ala Thr Cys
                1605                1610                1615
Ala Thr Thr Gly Cys Ala Ala Ala Ala Cys Gly Ala Ala Ala Ala Thr
            1620                1625                1630
Gly Gly Thr Gly Gly Gly Thr Thr Cys Gly Cys Thr Thr Cys Thr Thr
        1635                1640                1645
Ala Thr Gly Ala Ala Thr Thr Ala Ala Cys Thr Ala Gly Gly Thr Cys
    1650                1655                1660
Cys Thr Ala Thr Cys Cys Cys Thr Gly Gly Thr Thr Ala Gly Ala Gly
1665                1670                1675                1680
Thr Thr Gly Ala Thr Thr Ala Ala Cys Cys Cys Thr Gly Cys Cys Gly
                1685                1690                1695
Ala Ala Ala Cys Ala Thr Thr Thr Gly Gly Thr Gly Ala Thr Ala Thr
            1700                1705                1710
Cys Gly Thr Ala Ala Thr Thr Gly Ala Cys Thr Ala Cys Ala Gly Thr
        1715                1720                1725
Thr Ala Thr Gly Thr Gly Gly Ala Ala Thr Gly Cys Ala Cys Thr Ala
    1730                1735                1740
Gly Thr Gly Cys Gly Ala Cys Gly Ala Thr Gly Gly Ala Ala Gly Cys
1745                1750                1755                1760
Cys Thr Thr Ala Gly Cys Cys Thr Thr Gly Thr Thr Thr Ala Ala Gly
                1765                1770                1775
Ala Ala Gly Thr Thr Gly Cys Ala Cys Cys Cys Thr Gly Gly Gly Cys
            1780                1785                1790
Ala Thr Ala Gly Ala Ala Cys Cys Ala Ala Ala Gly Ala Ala Ala Thr
        1795                1800                1805
Thr Gly Ala Thr Gly Cys Cys Gly Cys Thr Ala Thr Thr Gly Cys Thr
    1810                1815                1820
Ala Ala Ala Gly Cys Cys Gly Cys Ala Ala Ala Thr Thr Thr Thr Cys
1825                1830                1835                1840
Thr Gly Gly Ala Gly Ala Ala Thr Ala Thr Gly Cys Ala Gly Ala Ala
                1845                1850                1855
Ala Ala Cys Ala Gly Ala Cys Gly Gly Gly Thr Cys Thr Thr Gly Gly
            1860                1865                1870
Thr Ala Thr Gly Gly Thr Thr Gly Thr Thr Gly Gly Gly Gly Thr Gly
        1875                1880                1885
Thr Cys Thr Gly Thr Thr Thr Thr Ala Cys Thr Thr Ala Thr Gly Cys
    1890                1895                1900
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Thr Gly Gly Thr Thr Gly Gly Thr Thr Thr Gly Gly Cys Ala Thr Cys
1905                1910                1915                1920
Ala Ala Ala Gly Gly Cys Thr Thr Ala Gly Thr Ala Gly Cys Thr Gly
                1925                1930                1935
Cys Thr Gly Gly Thr Ala Gly Ala Ala Cys Ala Thr Ala Cys Ala Ala
            1940                1945                1950
Thr Ala Ala Thr Thr Gly Thr Gly Thr Thr Gly Cys Cys Ala Thr Thr
        1955                1960                1965
Ala Gly Ala Ala Ala Gly Gly Cys Thr Thr Gly Thr Ala Ala Cys Thr
    1970                1975                1980
Thr Cys Cys Thr Gly Thr Thr Gly Thr Cys Ala Ala Ala Ala Gly Ala
1985                1990                1995                2000
Ala Thr Thr Gly Cys Cys Thr Gly Gly Cys Gly Gly Thr Gly Gly Thr
                2005                2010                2015
Thr Gly Gly Gly Gly Cys Gly Ala Ala Ala Gly Cys Thr Ala Cys Cys
            2020                2025                2030
Thr Ala Ala Gly Thr Thr Gly Cys Cys Ala Ala Ala Ala Cys Ala Ala
        2035                2040                2045
Ala Gly Thr Thr Thr Ala Thr Ala Cys Cys Ala Ala Thr Cys Thr Gly
    2050                2055                2060
Gly Ala Gly Gly Gly Ala Ala Ala Cys Ala Ala Gly Cys Cys Ala Cys
2065                2070                2075                2080
Ala Cys Thr Thr Ala Gly Thr Cys Ala Ala Thr Ala Cys Thr Gly Cys
                2085                2090                2095
Ala Thr Gly Gly Gly Thr Cys Ala Thr Gly Ala Thr Gly Gly Cys Cys
            2100                2105                2110
Thr Thr Gly Ala Thr Thr Gly Ala Ala Gly Cys Ala Gly Gly Ala Cys
        2115                2120                2125
Ala Ala Gly Gly Gly Gly Ala Ala Ala Gly Ala Gly Ala Thr Cys Cys
    2130                2135                2140
Ala Gly Cys Thr Cys Cys Gly Thr Thr Gly Cys Ala Thr Ala Gly Ala
2145                2150                2155                2160
Gly Cys Thr Gly Cys Cys Ala Gly Ala Thr Thr Gly Cys Thr Ala Ala
                2165                2170                2175
Thr Cys Ala Ala Thr Ala Gly Thr Cys Ala Ala Thr Thr Gly Gly Ala
            2180                2185                2190
Gly Thr Cys Ala Gly Gly Thr Gly Ala Cys Thr Thr Thr Cys Cys Ala
        2195                2200                2205
Cys Ala Ala Cys Ala Ala Gly Ala Ala Ala Thr Cys Ala Thr Gly Gly
    2210                2215                2220
Gly Thr Gly Thr Gly Thr Thr Thr Ala Ala Thr Ala Ala Gly Ala Ala
2225                2230                2235                2240
Cys Thr Gly Thr Ala Thr Gly Ala Thr Ala Ala Cys Ala Thr Ala Thr
                2245                2250                2255
Gly Cys Cys Gly Cys Ala Thr Ala Cys Ala Gly Ala Ala Ala Cys Ala
            2260                2265                2270
Thr Ala Thr Thr Cys Cys Cys Thr Ala Thr Ala Thr Gly Gly Gly Cys
        2275                2280                2285
Thr Cys Thr Ala Gly Gly Thr Gly Ala Ala Thr Ala Cys Thr Cys Cys
    2290                2295                2300
Cys Ala Thr Cys Gly Thr Gly Thr Cys Thr Thr Gly Gly Ala Thr Ala
2305                2310                2315                2320
Thr Gly Gly Gly Ala Ala Gly Thr Gly Cys Ala Gly Cys Thr Cys Cys
                2325                2330                2335
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Thr Gly Gly Ala Ala Gly Thr Gly Gly Ala Ala Gly Thr Gly Gly Thr
2340 2345 2350
Thr Cys Ala Gly Gly Ala Ala Thr Gly Ala Ala Thr Thr Thr Ala Gly
2355 2360 2365
Ala Thr Thr Thr Ala Gly Ala Thr Cys Ala Ala Gly Ala Thr Thr Cys
2370 2375 2380
Ala Gly Ala Cys Thr Ala Gly
2385 2390

<210> 960
<211> 796
<212> PRT
<213> Artificial Sequence

<220>
<223> SS4b-B8a Full Gene AA seq

<400> 960
Met Trp Arg Leu Lys Val Gly Lys Glu Ser Val Gly Glu Lys Glu Glu
1 5 10 15
Lys Trp Ile Lys Ser Ile Ser Asn His Leu Gly Arg Gln Val Trp Glu
20 25 30
Phe Cys Ser Gly Glu Asn Glu Asn Asp Asp Asp Glu Ala Ile Ala Val
35 40 45
Ala Asn Asn Ser Ala Ser Lys Phe Glu Asn Ala Arg Asn His Phe Arg
50 55 60
Asn Asn Arg Phe His Arg Lys Gln Ser Ser Asp Leu Phe Leu Ala Ile
65 70 75 80
Gln Cys Glu Lys Glu Ile Ile Arg Asn Gly Ala Lys Asn Glu Gly Thr
85 90 95
Thr Lys Val Lys Glu Gly Glu Asp Val Lys Lys Glu Ala Val Lys Asn
100 105 110
Thr Leu Glu Arg Ala Leu Ser Phe Tyr Ser Ala Val Gln Thr Ser Asp
115 120 125
Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro Met Phe Leu Leu Pro Gly
130 135 140
Leu Val Ile Ala Leu Tyr Val Thr Gly Val Leu Asn Ser Val Leu Ser
145 150 155 160
Lys His His Arg Gln Glu Met Cys Arg Tyr Ile Tyr Asn His Gln Asn
165 170 175
Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly Ser Ser Thr Met Phe
180 185 190
Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu Leu Gly Glu Ala Ala
195 200 205
Asp Gly Gly Glu His Gly Ala Met Thr Lys Ala Arg Ser Trp Ile Leu
210 215 220
Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser Trp Gly Lys Leu Trp Leu
225 230 235 240
Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn Pro Leu Pro Pro
245 250 255
Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro Phe His Pro Gly Arg Met
260 265 270
Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly

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        275                 280                 285
Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu Ser Leu Arg Lys
    290                 295                 300
Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile Asp Trp Asn Arg Ser Arg
305                 310                 315                 320
Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met Gln
                325                 330                 335
Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu Pro Leu Phe Ser
            340                 345                 350
Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met Lys Ile Ala Met
        355                 360                 365
Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile Cys Leu Gly
    370                 375                 380
Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro
385                 390                 395                 400
Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile Pro Asp Tyr Leu
                405                 410                 415
Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn Gly Ser Gln
            420                 425                 430
Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile Ser Thr Lys Leu
        435                 440                 445
Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His His Phe Val Lys
    450                 455                 460
His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro Asn Val Trp Phe
465                 470                 475                 480
Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His Gly
                485                 490                 495
Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ser Leu Met
            500                 505                 510
Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro Leu Glu Lys Asn
        515                 520                 525
Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Glu Asn
    530                 535                 540
Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu Glu
545                 550                 555                 560
Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr Ser
                565                 570                 575
Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Ala Leu Phe Lys
            580                 585                 590
Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Ala Ala Ile Ala
        595                 600                 605
Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys Thr Asp Gly Ser Trp
    610                 615                 620
Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly Ile
625                 630                 635                 640
Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Val Ala Ile
                645                 650                 655
Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly Gly
            660                 665                 670
Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu
        675                 680                 685
Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp Val Met Met Ala
    690                 695                 700
Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala Pro Leu His Arg
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705 710 715 720
Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser Gly Asp Phe Pro
725 730 735
Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr
740 745 750
Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Ser
755 760 765
His Arg Val Leu Asp Met Gly Ser Ala Ala Pro Gly Ser Gly Ser Gly
770 775 780
Ser Gly Met Asn Leu Asp Leu Asp Gln Asp Ser Asp
785 790 795

<210> 961
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> SS4b-B8a Fusion AA seq

<400> 961
Met Asn Leu Asp Leu Asp Gln Asp Ser Asp
1 5 10

<210> 962

<400> 962
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<210> 963
<211> 3387
<212> DNA
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<220>
<223> SS4b-B8b Full gene NT Seq

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gacgacgatg aagcaattgc tgtagctaac aattcagcct caaaatttga aaatgcaaga 180
aatcacttcc gtaataacag attccatagg aagcaatctt ccgacttatt cttggctata 240
caatgcgaga aagagatcat taggaatggt gctaagaatg aaggtactac caaagtgaaa 300
gaaggtgaag atgttaagaa agaagccgta aaaaatacac tagaaagagc attgtcgttc 360
tattctgctg tacagacctc tgacggtaat tgggcatcag acttgggagg acctatgttc 420
cttttaccag ggctagttat tgcgctatac gttacaggcg ttcttaacag tgtgttgtca 480
aaacatcaca ggcaagaaat gtgtcgttac atctataatc accaaaacga agatggaggg 540
tggggtttac atatagaagg ctcttctact atgtttgggt ctgcactgaa ttacgttgcg 600
ttaaggttac taggagaagc ggcagatggc ggtgagcatg gtgcgatgac caaagcaagg 660
tcctggatat tggaaagagg aggtgccaca gcaataactt cctggggcaa actttggctt 720
tccgtattag gagtgtatga atggtcggga aacaatccat tgccacccga attttggtta 780
cttccatata gccttccctt tcatccaggg agaatgtggt gtcattgtag aatggtttat 840

ctgccaatgt cgtatcttta tggtaagaga tttgttggtc caatcactcc aatagtttta 900
tcgttgagaa aagagttata taccattccg taccacgaga ttgattggaa tagatccaga 960
aacacgtgtg ctaaggagga cttatattac cctcacccta agatgcaaga tatcctatgg 1020
ggcagtatct accatgtcta cgaaccgcta ttttcaggtt ggccaggtaa gagattgagg 1080
gaaaaggcca tgaaaattgc aatggaacat atccattacg aagatgagaa ttccaggtac 1140
atatgccttg gacccgtgaa caaagttcta aatatgctgt gttgctgggt tgaggatcct 1200
tactctgatg ctttcaagtt tcacttgcag agaattcctg actatctatg gttagctgaa 1260
gatggaatga gaatgcaggg ttataatggt tcacagcttt gggacactgc attcagcata 1320
caagcgataa tctcaacgaa attgattgat acgtttggtc cgacattacg taaagcacac 1380
catttcgtca agcatagtca gattcaagag gattgtccag gtgatccaaa cgtatggttc 1440
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gattgcacag ctgagggatt gaaagcttca ctgatgttat ctaagttgcc ttctaaaatt 1560
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caaaacgaaa atggtgggtt cgcttcttat gaattaacta ggtcctatcc ctggttagag 1680
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aaagaaattg atgccgctat tgctaaagcc gcaaattttc tggagaatat gcagaaaaca 1860
gacgggtctt ggtatggttg ttggggtgtc tgttttactt atgctggttg gtttggcatc 1920
aaaggcttag tagctgctgg tagaacatac aataattgtg ttgccattag aaaggcttgt 1980
aacttcctgt tgtcaaaaga attgcctggc ggtggttggg gcgaaagcta cctaagttgc 2040
caaaacaaag tttataccaa tctggaggga aacaagccac acttagtcaa tactgcatgg 2100
gtcatgatgg ccttgattga agcaggacaa ggggaaagag atccagctcc gttgcataga 2160
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atatgggctc taggtgaata ctcccatcgt gtcttggata tgggaagtgc agctcctgga 2340
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ggcatcagca agtccgtgct gtcaaggatg attcatcaca aggttacaat cataggttct 2460
ggccccgctg cccacaccgc tgctatatac ttggcaagag cagagatgaa gcccacatta 2520
tatgagggaa tgatggccaa cggaattgct gctggtggcc aattgacaac aaccaccgat 2580
atcgaaaatt tcccagggtt tcctgaatcg ttgagtggca gtgaactgat ggagaggatg 2640
aggaaacaat ctgccaagtt tggcactaac ataattatcg agactgtctc taaagtcgat 2700
ttatcttcaa aaccattcag attatggacc gaatttaatg aggatgcaga gcctgtgacc 2760
actgatgcta taatcttggc cacgggtgct tccgctaaga gaatgcattt accaggggag 2820
gaaacctact ggcagcaggg aatatctgcc tgtgctgtat gtgatggtgc agtccctatc 2880
tttagaaaca agccattggc cgttattggt ggtggtgact ctgcgtgtga ggaagcggaa 2940
tttcttacga agtatgcgtc gaaagtatat atattagtaa gaaaggatca ttttcgtgca 3000
tctgtaataa tgcagagacg aattgagaaa aatccaaaca tcattgtttt gttcaacaca 3060
gttgcattag aagctaaggg tgatggtaag ttattgaata tgttgagaat taagaatact 3120
aaaagtaatg tggagaacga tttagaagta aatggactat tttacgcaat aggtcacagc 3180
cctgccacag atatagttaa aggacaagta gatgaagaag agacggggta tataaaaact 3240
gtgcctggat cgtctctgac ttctgtgcca ggtttttttg ctgcaggtga cgttcaggac 3300
tctaggtata gacaagcagt tacttctgct ggttccggat gcattgctgc tttggatgca 3360
gaacggtacc taagtgccca agagtaa 3387

<210> 964
<211> 1128
<212> PRT
<213> Artificial Sequence

<220>
<223> SS4b-B8b Full Gene AA seq

<400> 964
Met Trp Arg Leu Lys Val Gly Lys Glu Ser Val Gly Glu Lys Glu Glu

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 1               5                  10                  15
Lys Trp Ile Lys Ser Ile Ser Asn His Leu Gly Arg Gln Val Trp Glu
            20                  25                  30
Phe Cys Ser Gly Glu Asn Glu Asn Asp Asp Asp Glu Ala Ile Ala Val
        35                  40                  45
Ala Asn Asn Ser Ala Ser Lys Phe Glu Asn Ala Arg Asn His Phe Arg
    50                  55                  60
Asn Asn Arg Phe His Arg Lys Gln Ser Ser Asp Leu Phe Leu Ala Ile
65                  70                  75                  80
Gln Cys Glu Lys Glu Ile Ile Arg Asn Gly Ala Lys Asn Glu Gly Thr
                85                  90                  95
Thr Lys Val Lys Glu Gly Glu Asp Val Lys Lys Glu Ala Val Lys Asn
            100                 105                 110
Thr Leu Glu Arg Ala Leu Ser Phe Tyr Ser Ala Val Gln Thr Ser Asp
        115                 120                 125
Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro Met Phe Leu Leu Pro Gly
    130                 135                 140
Leu Val Ile Ala Leu Tyr Val Thr Gly Val Leu Asn Ser Val Leu Ser
145                 150                 155                 160
Lys His His Arg Gln Glu Met Cys Arg Tyr Ile Tyr Asn His Gln Asn
                165                 170                 175
Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly Ser Ser Thr Met Phe
            180                 185                 190
Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu Leu Gly Glu Ala Ala
        195                 200                 205
Asp Gly Gly Glu His Gly Ala Met Thr Lys Ala Arg Ser Trp Ile Leu
    210                 215                 220
Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser Trp Gly Lys Leu Trp Leu
225                 230                 235                 240
Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn Pro Leu Pro Pro
                245                 250                 255
Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro Phe His Pro Gly Arg Met
            260                 265                 270
Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly
        275                 280                 285
Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu Ser Leu Arg Lys
    290                 295                 300
Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile Asp Trp Asn Arg Ser Arg
305                 310                 315                 320
Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met Gln
                325                 330                 335
Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu Pro Leu Phe Ser
            340                 345                 350
Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met Lys Ile Ala Met
        355                 360                 365
Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile Cys Leu Gly
    370                 375                 380
Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro
385                 390                 395                 400
Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile Pro Asp Tyr Leu
                405                 410                 415
Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn Gly Ser Gln
            420                 425                 430
Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile Ser Thr Lys Leu
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        435                 440                 445
Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His His Phe Val Lys
    450                 455                 460
His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro Asn Val Trp Phe
465                 470                 475                 480
Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His Gly
                485                 490                 495
Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ser Leu Met
            500                 505                 510
Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro Leu Glu Lys Asn
        515                 520                 525
Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Glu Asn
    530                 535                 540
Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu Glu
545                 550                 555                 560
Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr Ser
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Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Ala Leu Phe Lys
            580                 585                 590
Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Ala Ala Ile Ala
        595                 600                 605
Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys Thr Asp Gly Ser Trp
    610                 615                 620
Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly Ile
625                 630                 635                 640
Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Val Ala Ile
                645                 650                 655
Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly Gly
            660                 665                 670
Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu
        675                 680                 685
Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp Val Met Met Ala
    690                 695                 700
Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala Pro Leu His Arg
705                 710                 715                 720
Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser Gly Asp Phe Pro
                725                 730                 735
Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr
            740                 745                 750
Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Ser
        755                 760                 765
His Arg Val Leu Asp Met Gly Ser Ala Ala Pro Gly Ser Gly Ser Gly
    770                 775                 780
Ser Gly Met Ile Lys His Ile Val Ser Pro Phe Arg Thr Asn Phe Val
785                 790                 795                 800
Gly Ile Ser Lys Ser Val Leu Ser Arg Met Ile His His Lys Val Thr
                805                 810                 815
Ile Ile Gly Ser Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Leu Ala
            820                 825                 830
Arg Ala Glu Met Lys Pro Thr Leu Tyr Glu Gly Met Met Ala Asn Gly
        835                 840                 845
Ile Ala Ala Gly Gly Gln Leu Thr Thr Thr Thr Asp Ile Glu Asn Phe
    850                 855                 860
Pro Gly Phe Pro Glu Ser Leu Ser Gly Ser Glu Leu Met Glu Arg Met
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865 870 875 880
Arg Lys Gln Ser Ala Lys Phe Gly Thr Asn Ile Ile Ile Glu Thr Val
885 890 895
Ser Lys Val Asp Leu Ser Ser Lys Pro Phe Arg Leu Trp Thr Glu Phe
900 905 910
Asn Glu Asp Ala Glu Pro Val Thr Thr Asp Ala Ile Ile Leu Ala Thr
915 920 925
Gly Ala Ser Ala Lys Arg Met His Leu Pro Gly Glu Glu Thr Tyr Trp
930 935 940
Gln Gln Gly Ile Ser Ala Cys Ala Val Cys Asp Gly Ala Val Pro Ile
945 950 955 960
Phe Arg Asn Lys Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Cys
965 970 975
Glu Glu Ala Glu Phe Leu Thr Lys Tyr Ala Ser Lys Val Tyr Ile Leu
980 985 990
Val Arg Lys Asp His Phe Arg Ala Ser Val Ile Met Gln Arg Arg Ile
995 1000 1005
Glu Lys Asn Pro Asn Ile Ile Val Leu Phe Asn Thr Val Ala Leu Glu
1010 1015 1020
Ala Lys Gly Asp Gly Lys Leu Leu Asn Met Leu Arg Ile Lys Asn Thr
1025 1030 1035 1040
Lys Ser Asn Val Glu Asn Asp Leu Glu Val Asn Gly Leu Phe Tyr Ala
1045 1050 1055
Ile Gly His Ser Pro Ala Thr Asp Ile Val Lys Gly Gln Val Asp Glu
1060 1065 1070
Glu Glu Thr Gly Tyr Ile Lys Thr Val Pro Gly Ser Ser Leu Thr Ser
1075 1080 1085
Val Pro Gly Phe Phe Ala Ala Gly Asp Val Gln Asp Ser Arg Tyr Arg
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Gln Ala Val Thr Ser Ala Gly Ser Gly Cys Ile Ala Ala Leu Asp Ala
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<400> 965
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<210> 966
<211> 2389
<212> DNA
<213> Artificial Sequence

<220>
<223> SS4b-D4 Full gene NT Seq

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gacgacgatg aagcaattgc tgtagctaac aattcagcct caaaatttga aaatgcaaga 180
aatcacttcc gtaataacag attccatagg aagcaatctt ccgacttatt cttggctata 240
caatgcgaga aagagatcat taggaatggt gctaagaatg aaggtactac caaagtgaaa 300

gaaggtgaag atgttaagaa agaagccgta aaaaatacac tagaaagagc attgtcgttc 360
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cttttaccag ggctagttat tgcgctatac gttacaggcg ttcttaacag tgtgttgtca 480
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ttaaggttac taggagaagc ggcagatggc ggtgagcatg gtgcgatgac caaagcaagg 660
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tccgtattag gagtgtatga atggtcggga aacaatccat tgccacccga attttggtta 780
cttccatata gccttccctt tcatccaggg agaatgtggt gtcattgtag aatggtttat 840
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atatgggctc taggtgaata ctcccatcgt gtcttggata tgggaagtgc agctcctgga 2340
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<211> 800
<212> PRT
<213> Artificial Sequence

<220>
<223> SS4b-D4 Full Gene AA seq

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Lys Trp Ile Lys Ser Ile Ser Asn His Leu Gly Arg Gln Val Trp Glu
            20                  25                  30
Phe Cys Ser Gly Glu Asn Glu Asn Asp Asp Asp Glu Ala Ile Ala Val
        35                  40                  45
Ala Asn Asn Ser Ala Ser Lys Phe Glu Asn Ala Arg Asn His Phe Arg
    50                  55                  60
Asn Asn Arg Phe His Arg Lys Gln Ser Ser Asp Leu Phe Leu Ala Ile

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65                  70                  75                  80
Gln Cys Glu Lys Glu Ile Ile Arg Asn Gly Ala Lys Asn Glu Gly Thr
                85                  90                  95
Thr Lys Val Lys Glu Gly Glu Asp Val Lys Lys Glu Ala Val Lys Asn
            100                 105                 110
Thr Leu Glu Arg Ala Leu Ser Phe Tyr Ser Ala Val Gln Thr Ser Asp
        115                 120                 125
Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro Met Phe Leu Leu Pro Gly
    130                 135                 140
Leu Val Ile Ala Leu Tyr Val Thr Gly Val Leu Asn Ser Val Leu Ser
145                 150                 155                 160
Lys His His Arg Gln Glu Met Cys Arg Tyr Ile Tyr Asn His Gln Asn
                165                 170                 175
Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly Ser Ser Thr Met Phe
            180                 185                 190
Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu Leu Gly Glu Ala Ala
        195                 200                 205
Asp Gly Gly Glu His Gly Ala Met Thr Lys Ala Arg Ser Trp Ile Leu
    210                 215                 220
Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser Trp Gly Lys Leu Trp Leu
225                 230                 235                 240
Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn Pro Leu Pro Pro
                245                 250                 255
Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro Phe His Pro Gly Arg Met
            260                 265                 270
Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly
        275                 280                 285
Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu Ser Leu Arg Lys
    290                 295                 300
Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile Asp Trp Asn Arg Ser Arg
305                 310                 315                 320
Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met Gln
                325                 330                 335
Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu Pro Leu Phe Ser
            340                 345                 350
Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met Lys Ile Ala Met
        355                 360                 365
Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile Cys Leu Gly
    370                 375                 380
Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro
385                 390                 395                 400
Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile Pro Asp Tyr Leu
                405                 410                 415
Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn Gly Ser Gln
            420                 425                 430
Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile Ser Thr Lys Leu
        435                 440                 445
Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His His Phe Val Lys
    450                 455                 460
His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro Asn Val Trp Phe
465                 470                 475                 480
Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His Gly
                485                 490                 495
Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ser Leu Met
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            500                 505                 510
Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro Leu Glu Lys Asn
        515                 520                 525
Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Glu Asn
    530                 535                 540
Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu Glu
545                 550                 555                 560
Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr Ser
                565                 570                 575
Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Ala Leu Phe Lys
            580                 585                 590
Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Ala Ala Ile Ala
        595                 600                 605
Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys Thr Asp Gly Ser Trp
    610                 615                 620
Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly Ile
625                 630                 635                 640
Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Val Ala Ile
                645                 650                 655
Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly Gly
            660                 665                 670
Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu
        675                 680                 685
Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp Val Met Met Ala
    690                 695                 700
Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala Pro Leu His Arg
705                 710                 715                 720
Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser Gly Asp Phe Pro
                725                 730                 735
Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr
            740                 745                 750
Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Ser
        755                 760                 765
His Arg Val Leu Asp Met Gly Ser Ala Ala Pro Gly Ser Gly Ser Gly
    770                 775                 780
Ser Gly Met Ala Val Gln Asn His Ile Leu Pro Leu Thr Arg Val Met
785                 790                 795                 800


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

<220>
<223> SS4b-D4 Fusion AA seq

<400> 968
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<210> 969
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<400> 969
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<210> 970
<211> 2398
<212> DNA
<213> Artificial Sequence

<220>
<223> SS4c-C4a Full gene NT Seq

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gacgacgatg aagcaattgc tgtagctaac aattcagcct caaaatttga aaatgcaaga 180
aatcacttcc gtaataacag attccatagg aagcaatctt ccgacttatt cttggctata 240
caatgcgaga aagagatcat taggaatggt gctaagaatg aaggtactac caaagtgaaa 300
gaaggtgaag atgttaagaa agaagccgta aaaaatacac tagaaagagc attgtcgttc 360
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catttcgtca agcatagtca gattcaagag gattgtccag gtgatccaaa cgtatggttc 1440
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atatgggctc taggtgaata ctcccatcgt gtcttggata tgggaagtgc agctcctgga 2340
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<211> 798
<212> PRT
<213> Artificial Sequence

<220>
<223> SS4c-C4a Full Gene AA seq

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

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Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile Cys Leu Gly
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Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro
385                 390                 395                 400
Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile Pro Asp Tyr Leu
                405                 410                 415
Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn Gly Ser Gln
            420                 425                 430
Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile Ser Thr Lys Leu
        435                 440                 445
Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His His Phe Val Lys
    450                 455                 460
His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro Asn Val Trp Phe
465                 470                 475                 480
Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His Gly
                485                 490                 495
Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ser Leu Met
            500                 505                 510
Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro Leu Glu Lys Asn
        515                 520                 525
Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Glu Asn
    530                 535                 540
Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu Glu
545                 550                 555                 560
Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr Ser
                565                 570                 575
Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Ala Leu Phe Lys
            580                 585                 590
Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Ala Ala Ile Ala
        595                 600                 605
Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys Thr Asp Gly Ser Trp
    610                 615                 620
Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly Ile
625                 630                 635                 640
Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Val Ala Ile
                645                 650                 655
Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly Gly
            660                 665                 670
Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu
        675                 680                 685
Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp Val Met Met Ala
    690                 695                 700
Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala Pro Leu His Arg
705                 710                 715                 720
Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser Gly Asp Phe Pro
                725                 730                 735
Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr
            740                 745                 750
Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Ser
        755                 760                 765
His Arg Val Leu Asp Met Gly Ser Ala Ala Pro Gly Ser Gly Ser Gly
    770                 775                 780
Ser Gly Met Ser Ala Ser Thr His Ser Pro Glu Pro Cys Leu
785                 790                 795
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<212> PRT
<213> Artificial Sequence

<220>
<223> SS4c-C4a Fusion AA seq

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<210> 973

<400> 973
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<210> 974
<211> 3189
<212> DNA
<213> Artificial Sequence

<220>
<223> SS4c-C4b Full gene NT Seq

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gacgacgatg aagcaattgc tgtagctaac aattcagcct caaaatttga aaatgcaaga 180
aatcacttcc gtaataacag attccatagg aagcaatctt ccgacttatt cttggctata 240
caatgcgaga aagagatcat taggaatggt gctaagaatg aaggtactac caaagtgaaa 300
gaaggtgaag atgttaagaa agaagccgta aaaaatacac tagaaagagc attgtcgttc 360
tattctgctg tacagacctc tgacggtaat tgggcatcag acttgggagg acctatgttc 420
cttttaccag ggctagttat tgcgctatac gttacaggcg ttcttaacag tgtgttgtca 480
aaacatcaca ggcaagaaat gtgtcgttac atctataatc accaaaacga agatggaggg 540
tggggtttac atatagaagg ctcttctact atgtttgggt ctgcactgaa ttacgttgcg 600
ttaaggttac taggagaagc ggcagatggc ggtgagcatg gtgcgatgac caaagcaagg 660
tcctggatat tggaaagagg aggtgccaca gcaataactt cctggggcaa actttggctt 720
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gagcacgtaa acaaccctta cccaaccgtg caggaaaaaa gagaactgct cgcgaaaact 3060
ggtctaacta aacttcaaat ttccaattgg ttcattaatg ctaggagaag aaaaatattt 3120
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<212> PRT
<213> Artificial Sequence

<220>
<223> SS4c-C4b Full Gene AA seq

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

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        115                 120                 125
Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro Met Phe Leu Leu Pro Gly
    130                 135                 140
Leu Val Ile Ala Leu Tyr Val Thr Gly Val Leu Asn Ser Val Leu Ser
145                 150                 155                 160
Lys His His Arg Gln Glu Met Cys Arg Tyr Ile Tyr Asn His Gln Asn
                165                 170                 175
Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly Ser Ser Thr Met Phe
            180                 185                 190
Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu Leu Gly Glu Ala Ala
        195                 200                 205
Asp Gly Gly Glu His Gly Ala Met Thr Lys Ala Arg Ser Trp Ile Leu
    210                 215                 220
Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser Trp Gly Lys Leu Trp Leu
225                 230                 235                 240
Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn Pro Leu Pro Pro
                245                 250                 255
Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro Phe His Pro Gly Arg Met
            260                 265                 270
Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly
        275                 280                 285
Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu Ser Leu Arg Lys
    290                 295                 300
Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile Asp Trp Asn Arg Ser Arg
305                 310                 315                 320
Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met Gln
                325                 330                 335
Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu Pro Leu Phe Ser
            340                 345                 350
Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met Lys Ile Ala Met
        355                 360                 365
Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile Cys Leu Gly
    370                 375                 380
Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro
385                 390                 395                 400
Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile Pro Asp Tyr Leu
                405                 410                 415
Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn Gly Ser Gln
            420                 425                 430
Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile Ser Thr Lys Leu
        435                 440                 445
Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His His Phe Val Lys
    450                 455                 460
His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro Asn Val Trp Phe
465                 470                 475                 480
Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His Gly
                485                 490                 495
Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ser Leu Met
            500                 505                 510
Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro Leu Glu Lys Asn
        515                 520                 525
Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Glu Asn
    530                 535                 540
Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu Glu
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Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr Ser
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Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Ala Leu Phe Lys
            580                 585                 590
Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Ala Ala Ile Ala
        595                 600                 605
Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys Thr Asp Gly Ser Trp
    610                 615                 620
Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly Ile
625                 630                 635                 640
Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Val Ala Ile
                645                 650                 655
Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly Gly
            660                 665                 670
Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu
        675                 680                 685
Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp Val Met Met Ala
    690                 695                 700
Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala Pro Leu His Arg
705                 710                 715                 720
Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser Gly Asp Phe Pro
                725                 730                 735
Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr
            740                 745                 750
Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Ser
        755                 760                 765
His Arg Val Leu Asp Met Gly Ser Ala Ala Pro Gly Ser Gly Ser Gly
    770                 775                 780
Ser Gly Met Gly Thr Ser Ile Val Asn Leu Asn Gln Lys Ile Glu Leu
785                 790                 795                 800
Pro Pro Ile Gln Val Leu Phe Glu Ser Leu Asn Arg Glu Asn Glu Thr
                805                 810                 815
Lys Pro His Phe Glu Glu Arg Arg Leu Tyr Gln Pro Asn Pro Ser Phe
            820                 825                 830
Val Pro Arg Thr Asn Ile Ala Val Gly Ser Pro Val Asn Pro Val Pro
        835                 840                 845
Val Ser Ser Pro Val Phe Phe Ile Gly Pro Ser Pro Gln Arg Ser Ile
    850                 855                 860
Gln Asn His Asn Ala Ile Met Thr Gln Asn Ile Arg Gln Tyr Pro Val
865                 870                 875                 880
Ile Tyr Asn Asn Asn Arg Glu Val Ile Ser Thr Gly Glu Arg Asn Tyr
                885                 890                 895
Ile Ile Thr Val Gly Gly Pro Pro Val Thr Ser Ser Gln Pro Glu Tyr
            900                 905                 910
Glu His Ile Ser Thr Pro Asn Phe Tyr Gln Glu Gln Arg Leu Ala Gln
        915                 920                 925
Pro His Pro Val Asn Glu Ser Met Met Ile Gly Gly Tyr Thr Asn Pro
    930                 935                 940
Gln Pro Ile Ser Ile Ser Arg Gly Lys Met Leu Ser Gly Asn Ile Ser
945                 950                 955                 960
Thr Asn Ser Val Arg Gly Ser Asn Asn Gly Tyr Ser Ala Lys Glu Lys
                965                 970                 975
Lys His Lys Ala His Gly Lys Arg Ser Asn Leu Pro Lys Ala Thr Val
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            980                 985                 990
Ser Ile Leu Asn Lys Trp Leu His Glu His Val Asn Asn Pro Tyr Pro
        995                 1000                1005
Thr Val Gln Glu Lys Arg Glu Leu Leu Ala Lys Thr Gly Leu Thr Lys
    1010                1015                1020
Leu Gln Ile Ser Asn Trp Phe Ile Asn Ala Arg Arg Arg Lys Ile Phe
1025                1030                1035                1040
Ser Gly Gln Asn Asp Ala Asn Asn Phe Arg Arg Lys Phe Ser Ser Ser
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<400> 976
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<210> 977

<400> 977
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<210> 978
<211> 2386
<212> DNA
<213> Artificial Sequence

<220>
<223> SS4e-B2 Full gene NT Seq

<400> 978
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<211> 794
<212> PRT
<213> Artificial Sequence

<220>
<223> SS4e-B2 Full Gene AA seq

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

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Asp Gly Gly Glu His Gly Ala Met Thr Lys Ala Arg Ser Trp Ile Leu
    210                 215                 220
Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser Trp Gly Lys Leu Trp Leu
225                 230                 235                 240
Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn Pro Leu Pro Pro
                245                 250                 255
Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro Phe His Pro Gly Arg Met
            260                 265                 270
Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu Tyr Gly
        275                 280                 285
Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu Ser Leu Arg Lys
    290                 295                 300
Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile Asp Trp Asn Arg Ser Arg
305                 310                 315                 320
Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys Met Gln
                325                 330                 335
Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu Pro Leu Phe Ser
            340                 345                 350
Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met Lys Ile Ala Met
        355                 360                 365
Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile Cys Leu Gly
    370                 375                 380
Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu Asp Pro
385                 390                 395                 400
Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile Pro Asp Tyr Leu
                405                 410                 415
Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn Gly Ser Gln
            420                 425                 430
Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile Ser Thr Lys Leu
        435                 440                 445
Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His His Phe Val Lys
    450                 455                 460
His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro Asn Val Trp Phe
465                 470                 475                 480
Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp His Gly
                485                 490                 495
Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ser Leu Met
            500                 505                 510
Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro Leu Glu Lys Asn
        515                 520                 525
Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn Glu Asn
    530                 535                 540
Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp Leu Glu
545                 550                 555                 560
Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp Tyr Ser
                565                 570                 575
Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Ala Leu Phe Lys
            580                 585                 590
Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Ala Ala Ile Ala
        595                 600                 605
Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys Thr Asp Gly Ser Trp
    610                 615                 620
Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe Gly Ile
625                 630                 635                 640
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Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Val Ala Ile
                645                 650                 655
Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu Pro Gly Gly Gly
            660                 665                 670
Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr Asn Leu
        675                 680                 685
Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp Val Met Met Ala
    690                 695                 700
Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala Pro Leu His Arg
705                 710                 715                 720
Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser Gly Asp Phe Pro
                725                 730                 735
Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile Thr Tyr
            740                 745                 750
Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu Tyr Ser
        755                 760                 765
His Arg Val Leu Asp Met Gly Ser Ala Ala Pro Gly Ser Gly Ser Gly
    770                 775                 780
Ser Gly Met Asp Gln Pro Arg Thr Ile Val
785                 790
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<210> 980
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> SS4e-B2 Fusion AA seq

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Met Asp Gln Pro Arg Thr Ile
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<210> 981

<400> 981
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<210> 982
<211> 2391
<212> DNA
<213> Artificial Sequence

<220>
<223> SS5a-E8 Full gene NT Seq

<400> 982
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attaaaagca ttagtaacca tttgggcaga caagtctggg agttttgctc tggtgaaaat 180
gaaaacgacg acgatgaagc aattgctgta gctaacaatt cagcctcaaa atttgaaaat 240
gcaagaaatc acttccgtaa taacagattc cataggaagc aatcttccga cttattcttg 300
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gctatacaat gcgagaaaga gatcattagg aatggtgcta agaatgaagg tactaccaaa 360
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tcgttctatt ctgctgtaca gacctctgac ggtaattggg catcagactt gggaggacct 480
atgttccttt taccagggct agttattgcg ctatacgtta caggcgttct taacagtgtg 540
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gttgcgttaa ggttactagg agaagcggca gatggcggtg agcatggtgc gatgaccaaa 720
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catagagctg ccagattgct aatcaatagt caattggagt caggtgactt tccacaacaa 2280
gaaatcatgg gtgtgtttaa taagaactgt atgataacat atgccgcata cagaaacata 2340
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<211> 796
<212> PRT
<213> Artificial Sequence

<220>
<223> SS5a-E8 Full Gene AA seq

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            20                  25                  30
Val Gly Glu Lys Glu Glu Lys Trp Ile Lys Ser Ile Ser Asn His Leu
        35                  40                  45
Gly Arg Gln Val Trp Glu Phe Cys Ser Gly Glu Asn Glu Asn Asp Asp
    50                  55                  60
Asp Glu Ala Ile Ala Val Ala Asn Asn Ser Ala Ser Lys Phe Glu Asn

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65                  70                  75                  80
Ala Arg Asn His Phe Arg Asn Asn Arg Phe His Arg Lys Gln Ser Ser
                85                  90                  95
Asp Leu Phe Leu Ala Ile Gln Cys Glu Lys Glu Ile Ile Arg Asn Gly
            100                 105                 110
Ala Lys Asn Glu Gly Thr Thr Lys Val Lys Glu Gly Glu Asp Val Lys
        115                 120                 125
Lys Glu Ala Val Lys Asn Thr Leu Glu Arg Ala Leu Ser Phe Tyr Ser
    130                 135                 140
Ala Val Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro
145                 150                 155                 160
Met Phe Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val Thr Gly Val
                165                 170                 175
Leu Asn Ser Val Leu Ser Lys His His Arg Gln Glu Met Cys Arg Tyr
            180                 185                 190
Ile Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile Glu
        195                 200                 205
Gly Ser Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg
    210                 215                 220
Leu Leu Gly Glu Ala Ala Asp Gly Gly Glu His Gly Ala Met Thr Lys
225                 230                 235                 240
Ala Arg Ser Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser
                245                 250                 255
Trp Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp Ser Gly
            260                 265                 270
Asn Asn Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro
        275                 280                 285
Phe His Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr Leu Pro
    290                 295                 300
Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr Pro Ile
305                 310                 315                 320
Val Leu Ser Leu Arg Lys Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile
                325                 330                 335
Asp Trp Asn Arg Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr
            340                 345                 350
Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His Val
        355                 360                 365
Tyr Glu Pro Leu Phe Ser Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys
    370                 375                 380
Ala Met Lys Ile Ala Met Glu His Ile His Tyr Glu Asp Glu Asn Ser
385                 390                 395                 400
Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu Cys
                405                 410                 415
Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Phe His Leu Gln
            420                 425                 430
Arg Ile Pro Asp Tyr Leu Trp Leu Ala Glu Asp Gly Met Arg Met Gln
        435                 440                 445
Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala
    450                 455                 460
Ile Ile Ser Thr Lys Leu Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys
465                 470                 475                 480
Ala His His Phe Val Lys His Ser Gln Ile Gln Glu Asp Cys Pro Gly
                485                 490                 495
Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp Pro Phe
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            500                 505                 510
Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly
        515                 520                 525
Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Lys Ile Val Gly
    530                 535                 540
Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val Leu Leu
545                 550                 555                 560
Ser Leu Gln Asn Glu Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg
                565                 570                 575
Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp
            580                 585                 590
Ile Val Ile Asp Tyr Ser Tyr Val Glu Cys Thr Ser Ala Thr Met Glu
        595                 600                 605
Ala Leu Ala Leu Phe Lys Lys Leu His Pro Gly His Arg Thr Lys Glu
    610                 615                 620
Ile Asp Ala Ala Ile Ala Lys Ala Ala Asn Phe Leu Glu Asn Met Gln
625                 630                 635                 640
Lys Thr Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr
                645                 650                 655
Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr
            660                 665                 670
Asn Asn Cys Val Ala Ile Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys
        675                 680                 685
Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn
    690                 695                 700
Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val Asn Thr
705                 710                 715                 720
Ala Trp Val Met Met Ala Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp
                725                 730                 735
Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu
            740                 745                 750
Glu Ser Gly Asp Phe Pro Gln Gln Glu Ile Met Gly Val Phe Asn Lys
        755                 760                 765
Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp
    770                 775                 780
Ala Leu Gly Glu Tyr Ser His Arg Val Leu Asp Met
785                 790                 795


<210> 984
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> SS5a-E8 Fusion AA seq

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Met Thr Thr Asp Asn Ala Ala Ala Tyr Ser
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<210> 985
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<400> 985
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<210> 986
<211> 2397
<212> DNA
<213> Artificial Sequence

<220>
<223> SS5d-E7 Full gene NT Seq

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agtggttcag gaatgtggag actgaaagta ggcaaagaat ctgttggcga aaaggaagaa 120
aagtggatta aaagcattag taaccatttg ggcagacaag tctgggagtt ttgctctggt 180
gaaaatgaaa acgacgacga tgaagcaatt gctgtagcta acaattcagc ctcaaaattt 240
gaaaatgcaa gaaatcactt ccgtaataac agattccata ggaagcaatc ttccgactta 300
ttcttggcta tacaatgcga gaaagagatc attaggaatg gtgctaagaa tgaaggtact 360
accaaagtga aagaaggtga agatgttaag aaagaagccg taaaaaatac actagaaaga 420
gcattgtcgt tctattctgc tgtacagacc tctgacggta attgggcatc agacttggga 480
ggacctatgt tccttttacc agggctagtt attgcgctat acgttacagg cgttcttaac 540
agtgtgttgt caaaacatca caggcaagaa atgtgtcgtt acatctataa tcaccaaaac 600
gaagatggag ggtggggttt acatatagaa ggctcttcta ctatgtttgg gtctgcactg 660
aattacgttg cgttaaggtt actaggagaa gcggcagatg gcggtgagca tggtgcgatg 720
accaaagcaa ggtcctggat attggaaaga ggaggtgcca cagcaataac ttcctggggc 780
aaactttggc tttccgtatt aggagtgtat gaatggtcgg gaaacaatcc attgccaccc 840
gaattttggt tacttccata tagccttccc tttcatccag ggagaatgtg gtgtcattgt 900
agaatggttt atctgccaat gtcgtatctt tatggtaaga gatttgttgg tccaatcact 960
ccaatagttt tatcgttgag aaaagagtta tataccattc cgtaccacga gattgattgg 1020
aatagatcca gaaacacgtg tgctaaggag gacttatatt accctcaccc taagatgcaa 1080
gatatcctat ggggcagtat ctaccatgtc tacgaaccgc tattttcagg ttggccaggt 1140
aagagattga gggaaaaggc catgaaaatt gcaatggaac atatccatta cgaagatgag 1200
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gcattcagca tacaagcgat aatctcaacg aaattgattg atacgtttgg tccgacatta 1440
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aacgtatggt tcagacacat tcataaagga gcttggcctt ttagcactag agatcatggt 1560
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caacaagaaa tcatgggtgt gtttaataag aactgtatga taacatatgc cgcatacaga 2340
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<211> 798
<212> PRT
<213> Artificial Sequence

<220>
<223> SS5d-E7 Full Gene AA seq

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

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His Val Tyr Glu Pro Leu Phe Ser Gly Trp Pro Gly Lys Arg Leu Arg
    370                 375                 380
Glu Lys Ala Met Lys Ile Ala Met Glu His Ile His Tyr Glu Asp Glu
385                 390                 395                 400
Asn Ser Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met
                405                 410                 415
Leu Cys Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Phe His
            420                 425                 430
Leu Gln Arg Ile Pro Asp Tyr Leu Trp Leu Ala Glu Asp Gly Met Arg
        435                 440                 445
Met Gln Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile
    450                 455                 460
Gln Ala Ile Ile Ser Thr Lys Leu Ile Asp Thr Phe Gly Pro Thr Leu
465                 470                 475                 480
Arg Lys Ala His His Phe Val Lys His Ser Gln Ile Gln Glu Asp Cys
                485                 490                 495
Pro Gly Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp
            500                 505                 510
Pro Phe Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala
        515                 520                 525
Glu Gly Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Lys Ile
    530                 535                 540
Val Gly Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val
545                 550                 555                 560
Leu Leu Ser Leu Gln Asn Glu Asn Gly Gly Phe Ala Ser Tyr Glu Leu
                565                 570                 575
Thr Arg Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe
            580                 585                 590
Gly Asp Ile Val Ile Asp Tyr Ser Tyr Val Glu Cys Thr Ser Ala Thr
        595                 600                 605
Met Glu Ala Leu Ala Leu Phe Lys Lys Leu His Pro Gly His Arg Thr
    610                 615                 620
Lys Glu Ile Asp Ala Ala Ile Ala Lys Ala Ala Asn Phe Leu Glu Asn
625                 630                 635                 640
Met Gln Lys Thr Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe
                645                 650                 655
Thr Tyr Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg
            660                 665                 670
Thr Tyr Asn Asn Cys Val Ala Ile Arg Lys Ala Cys Asn Phe Leu Leu
        675                 680                 685
Ser Lys Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys
    690                 695                 700
Gln Asn Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val
705                 710                 715                 720
Asn Thr Ala Trp Val Met Met Ala Leu Ile Glu Ala Gly Gln Gly Glu
                725                 730                 735
Arg Asp Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu Ile Asn Ser
            740                 745                 750
Gln Leu Glu Ser Gly Asp Phe Pro Gln Gln Glu Ile Met Gly Val Phe
        755                 760                 765
Asn Lys Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro
    770                 775                 780
Ile Trp Ala Leu Gly Glu Tyr Ser His Arg Val Leu Asp Met
785                 790                 795
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<210> 988
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> SS5d-E7 Fusion AA seq

<400> 988
Met Ala Leu Gly Asn Glu Ile Ala Asn Leu Gln Glu
 1               5                  10


<210> 989

<400> 989
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<210> 990
<211> 2427
<212> DNA
<213> Artificial Sequence

<220>
<223> SS5d-G5 Full gene NT Seq

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gagagtggaa gtgcagctcc tggaagtgga agtggttcag gaatgtggag actgaaagta 120
ggcaaagaat ctgttggcga aaaggaagaa aagtggatta aaagcattag taaccatttg 180
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gctgtagcta acaattcagc ctcaaaattt gaaaatgcaa gaaatcactt ccgtaataac 300
agattccata ggaagcaatc ttccgactta ttcttggcta tacaatgcga gaaagagatc 360
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gaagcaggac aaggggaaag agatccagct ccgttgcata gagctgccag attgctaatc 2280
aatagtcaat tggagtcagg tgactttcca caacaagaaa tcatgggtgt gtttaataag 2340
aactgtatga taacatatgc cgcatacaga aacatattcc ctatatgggc tctaggtgaa 2400
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<210> 991
<211> 808
<212> PRT
<213> Artificial Sequence

<220>
<223> SS5d-G5 Full Gene AA seq

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

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Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu Leu Gly Glu
225                 230                 235                 240
Ala Ala Asp Gly Gly Glu His Gly Ala Met Thr Lys Ala Arg Ser Trp
                245                 250                 255
Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser Trp Gly Lys Leu
            260                 265                 270
Trp Leu Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn Pro Leu
        275                 280                 285
Pro Pro Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro Phe His Pro Gly
    290                 295                 300
Arg Met Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser Tyr Leu
305                 310                 315                 320
Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu Ser Leu
                325                 330                 335
Arg Lys Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile Asp Trp Asn Arg
            340                 345                 350
Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His Pro Lys
        355                 360                 365
Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu Pro Leu
    370                 375                 380
Phe Ser Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met Lys Ile
385                 390                 395                 400
Ala Met Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile Cys
                405                 410                 415
Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val Glu
            420                 425                 430
Asp Pro Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile Pro Asp
        435                 440                 445
Tyr Leu Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn Gly
    450                 455                 460
Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile Ser Thr
465                 470                 475                 480
Lys Leu Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His His Phe
                485                 490                 495
Val Lys His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro Asn Val
            500                 505                 510
Trp Phe Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg Asp
        515                 520                 525
His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala Ser
    530                 535                 540
Leu Met Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro Leu Glu
545                 550                 555                 560
Lys Asn Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln Asn
                565                 570                 575
Glu Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro Trp
            580                 585                 590
Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile Asp
        595                 600                 605
Tyr Ser Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Ala Leu
    610                 615                 620
Phe Lys Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Ala Ala
625                 630                 635                 640
Ile Ala Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys Thr Asp Gly
                645                 650                 655
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Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp Phe
            660                 665                 670
Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys Val
        675                 680                 685
Ala Ile Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu Pro Gly
    690                 695                 700
Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr Thr
705                 710                 715                 720
Asn Leu Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp Val Met
                725                 730                 735
Met Ala Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala Pro Leu
            740                 745                 750
His Arg Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser Gly Asp
        755                 760                 765
Phe Pro Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met Ile
    770                 775                 780
Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Glu
785                 790                 795                 800
Tyr Ser His Arg Val Leu Asp Met
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<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> SS5d-G5 Fusion AA seq

<400> 992
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Pro Val Glu Glu Glu Ser
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<210> 993

<400> 993
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<210> 994
<211> 2397
<212> DNA
<213> Artificial Sequence

<220>
<223> SS5d-G7 Full gene NT Seq

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agtggttcag gaatgtggag actgaaagta ggcaaagaat ctgttggcga aaaggaagaa 120
aagtggatta aaagcattag taaccatttg ggcagacaag tctgggagtt ttgctctggt 180
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gaaaatgaaa acgacgacga tgaagcaatt gctgtagcta acaattcagc ctcaaaattt 240
gaaaatgcaa gaaatcactt ccgtaataac agattccata ggaagcaatc ttccgactta 300
ttcttggcta tacaatgcga gaaagagatc attaggaatg gtgctaagaa tgaaggtact 360
accaaagtga aagaaggtga agatgttaag aaagaagccg taaaaaatac actagaaaga 420
gcattgtcgt tctattctgc tgtacagacc tctgacggta attgggcatc agacttggga 480
ggacctatgt tccttttacc agggctagtt attgcgctat acgttacagg cgttcttaac 540
agtgtgttgt caaaacatca caggcaagaa atgtgtcgtt acatctataa tcaccaaaac 600
gaagatggag ggtggggttt acatatagaa ggctcttcta ctatgtttgg gtctgcactg 660
aattacgttg cgttaaggtt actaggagaa gcggcagatg gcggtgagca tggtgcgatg 720
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agaatggttt atctgccaat gtcgtatctt tatggtaaga gatttgttgg tccaatcact 960
ccaatagttt tatcgttgag aaaagagtta tataccattc cgtaccacga gattgattgg 1020
aatagatcca gaaacacgtg tgctaaggag gacttatatt accctcaccc taagatgcaa 1080
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aatactgcat gggtcatgat ggccttgatt gaagcaggac aaggggaaag agatccagct 2220
ccgttgcata gagctgccag attgctaatc aatagtcaat tggagtcagg tgactttcca 2280
caacaagaaa tcatgggtgt gtttaataag aactgtatga taacatatgc cgcatacaga 2340
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<211> 798
<212> PRT
<213> Artificial Sequence

<220>
<223> SS5d-G7 Full Gene AA seq

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Pro Gly Ser Gly Ser Gly Ser Gly Met Trp Arg Leu Lys Val Gly Lys
            20                  25                  30
Glu Ser Val Gly Glu Lys Glu Glu Lys Trp Ile Lys Ser Ile Ser Asn
        35                  40                  45
His Leu Gly Arg Gln Val Trp Glu Phe Cys Ser Gly Glu Asn Glu Asn

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    50                  55                  60
Asp Asp Asp Glu Ala Ile Ala Val Ala Asn Asn Ser Ala Ser Lys Phe
65                  70                  75                  80
Glu Asn Ala Arg Asn His Phe Arg Asn Asn Arg Phe His Arg Lys Gln
                85                  90                  95
Ser Ser Asp Leu Phe Leu Ala Ile Gln Cys Glu Lys Glu Ile Ile Arg
            100                 105                 110
Asn Gly Ala Lys Asn Glu Gly Thr Thr Lys Val Lys Glu Gly Glu Asp
        115                 120                 125
Val Lys Lys Glu Ala Val Lys Asn Thr Leu Glu Arg Ala Leu Ser Phe
    130                 135                 140
Tyr Ser Ala Val Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu Gly
145                 150                 155                 160
Gly Pro Met Phe Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val Thr
                165                 170                 175
Gly Val Leu Asn Ser Val Leu Ser Lys His His Arg Gln Glu Met Cys
            180                 185                 190
Arg Tyr Ile Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His
        195                 200                 205
Ile Glu Gly Ser Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala
    210                 215                 220
Leu Arg Leu Leu Gly Glu Ala Ala Asp Gly Gly Glu His Gly Ala Met
225                 230                 235                 240
Thr Lys Ala Arg Ser Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile
                245                 250                 255
Thr Ser Trp Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp
            260                 265                 270
Ser Gly Asn Asn Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr Ser
        275                 280                 285
Leu Pro Phe His Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr
    290                 295                 300
Leu Pro Met Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr
305                 310                 315                 320
Pro Ile Val Leu Ser Leu Arg Lys Glu Leu Tyr Thr Ile Pro Tyr His
                325                 330                 335
Glu Ile Asp Trp Asn Arg Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu
            340                 345                 350
Tyr Tyr Pro His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr
        355                 360                 365
His Val Tyr Glu Pro Leu Phe Ser Gly Trp Pro Gly Lys Arg Leu Arg
    370                 375                 380
Glu Lys Ala Met Lys Ile Ala Met Glu His Ile His Tyr Glu Asp Glu
385                 390                 395                 400
Asn Ser Arg Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met
                405                 410                 415
Leu Cys Cys Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Phe His
            420                 425                 430
Leu Gln Arg Ile Pro Asp Tyr Leu Trp Leu Ala Glu Asp Gly Met Arg
        435                 440                 445
Met Gln Gly Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile
    450                 455                 460
Gln Ala Ile Ile Ser Thr Lys Leu Ile Asp Thr Phe Gly Pro Thr Leu
465                 470                 475                 480
Arg Lys Ala His His Phe Val Lys His Ser Gln Ile Gln Glu Asp Cys
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                485                 490                 495
Pro Gly Asp Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp
            500                 505                 510
Pro Phe Ser Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala
        515                 520                 525
Glu Gly Leu Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Lys Ile
    530                 535                 540
Val Gly Glu Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val
545                 550                 555                 560
Leu Leu Ser Leu Gln Asn Glu Asn Gly Gly Phe Ala Ser Tyr Glu Leu
                565                 570                 575
Thr Arg Ser Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe
            580                 585                 590
Gly Asp Ile Val Ile Asp Tyr Ser Tyr Val Glu Cys Thr Ser Ala Thr
        595                 600                 605
Met Glu Ala Leu Ala Leu Phe Lys Lys Leu His Pro Gly His Arg Thr
    610                 615                 620
Lys Glu Ile Asp Ala Ala Ile Ala Lys Ala Ala Asn Phe Leu Glu Asn
625                 630                 635                 640
Met Gln Lys Thr Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe
                645                 650                 655
Thr Tyr Ala Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg
            660                 665                 670
Thr Tyr Asn Asn Cys Val Ala Ile Arg Lys Ala Cys Asn Phe Leu Leu
        675                 680                 685
Ser Lys Glu Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys
    690                 695                 700
Gln Asn Lys Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val
705                 710                 715                 720
Asn Thr Ala Trp Val Met Met Ala Leu Ile Glu Ala Gly Gln Gly Glu
                725                 730                 735
Arg Asp Pro Ala Pro Leu His Arg Ala Ala Arg Leu Leu Ile Asn Ser
            740                 745                 750
Gln Leu Glu Ser Gly Asp Phe Pro Gln Gln Glu Ile Met Gly Val Phe
        755                 760                 765
Asn Lys Asn Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro
    770                 775                 780
Ile Trp Ala Leu Gly Glu Tyr Ser His Arg Val Leu Asp Met
785                 790                 795


<210> 996
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> SS5d-G7 Fusion AA seq

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Met Ser Ser Ser Lys Lys Ile Thr Ser Val Lys Gln
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<210> 997

<400> 997
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<210> 998
<211> 2382
<212> DNA
<213> Artificial Sequence

<220>
<223> SS5e-C10 Full gene NT Seq

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attagtaacc atttgggcag acaagtctgg gagttttgct ctggtgaaaa tgaaaacgac 180
gacgatgaag caattgctgt agctaacaat tcagcctcaa aatttgaaaa tgcaagaaat 240
cacttccgta ataacagatt ccataggaag caatcttccg acttattctt ggctatacaa 300
tgcgagaaag agatcattag gaatggtgct aagaatgaag gtactaccaa agtgaaagaa 360
ggtgaagatg ttaagaaaga agccgtaaaa aatacactag aaagagcatt gtcgttctat 420
tctgctgtac agacctctga cggtaattgg gcatcagact tgggaggacc tatgttcctt 480
ttaccagggc tagttattgc gctatacgtt acaggcgttc ttaacagtgt gttgtcaaaa 540
catcacaggc aagaaatgtg tcgttacatc tataatcacc aaaacgaaga tggagggtgg 600
ggtttacata tagaaggctc ttctactatg tttgggtctg cactgaatta cgttgcgtta 660
aggttactag gagaagcggc agatggcggt gagcatggtg cgatgaccaa agcaaggtcc 720
tggatattgg aaagaggagg tgccacagca ataacttcct ggggcaaact ttggctttcc 780
gtattaggag tgtatgaatg gtcgggaaac aatccattgc cacccgaatt ttggttactt 840
ccatatagcc ttccctttca tccagggaga atgtggtgtc attgtagaat ggtttatctg 900
ccaatgtcgt atctttatgg taagagattt gttggtccaa tcactccaat agttttatcg 960
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tgccttggac ccgtgaacaa agttctaaat atgctgtgtt gctgggttga ggatccttac 1260
tctgatgctt tcaagtttca cttgcagaga attcctgact atctatggtt agctgaagat 1320
ggaatgagaa tgcagggtta taatggttca cagctttggg acactgcatt cagcatacaa 1380
gcgataatct caacgaaatt gattgatacg tttggtccga cattacgtaa agcacaccat 1440
ttcgtcaagc atagtcagat tcaagaggat tgtccaggtg atccaaacgt atggttcaga 1500
cacattcata aaggagcttg gccttttagc actagagatc atggttggct tatatcggat 1560
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ggtgtgttta ataagaactg tatgataaca tatgccgcat acagaaacat attccctata 2340
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<210> 999
<211> 793
<212> PRT
<213> Artificial Sequence

<220>
<223> SS5e-C10 Full Gene AA seq

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

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Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu Pro
        355                 360                 365
Leu Phe Ser Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met Lys
    370                 375                 380
Ile Ala Met Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr Ile
385                 390                 395                 400
Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp Val
                405                 410                 415
Glu Asp Pro Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile Pro
            420                 425                 430
Asp Tyr Leu Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr Asn
        435                 440                 445
Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile Ser
    450                 455                 460
Thr Lys Leu Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His His
465                 470                 475                 480
Phe Val Lys His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro Asn
                485                 490                 495
Val Trp Phe Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr Arg
            500                 505                 510
Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys Ala
        515                 520                 525
Ser Leu Met Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro Leu
    530                 535                 540
Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu Gln
545                 550                 555                 560
Asn Glu Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr Pro
                565                 570                 575
Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val Ile
            580                 585                 590
Asp Tyr Ser Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu Ala
        595                 600                 605
Leu Phe Lys Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp Ala
    610                 615                 620
Ala Ile Ala Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys Thr Asp
625                 630                 635                 640
Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly Trp
                645                 650                 655
Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn Cys
            660                 665                 670
Val Ala Ile Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu Pro
        675                 680                 685
Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val Tyr
    690                 695                 700
Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp Val
705                 710                 715                 720
Met Met Ala Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala Pro
                725                 730                 735
Leu His Arg Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser Gly
            740                 745                 750
Asp Phe Pro Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys Met
        755                 760                 765
Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly
    770                 775                 780
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Glu Tyr Ser His Arg Val Leu Asp Met
785 790

<210> 1000
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> SS5e-C10 Fusion AA seq

<400> 1000
Met Arg Gly Leu Thr Pro Lys
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<210> 1001

<400> 1001
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<210> 1002
<211> 2385
<212> DNA
<213> Artificial Sequence

<220>
<223> SS5e-G8 Full gene NT Seq

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agcattagta accatttggg cagacaagtc tgggagtttt gctctggtga aaatgaaaac 180
gacgacgatg aagcaattgc tgtagctaac aattcagcct caaaatttga aaatgcaaga 240
aatcacttcc gtaataacag attccatagg aagcaatctt ccgacttatt cttggctata 300
caatgcgaga aagagatcat taggaatggt gctaagaatg aaggtactac caaagtgaaa 360
gaaggtgaag atgttaagaa agaagccgta aaaaatacac tagaaagagc attgtcgttc 420
tattctgctg tacagacctc tgacggtaat tgggcatcag acttgggagg acctatgttc 480
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cttccatata gccttccctt tcatccaggg agaatgtggt gtcattgtag aatggtttat 900
ctgccaatgt cgtatcttta tggtaagaga tttgttggtc caatcactcc aatagtttta 960
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atatgccttg gacccgtgaa caaagttcta aatatgctgt gttgctgggt tgaggatcct 1260
tactctgatg ctttcaagtt tcacttgcag agaattcctg actatctatg gttagctgaa 1320
gatggaatga gaatgcaggg ttataatggt tcacagcttt gggacactgc attcagcata 1380

caagcgataa tctcaacgaa attgattgat acgtttggtc cgacattacg taaagcacac 1440
catttcgtca agcatagtca gattcaagag gattgtccag gtgatccaaa cgtatggttc 1500
agacacattc ataaaggagc ttggcctttt agcactagag atcatggttg gcttatatcg 1560
gattgcacag ctgagggatt gaaagcttca ctgatgttat ctaagttgcc ttctaaaatt 1620
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caaaacgaaa atggtgggtt cgcttcttat gaattaacta ggtcctatcc ctggttagag 1740
ttgattaacc ctgccgaaac atttggtgat atcgtaattg actacagtta tgtggaatgc 1800
actagtgcga cgatggaagc cttagccttg tttaagaagt tgcaccctgg gcatagaacc 1860
aaagaaattg atgccgctat tgctaaagcc gcaaattttc tggagaatat gcagaaaaca 1920
gacgggtctt ggtatggttg ttggggtgtc tgttttactt atgctggttg gtttggcatc 1980
aaaggcttag tagctgctgg tagaacatac aataattgtg ttgccattag aaaggcttgt 2040
aacttcctgt tgtcaaaaga attgcctggc ggtggttggg gcgaaagcta cctaagttgc 2100
caaaacaaag tttataccaa tctggaggga aacaagccac acttagtcaa tactgcatgg 2160
gtcatgatgg ccttgattga agcaggacaa ggggaaagag atccagctcc gttgcataga 2220
gctgccagat tgctaatcaa tagtcaattg gagtcaggtg actttccaca acaagaaatc 2280
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<210> 1003
<211> 794
<212> PRT
<213> Artificial Sequence

<220>
<223> SS5e-G8 Full Gene AA seq

<400> 1003
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Ser Gly Ser Gly Met Trp Arg Leu Lys Val Gly Lys Glu Ser Val Gly
            20                  25                  30
Glu Lys Glu Glu Lys Trp Ile Lys Ser Ile Ser Asn His Leu Gly Arg
        35                  40                  45
Gln Val Trp Glu Phe Cys Ser Gly Glu Asn Glu Asn Asp Asp Asp Glu
    50                  55                  60
Ala Ile Ala Val Ala Asn Asn Ser Ala Ser Lys Phe Glu Asn Ala Arg
65                  70                  75                  80
Asn His Phe Arg Asn Asn Arg Phe His Arg Lys Gln Ser Ser Asp Leu
                85                  90                  95
Phe Leu Ala Ile Gln Cys Glu Lys Glu Ile Ile Arg Asn Gly Ala Lys
            100                 105                 110
Asn Glu Gly Thr Thr Lys Val Lys Glu Gly Glu Asp Val Lys Lys Glu
        115                 120                 125
Ala Val Lys Asn Thr Leu Glu Arg Ala Leu Ser Phe Tyr Ser Ala Val
    130                 135                 140
Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro Met Phe
145                 150                 155                 160
Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val Thr Gly Val Leu Asn
                165                 170                 175
Ser Val Leu Ser Lys His His Arg Gln Glu Met Cys Arg Tyr Ile Tyr
            180                 185                 190
Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly Ser
        195                 200                 205

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Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu Leu
    210                 215                 220
Gly Glu Ala Ala Asp Gly Gly Glu His Gly Ala Met Thr Lys Ala Arg
225                 230                 235                 240
Ser Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser Trp Gly
                245                 250                 255
Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn
            260                 265                 270
Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro Phe His
        275                 280                 285
Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser
    290                 295                 300
Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu
305                 310                 315                 320
Ser Leu Arg Lys Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile Asp Trp
                325                 330                 335
Asn Arg Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His
            340                 345                 350
Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu
        355                 360                 365
Pro Leu Phe Ser Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met
    370                 375                 380
Lys Ile Ala Met Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr
385                 390                 395                 400
Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp
                405                 410                 415
Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile
            420                 425                 430
Pro Asp Tyr Leu Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr
        435                 440                 445
Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile
    450                 455                 460
Ser Thr Lys Leu Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His
465                 470                 475                 480
His Phe Val Lys His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro
                485                 490                 495
Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr
            500                 505                 510
Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys
        515                 520                 525
Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro
    530                 535                 540
Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu
545                 550                 555                 560
Gln Asn Glu Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr
                565                 570                 575
Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val
            580                 585                 590
Ile Asp Tyr Ser Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu
        595                 600                 605
Ala Leu Phe Lys Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp
    610                 615                 620
Ala Ala Ile Ala Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys Thr
625                 630                 635                 640
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Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly
                645                 650                 655
Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn
            660                 665                 670
Cys Val Ala Ile Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu
        675                 680                 685
Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val
    690                 695                 700
Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp
705                 710                 715                 720
Val Met Met Ala Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala
                725                 730                 735
Pro Leu His Arg Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser
            740                 745                 750
Gly Asp Phe Pro Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys
        755                 760                 765
Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu
    770                 775                 780
Gly Glu Tyr Ser His Arg Val Leu Asp Met
785                 790
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<210> 1004
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> SS5e-G8 Fusion AA seq

<400> 1004
Met Ala Asn Gln Ile Ala Asn Gln
 1               5

<210> 1005

<400> 1005
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<210> 1006
<211> 2385
<212> DNA
<213> Artificial Sequence

<220>
<223> SS5f-E11 Full gene NT Seq

<400> 1006
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agcattagta accatttggg cagacaagtc tgggagtttt gctctggtga aaatgaaaac 180
gacgacgatg aagcaattgc tgtagctaac aattcagcct caaaatttga aaatgcaaga 240

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aatcacttcc gtaataacag attccatagg aagcaatctt ccgacttatt cttggctata 300
caatgcgaga aagagatcat taggaatggt gctaagaatg aaggtactac caaagtgaaa 360
gaaggtgaag atgttaagaa agaagccgta aaaaatacac tagaaagagc attgtcgttc 420
tattctgctg tacagacctc tgacggtaat tgggcatcag acttgggagg acctatgttc 480
cttttaccag ggctagttat tgcgctatac gttacaggcg ttcttaacag tgtgttgtca 540
aaacatcaca ggcaagaaat gtgtcgttac atctataatc accaaaacga agatggaggg 600
tggggtttac atatagaagg ctcttctact atgtttgggt ctgcactgaa ttacgttgcg 660
ttaaggttac taggagaagc ggcagatggc ggtgagcatg gtgcgatgac caaagcaagg 720
tcctggatat tggaaagagg aggtgccaca gcaataactt cctggggcaa actttggctt 780
tccgtattag gagtgtatga atggtcggga aacaatccat tgccacccga attttggtta 840
cttccatata gccttccctt tcatccaggg agaatgtggt gtcattgtag aatggtttat 900
ctgccaatgt cgtatcttta tggtaagaga tttgttggtc caatcactcc aatagtttta 960
tcgttgagaa aagagttata taccattccg taccacgaga ttgattggaa tagatccaga 1020
aacacgtgtg ctaaggagga cttatattac cctcacccta agatgcaaga tatcctatgg 1080
ggcagtatct accatgtcta cgaaccgcta ttttcaggtt ggccaggtaa gagattgagg 1140
gaaaaggcca tgaaaattgc aatggaacat atccattacg aagatgagaa ttccaggtac 1200
atatgccttg gacccgtgaa caaagttcta aatatgctgt gttgctgggt tgaggatcct 1260
tactctgatg ctttcaagtt tcacttgcag agaattcctg actatctatg gttagctgaa 1320
gatggaatga gaatgcaggg ttataatggt tcacagcttt gggacactgc attcagcata 1380
caagcgataa tctcaacgaa attgattgat acgtttggtc cgacattacg taaagcacac 1440
catttcgtca agcatagtca gattcaagag gattgtccag gtgatccaaa cgtatggttc 1500
agacacattc ataaaggagc ttggcctttt agcactagag atcatggttg gcttatatcg 1560
gattgcacag ctgagggatt gaaagcttca ctgatgttat ctaagttgcc ttctaaaatt 1620
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caaaacgaaa atggtgggtt cgcttcttat gaattaacta ggtcctatcc ctggttagag 1740
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gacgggtctt ggtatggttg ttggggtgtc tgttttactt atgctggttg gtttggcatc 1980
aaaggcttag tagctgctgg tagaacatac aataattgtg ttgccattag aaaggcttgt 2040
aacttcctgt tgtcaaaaga attgcctggc ggtggttggg gcgaaagcta cctaagttgc 2100
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gtcatgatgg ccttgattga agcaggacaa ggggaaagag atccagctcc gttgcataga 2220
gctgccagat tgctaatcaa tagtcaattg gagtcaggtg actttccaca acaagaaatc 2280
atgggtgtgt ttaataagaa ctgtatgata acatatgccg catacagaaa catattccct 2340
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<210> 1007
<211> 794
<212> PRT
<213> Artificial Sequence

<220>
<223> SS5f-E11 Full Gene AA seq

<400> 1007

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Met Val Asp Ala Arg Gly Ser Asn Gly Ser Ala Ala Pro Gly Ser Gly
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Ser Gly Ser Gly Met Trp Arg Leu Lys Val Gly Lys Glu Ser Val Gly
            20                  25                  30
Glu Lys Glu Glu Lys Trp Ile Lys Ser Ile Ser Asn His Leu Gly Arg
        35                  40                  45
Gln Val Trp Glu Phe Cys Ser Gly Glu Asn Glu Asn Asp Asp Asp Glu
    50                  55                  60
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Ala Ile Ala Val Ala Asn Asn Ser Ala Ser Lys Phe Glu Asn Ala Arg
65                  70                  75                  80
Asn His Phe Arg Asn Asn Arg Phe His Arg Lys Gln Ser Ser Asp Leu
                85                  90                  95
Phe Leu Ala Ile Gln Cys Glu Lys Glu Ile Ile Arg Asn Gly Ala Lys
            100                 105                 110
Asn Glu Gly Thr Thr Lys Val Lys Glu Gly Glu Asp Val Lys Lys Glu
        115                 120                 125
Ala Val Lys Asn Thr Leu Glu Arg Ala Leu Ser Phe Tyr Ser Ala Val
    130                 135                 140
Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro Met Phe
145                 150                 155                 160
Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val Thr Gly Val Leu Asn
                165                 170                 175
Ser Val Leu Ser Lys His His Arg Gln Glu Met Cys Arg Tyr Ile Tyr
            180                 185                 190
Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly Ser
        195                 200                 205
Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu Leu
    210                 215                 220
Gly Glu Ala Ala Asp Gly Gly Glu His Gly Ala Met Thr Lys Ala Arg
225                 230                 235                 240
Ser Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser Trp Gly
                245                 250                 255
Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn Asn
            260                 265                 270
Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro Phe His
        275                 280                 285
Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr Leu Pro Met Ser
    290                 295                 300
Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val Leu
305                 310                 315                 320
Ser Leu Arg Lys Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile Asp Trp
                325                 330                 335
Asn Arg Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro His
            340                 345                 350
Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr Glu
        355                 360                 365
Pro Leu Phe Ser Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala Met
    370                 375                 380
Lys Ile Ala Met Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg Tyr
385                 390                 395                 400
Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys Trp
                405                 410                 415
Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg Ile
            420                 425                 430
Pro Asp Tyr Leu Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly Tyr
        435                 440                 445
Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile Ile
    450                 455                 460
Ser Thr Lys Leu Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala His
465                 470                 475                 480
His Phe Val Lys His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp Pro
                485                 490                 495
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Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp Pro Phe Ser Thr
            500                 505                 510
Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu Lys
        515                 520                 525
Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu Pro
    530                 535                 540
Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser Leu
545                 550                 555                 560
Gln Asn Glu Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser Tyr
                565                 570                 575
Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile Val
            580                 585                 590
Ile Asp Tyr Ser Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala Leu
        595                 600                 605
Ala Leu Phe Lys Lys Leu His Pro Gly His Arg Thr Lys Glu Ile Asp
    610                 615                 620
Ala Ala Ile Ala Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys Thr
625                 630                 635                 640
Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala Gly
                645                 650                 655
Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn Asn
            660                 665                 670
Cys Val Ala Ile Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu Leu
        675                 680                 685
Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys Val
    690                 695                 700
Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala Trp
705                 710                 715                 720
Val Met Met Ala Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro Ala
                725                 730                 735
Pro Leu His Arg Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu Ser
            740                 745                 750
Gly Asp Phe Pro Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn Cys
        755                 760                 765
Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu
    770                 775                 780
Gly Glu Tyr Ser His Arg Val Leu Asp Met
785                 790


<210> 1008
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> SS5f-E11 Fusion AA seq

<400> 1008
Met Val Asp Ala Arg Gly Ser Asn
 1               5


<210> 1009
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<400> 1009
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<210> 1010
<211> 2388
<212> DNA
<213> Artificial Sequence

<220>
<223> SS5f-F8 Full gene NT Seq

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ggaatgtgga gactgaaagt aggcaaagaa tctgttggcg aaaaggaaga aaagtggatt 120
aaaagcatta gtaaccattt gggcagacaa gtctgggagt tttgctctgg tgaaaatgaa 180
aacgacgacg atgaagcaat tgctgtagct aacaattcag cctcaaaatt tgaaaatgca 240
agaaatcact tccgtaataa cagattccat aggaagcaat cttccgactt attcttggct 300
atacaatgcg agaaagagat cattaggaat ggtgctaaga atgaaggtac taccaaagtg 360
aaagaaggtg aagatgttaa gaaagaagcc gtaaaaaata cactagaaag agcattgtcg 420
ttctattctg ctgtacagac ctctgacggt aattgggcat cagacttggg aggacctatg 480
ttccttttac cagggctagt tattgcgcta tacgttacag gcgttcttaa cagtgtgttg 540
tcaaaacatc acaggcaaga aatgtgtcgt tacatctata atcaccaaaa cgaagatgga 600
gggtggggtt tacatataga aggctcttct actatgtttg ggtctgcact gaattacgtt 660
gcgttaaggt tactaggaga agcggcagat ggcggtgagc atggtgcgat gaccaaagca 720
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ctttccgtat taggagtgta tgaatggtcg ggaaacaatc cattgccacc cgaattttgg 840
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tacatatgcc ttggacccgt gaacaaagtt ctaaatatgc tgtgttgctg ggttgaggat 1260
ccttactctg atgctttcaa gtttcacttg cagagaattc ctgactatct atggttagct 1320
gaagatggaa tgagaatgca gggttataat ggttcacagc tttgggacac tgcattcagc 1380
atacaagcga taatctcaac gaaattgatt gatacgtttg gtccgacatt acgtaaagca 1440
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atcatgggtg tgtttaataa gaactgtatg ataacatatg ccgcatacag aaacatattc 2340
cctatatggg ctctaggtga atactcccat cgtgtcttgg atatgtga 2388

<210> 1011
<211> 795
<212> PRT
<213> Artificial Sequence

<220>
<223> SS5f-F8 Full Gene AA seq

<400> 1011
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Gly Ser Gly Ser Gly Met Trp Arg Leu Lys Val Gly Lys Glu Ser Val
            20                  25                  30
Gly Glu Lys Glu Glu Lys Trp Ile Lys Ser Ile Ser Asn His Leu Gly
        35                  40                  45
Arg Gln Val Trp Glu Phe Cys Ser Gly Glu Asn Glu Asn Asp Asp Asp
    50                  55                  60
Glu Ala Ile Ala Val Ala Asn Asn Ser Ala Ser Lys Phe Glu Asn Ala
65                  70                  75                  80
Arg Asn His Phe Arg Asn Asn Arg Phe His Arg Lys Gln Ser Ser Asp
                85                  90                  95
Leu Phe Leu Ala Ile Gln Cys Glu Lys Glu Ile Ile Arg Asn Gly Ala
            100                 105                 110
Lys Asn Glu Gly Thr Thr Lys Val Lys Glu Gly Glu Asp Val Lys Lys
        115                 120                 125
Glu Ala Val Lys Asn Thr Leu Glu Arg Ala Leu Ser Phe Tyr Ser Ala
    130                 135                 140
Val Gln Thr Ser Asp Gly Asn Trp Ala Ser Asp Leu Gly Gly Pro Met
145                 150                 155                 160
Phe Leu Leu Pro Gly Leu Val Ile Ala Leu Tyr Val Thr Gly Val Leu
                165                 170                 175
Asn Ser Val Leu Ser Lys His His Arg Gln Glu Met Cys Arg Tyr Ile
            180                 185                 190
Tyr Asn His Gln Asn Glu Asp Gly Gly Trp Gly Leu His Ile Glu Gly
        195                 200                 205
Ser Ser Thr Met Phe Gly Ser Ala Leu Asn Tyr Val Ala Leu Arg Leu
    210                 215                 220
Leu Gly Glu Ala Ala Asp Gly Gly Glu His Gly Ala Met Thr Lys Ala
225                 230                 235                 240
Arg Ser Trp Ile Leu Glu Arg Gly Gly Ala Thr Ala Ile Thr Ser Trp
                245                 250                 255
Gly Lys Leu Trp Leu Ser Val Leu Gly Val Tyr Glu Trp Ser Gly Asn
            260                 265                 270
Asn Pro Leu Pro Pro Glu Phe Trp Leu Leu Pro Tyr Ser Leu Pro Phe
        275                 280                 285
His Pro Gly Arg Met Trp Cys His Cys Arg Met Val Tyr Leu Pro Met
    290                 295                 300
Ser Tyr Leu Tyr Gly Lys Arg Phe Val Gly Pro Ile Thr Pro Ile Val
305                 310                 315                 320
Leu Ser Leu Arg Lys Glu Leu Tyr Thr Ile Pro Tyr His Glu Ile Asp
                325                 330                 335
Trp Asn Arg Ser Arg Asn Thr Cys Ala Lys Glu Asp Leu Tyr Tyr Pro
            340                 345                 350
His Pro Lys Met Gln Asp Ile Leu Trp Gly Ser Ile Tyr His Val Tyr

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        355                 360                 365
Glu Pro Leu Phe Ser Gly Trp Pro Gly Lys Arg Leu Arg Glu Lys Ala
    370                 375                 380
Met Lys Ile Ala Met Glu His Ile His Tyr Glu Asp Glu Asn Ser Arg
385                 390                 395                 400
Tyr Ile Cys Leu Gly Pro Val Asn Lys Val Leu Asn Met Leu Cys Cys
                405                 410                 415
Trp Val Glu Asp Pro Tyr Ser Asp Ala Phe Lys Phe His Leu Gln Arg
            420                 425                 430
Ile Pro Asp Tyr Leu Trp Leu Ala Glu Asp Gly Met Arg Met Gln Gly
        435                 440                 445
Tyr Asn Gly Ser Gln Leu Trp Asp Thr Ala Phe Ser Ile Gln Ala Ile
    450                 455                 460
Ile Ser Thr Lys Leu Ile Asp Thr Phe Gly Pro Thr Leu Arg Lys Ala
465                 470                 475                 480
His His Phe Val Lys His Ser Gln Ile Gln Glu Asp Cys Pro Gly Asp
                485                 490                 495
Pro Asn Val Trp Phe Arg His Ile His Lys Gly Ala Trp Pro Phe Ser
            500                 505                 510
Thr Arg Asp His Gly Trp Leu Ile Ser Asp Cys Thr Ala Glu Gly Leu
        515                 520                 525
Lys Ala Ser Leu Met Leu Ser Lys Leu Pro Ser Lys Ile Val Gly Glu
    530                 535                 540
Pro Leu Glu Lys Asn Arg Leu Cys Asp Ala Val Asn Val Leu Leu Ser
545                 550                 555                 560
Leu Gln Asn Glu Asn Gly Gly Phe Ala Ser Tyr Glu Leu Thr Arg Ser
                565                 570                 575
Tyr Pro Trp Leu Glu Leu Ile Asn Pro Ala Glu Thr Phe Gly Asp Ile
            580                 585                 590
Val Ile Asp Tyr Ser Tyr Val Glu Cys Thr Ser Ala Thr Met Glu Ala
        595                 600                 605
Leu Ala Leu Phe Lys Lys Leu His Pro Gly His Arg Thr Lys Glu Ile
    610                 615                 620
Asp Ala Ala Ile Ala Lys Ala Ala Asn Phe Leu Glu Asn Met Gln Lys
625                 630                 635                 640
Thr Asp Gly Ser Trp Tyr Gly Cys Trp Gly Val Cys Phe Thr Tyr Ala
                645                 650                 655
Gly Trp Phe Gly Ile Lys Gly Leu Val Ala Ala Gly Arg Thr Tyr Asn
            660                 665                 670
Asn Cys Val Ala Ile Arg Lys Ala Cys Asn Phe Leu Leu Ser Lys Glu
        675                 680                 685
Leu Pro Gly Gly Gly Trp Gly Glu Ser Tyr Leu Ser Cys Gln Asn Lys
    690                 695                 700
Val Tyr Thr Asn Leu Glu Gly Asn Lys Pro His Leu Val Asn Thr Ala
705                 710                 715                 720
Trp Val Met Met Ala Leu Ile Glu Ala Gly Gln Gly Glu Arg Asp Pro
                725                 730                 735
Ala Pro Leu His Arg Ala Ala Arg Leu Leu Ile Asn Ser Gln Leu Glu
            740                 745                 750
Ser Gly Asp Phe Pro Gln Gln Glu Ile Met Gly Val Phe Asn Lys Asn
        755                 760                 765
Cys Met Ile Thr Tyr Ala Ala Tyr Arg Asn Ile Phe Pro Ile Trp Ala
    770                 775                 780
Leu Gly Glu Tyr Ser His Arg Val Leu Asp Met
```

785 790 795

<210> 1012
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> SS5f-F8 Fusion AA seq

<400> 1012
Met His Gly Lys Glu Leu Ala Gly Leu
1 5

<210> 1013
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> EXG1 YLR300W Saccharomyces cerevisiae

<400> 1013
Met Leu Ser Leu Lys Thr Leu Leu Cys Thr Leu Leu Thr Val Ser Ser
1 5 10 15
Val Leu Ala Thr Pro Val Pro Ala Arg Asp Pro Ser Ser Ile Gln Phe
20 25 30
Val His Glu Glu Asn Lys Lys Arg Tyr Tyr Asp Tyr Asp His Gly Ser
35 40 45
Leu Gly Glu Pro Ile Arg Gly Val Asn Ile Gly Gly Trp Leu Leu Leu
50 55 60
Glu Pro Tyr Ile Thr Pro Ser Leu Phe Glu Ala Phe Arg Thr Asn Asp
65 70 75 80
Asp Asn Asp Glu Gly Ile Pro Val Asp Glu Tyr His Phe Cys Gln Tyr
85 90 95
Leu Gly Lys Asp Leu Ala Lys Ser Arg Leu Gln Ser His Trp Ser Thr
100 105 110
Phe Tyr Gln Glu Gln Asp Phe Ala Asn Ile Ala Ser Gln Gly Phe Asn
115 120 125
Leu Val Arg Ile Pro Ile Gly Tyr Trp Ala Phe Gln Thr Leu Asp Asp
130 135 140
Asp Pro Tyr Val Ser Gly Leu Gln Glu Ser Tyr Leu Asp Gln Ala Ile
145 150 155 160
Gly Trp Ala Arg Asn Asn Ser Leu Lys Val Trp Val Asp Leu His Gly
165 170 175
Ala Ala Gly Ser Gln Asn Gly Phe Asp Asn Ser Gly Leu Arg Asp Ser
180 185 190
Tyr Lys Phe Leu Glu Asp Ser Asn Leu Ala Val Thr Thr Asn Val Leu
195 200 205
Asn Tyr Ile Leu Lys Lys Tyr Ser Ala Glu Glu Tyr Leu Asp Thr Val
210 215 220
Ile Gly Ile Glu Leu Ile Asn Glu Pro Leu Gly Pro Val Leu Asp Met

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

<210> 1014
<211> 421
<212> PRT
<213> Artificial Sequence

<220>
<223> EXG1 Yarrowia lipolytica

<400> 1014
Met Lys Leu Thr Lys Leu Val Ala Leu Ala Gly Ala Ala Leu Ala Ser
1 5 10 15
Pro Ile Gln Leu Val Pro Arg Glu Gly Ser Phe Leu Gly Phe Asn Tyr
20 25 30
Gly Ser Glu Lys Val His Gly Val Asn Leu Gly Gly Trp Phe Val Leu
35 40 45
Glu Pro Phe Ile Thr Pro Ser Leu Phe Glu Ala Phe Gly Asn Asn Asp
50 55 60
Ala Asn Val Pro Val Asp Glu Tyr His Tyr Thr Ala Trp Leu Gly Lys
65 70 75 80
Glu Glu Ala Glu Lys Arg Leu Thr Asp His Trp Asn Thr Trp Ile Thr
85 90 95
Glu Tyr Asp Ile Lys Ala Ile Ala Glu Asn Tyr Lys Leu Asn Leu Val
100 105 110
Arg Ile Pro Ile Gly Tyr Trp Ala Phe Ser Leu Leu Pro Asn Asp Pro
115 120 125

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

<210> 1015
<211> 631
<212> PRT
<213> Artificial Sequence

<220>
<223> Glugan 1, 4, alpha glucosidase

<400> 1015

```
Met Pro Arg Leu Ser Tyr Ala Leu Cys Ala Leu Ser Leu Gly His Ala
 1               5                  10                  15
Ala Ile Ala Ala Pro Gln Leu Ser Ala Arg Ala Thr Gly Ser Leu Asp
            20                  25                  30
Ser Trp Leu Gly Thr Glu Thr Thr Val Ala Leu Asn Gly Ile Leu Ala
```

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

```
465                 470                 475                 480
Ala Thr Gly Thr Tyr Ser Thr Ala Thr Ala Thr Ser Trp Pro Ser Thr
                485                 490                 495
Leu Thr Ser Gly Ser Pro Gly Ser Thr Thr Thr Val Gly Thr Thr Thr
            500                 505                 510
Ser Thr Thr Ser Gly Thr Ala Ala Glu Thr Ala Cys Ala Thr Pro Thr
        515                 520                 525
Ala Val Ala Val Thr Phe Asn Glu Ile Ala Thr Thr Thr Tyr Gly Glu
    530                 535                 540
Asn Val Tyr Ile Val Gly Ser Ile Ser Glu Leu Gly Asn Trp Asp Thr
545                 550                 555                 560
Ser Lys Ala Val Ala Leu Ser Ala Ser Lys Tyr Thr Ser Ser Asn Asn
                565                 570                 575
Leu Trp Tyr Val Ser Val Thr Leu Pro Ala Gly Thr Thr Phe Glu Tyr
            580                 585                 590
Lys Tyr Ile Arg Lys Glu Ser Asp Gly Ser Ile Val Trp Glu Ser Asp
        595                 600                 605
Pro Asn Arg Ser Tyr Thr Val Pro Ala Ala Cys Gly Val Ser Thr Ala
    610                 615                 620
Thr Glu Asn Asp Thr Trp Gln
625                 630
```

<210> 1016
<211> 378
<212> PRT
<213> Artificial Sequence

<220>
<223> polygalacturonase 1 [Aspergillus aculeatus]
CAE46193.1 GI:34366090

<400> 1016

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

```
                165                 170                 175
Leu Thr Leu Lys Asp Ile Thr Ile Asp Asn Ser Asp Gly Asp Asp Asn
            180                 185                 190
Gly Gly His Asn Thr Asp Ala Phe Asp Ile Gly Thr Ser Thr Tyr Val
        195                 200                 205
Thr Ile Ser Gly Ala Thr Val Tyr Asn Gln Asp Asp Cys Val Ala Val
    210                 215                 220
Asn Ser Gly Glu Asn Ile Tyr Phe Ser Gly Gly Tyr Cys Ser Gly Gly
225                 230                 235                 240
His Gly Leu Ser Ile Gly Ser Val Gly Gly Arg Ser Asp Asn Thr Val
                245                 250                 255
Lys Asn Val Thr Phe Val Asp Ser Thr Ile Ile Asn Ser Asp Asn Gly
            260                 265                 270
Val Arg Ile Lys Thr Asn Ile Asp Thr Thr Gly Ser Val Ser Asp Val
        275                 280                 285
Thr Tyr Lys Asp Ile Thr Leu Thr Ser Ile Ala Lys Tyr Gly Ile Val
    290                 295                 300
Val Gln Gln Asn Tyr Gly Asp Thr Ser Ser Thr Pro Thr Thr Gly Val
305                 310                 315                 320
Pro Ile Thr Asp Phe Val Leu Asp Asn Val His Gly Ser Val Val Ser
                325                 330                 335
Ser Gly Thr Asn Ile Leu Ile Ser Cys Gly Ser Gly Ser Cys Ser Asp
            340                 345                 350
Trp Thr Trp Thr Asp Val Ser Val Ser Gly Gly Lys Thr Ser Ser Lys
        355                 360                 365
Cys Thr Asn Val Pro Ser Gly Ala Ser Cys
    370                 375
```

<210> 1017
<211> 369
<212> PRT
<213> Artificial Sequence

<220>
<223> polygalacturonase 2 [Aspergillus aculeatus]
CAE46194.1 GI:34366092

<400> 1017

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

```
        115                 120                 125
Gly Lys Thr Lys Pro Lys Phe Met Tyr Val His Asp Val Glu Asp Ser
    130                 135                 140
Thr Ile Lys Gly Leu Gln Ile Lys Asn Thr Pro Val Gln Ala Ile Ser
145                 150                 155                 160
Val Gln Ala Thr Asn Val Tyr Leu Thr Asp Ile Thr Ile Asp Asn Ser
                165                 170                 175
Asp Gly Asp Asp Asn Gly Gly His Asn Thr Asp Gly Phe Asp Ile Ser
            180                 185                 190
Glu Ser Thr Gly Val Tyr Ile Ser Gly Ala Thr Val Lys Asn Gln Asp
        195                 200                 205
Asp Cys Ile Ala Ile Asn Ser Gly Glu Asn Ile Leu Phe Thr Gly Gly
    210                 215                 220
Thr Cys Ser Gly Gly His Gly Leu Ser Ile Gly Ser Val Gly Gly Arg
225                 230                 235                 240
Asp Asp Asn Thr Val Lys Asn Val Thr Ile Ser Asp Ser Thr Val Thr
                245                 250                 255
Asp Ser Ala Asn Gly Val Arg Ile Lys Thr Ile Tyr Gly Asp Thr Gly
            260                 265                 270
Asp Val Ser Glu Ile Thr Tyr Ser Asn Ile Gln Leu Ser Gly Ile Thr
        275                 280                 285
Asp Tyr Gly Ile Val Ile Glu Gln Asp Tyr Glu Asn Gly Ser Pro Thr
    290                 295                 300
Gly Thr Pro Ser Thr Gly Val Pro Ile Thr Asp Val Thr Val Asp Gly
305                 310                 315                 320
Val Thr Gly Ser Ile Glu Asp Asp Ala Val Gln Val Tyr Ile Leu Cys
                325                 330                 335
Gly Asp Gly Ser Cys Ser Asp Trp Thr Trp Ser Gly Val Asp Ile Thr
            340                 345                 350
Gly Gly Glu Thr Ser Ser Asp Cys Glu Asn Val Pro Ser Gly Ala Ser
        355                 360                 365
Cys
```

<210> 1018
<211> 384
<212> PRT
<213> Artificial Sequence

<220>
<223> polygalacturonase 3 [Aspergillus aculeatus]
CAE46195.1 GI:34366094

<400> 1018

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

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

<210> 1019
<211> 339
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Crystal Structure Of Polygalacturonase
From Aspergillus Aculeatus At Ph4.5 1IB4_A
GI:15988280

<400> 1019

```
Ala Thr Thr Cys Thr Phe Ser Gly Ser Asn Gly Ala Ser Ser Ala Ser
 1               5                  10                  15
```

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

<210> 1020
<211> 339
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain B, Crystal Structure Of Polygalacturonase
From Aspergillus Aculeatus At Ph4.5 1IB4_B
GI:15988281

<400> 1020
Ala Thr Thr Cys Thr Phe Ser Gly Ser Asn Gly Ala Ser Ser Ala Ser
 1               5                  10                  15
Lys Ser Lys Thr Ser Cys Ser Thr Ile Val Leu Ser Asn Val Ala Val
            20                  25                  30
Pro Ser Gly Thr Thr Leu Asp Leu Thr Lys Leu Asn Asp Gly Thr His
        35                  40                  45
Val Ile Phe Ser Gly Glu Thr Thr Phe Gly Tyr Lys Glu Trp Ser Gly
    50                  55                  60
Pro Leu Ile Ser Val Ser Gly Ser Asp Leu Thr Ile Thr Gly Ala Ser
65                  70                  75                  80
Gly His Ser Ile Asn Gly Asp Gly Ser Arg Trp Trp Asp Gly Glu Gly
                85                  90                  95
Gly Asn Gly Gly Lys Thr Lys Pro Lys Phe Phe Ala Ala His Ser Leu
            100                 105                 110
Thr Asn Ser Val Ile Ser Gly Leu Lys Ile Val Asn Ser Pro Val Gln
        115                 120                 125
Val Phe Ser Val Ala Gly Ser Asp Tyr Leu Thr Leu Lys Asp Ile Thr
    130                 135                 140
Ile Asp Asn Ser Asp Gly Asp Asp Asn Gly Gly His Asn Thr Asp Ala
145                 150                 155                 160
Phe Asp Ile Gly Thr Ser Thr Tyr Val Thr Ile Ser Gly Ala Thr Val
                165                 170                 175
Tyr Asn Gln Asp Asp Cys Val Ala Val Asn Ser Gly Glu Asn Ile Tyr
            180                 185                 190
Phe Ser Gly Gly Tyr Cys Ser Gly Gly His Gly Leu Ser Ile Gly Ser
        195                 200                 205
Val Gly Gly Arg Ser Asp Asn Thr Val Lys Asn Val Thr Phe Val Asp
    210                 215                 220
Ser Thr Ile Ile Asn Ser Asp Asn Gly Val Arg Ile Lys Thr Asn Ile
225                 230                 235                 240
Asp Thr Thr Gly Ser Val Ser Asp Val Thr Tyr Lys Asp Ile Thr Leu
                245                 250                 255
Thr Ser Ile Ala Lys Tyr Gly Ile Val Val Gln Gln Asn Tyr Gly Asp
            260                 265                 270
Thr Ser Ser Thr Pro Thr Thr Gly Val Pro Ile Thr Asp Phe Val Leu
        275                 280                 285
Asp Asn Val His Gly Ser Val Val Ser Ser Gly Thr Asn Ile Leu Ile
    290                 295                 300
Ser Cys Gly Ser Gly Ser Cys Ser Asp Trp Thr Trp Thr Asp Val Ser
305                 310                 315                 320
Val Ser Gly Gly Lys Thr Ser Ser Lys Cys Thr Asn Val Pro Ser Gly
                325                 330                 335
Ala Ser Cys

<210> 1021
<211> 339
<212> PRT
<213> Artificial Sequence

<220>
<223> Chain A, Polygalacturonase From Aspergillus

Aculeatus 1IA5_A GI:15988279

<400> 1021

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

<210> 1022
<211> 378
<212> PRT
<213> Artificial Sequence

<220>
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Ala Glu Glu Ile Ala Lys Arg Ala Thr Thr Cys Thr Phe Ser Gly Ser
        35                  40                  45
Asn Gly Ala Ser Ser Ala Ser Lys Ser Lys Thr Ser Cys Ser Thr Ile
    50                  55                  60
Val Leu Ser Asn Val Ala Val Pro Ser Gly Thr Thr Leu Asp Leu Thr
65                  70                  75                  80
Lys Leu Asn Asp Gly Thr His Val Ile Phe Ser Gly Glu Thr Thr Phe
                85                  90                  95
Gly Tyr Lys Glu Trp Ser Gly Pro Leu Ile Ser Val Ser Gly Ser Asp
            100                 105                 110
Leu Thr Ile Thr Gly Ala Ser Gly His Ser Ile Asn Gly Asp Gly Ser
        115                 120                 125
Arg Trp Trp Asp Gly Glu Gly Gly Asn Gly Gly Lys Thr Lys Pro Lys
    130                 135                 140
Phe Phe Ala Ala His Ser Leu Thr Asn Ser Val Ile Ser Gly Leu Lys
145                 150                 155                 160
Ile Val Asn Ser Pro Val Gln Val Phe Ser Val Ala Gly Ser Asp Tyr
                165                 170                 175
Leu Thr Leu Lys Asp Ile Thr Ile Asp Asn Ser Asp Gly Asp Asp Asn
            180                 185                 190
Gly Gly His Asn Thr Asp Ala Phe Asp Ile Gly Thr Ser Thr Tyr Val
        195                 200                 205
Thr Ile Ser Gly Ala Thr Val Tyr Asn Gln Asp Asp Cys Val Ala Val
    210                 215                 220
Asn Ser Gly Glu Asn Ile Tyr Phe Ser Gly Gly Tyr Cys Ser Gly Gly
225                 230                 235                 240
His Gly Leu Ser Ile Gly Ser Val Gly Gly Arg Ser Asp Asn Thr Val
                245                 250                 255
Lys Asn Val Thr Phe Val Asp Ser Thr Ile Ile Asn Ser Asp Asn Gly
            260                 265                 270
Val Arg Ile Lys Thr Asn Ile Asp Thr Thr Gly Ser Val Ser Asp Val
        275                 280                 285
Thr Tyr Lys Asp Ile Thr Leu Thr Ser Ile Ala Lys Tyr Gly Ile Val
    290                 295                 300
Val Gln Gln Asn Tyr Gly Asp Thr Ser Ser Thr Pro Thr Thr Gly Val
305                 310                 315                 320
Pro Ile Thr Asp Phe Val Leu Asp Asn Val His Gly Ser Val Val Ser
                325                 330                 335
Ser Gly Thr Asn Ile Leu Ile Ser Cys Gly Ser Gly Ser Cys Ser Asp
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Cys Thr Asn Val Pro Ser Gly Ala Ser Cys
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<220>
<223> EXG2 YDR261C Saccharomyces cerevisiae

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

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Asn Ile Ile Asn Tyr Gly Asp Ser Ile His Lys Glu Leu Ser Phe His
        355                 360                 365
Pro Ala Val Val Gly Glu Trp Ser Gly Ala Ile Thr Asp Cys Ala Thr
    370                 375                 380
Trp Leu Asn Gly Val Gly Val Gly Ala Arg Tyr Asp Gly Ser Tyr Tyr
385                 390                 395                 400
Asn Thr Thr Leu Phe Thr Thr Asn Asp Lys Pro Val Gly Thr Cys Ile
                405                 410                 415
Ser Gln Asn Ser Leu Ala Asp Trp Thr Gln Asp Tyr Arg Asp Arg Val
            420                 425                 430
Arg Gln Phe Ile Glu Ala Gln Leu Ala Thr Tyr Ser Ser Lys Thr Thr
        435                 440                 445
Gly Trp Ile Phe Trp Asn Trp Lys Thr Glu Asp Ala Val Glu Trp Asp
    450                 455                 460
Tyr Leu Lys Leu Lys Glu Ala Asn Leu Phe Pro Ser Pro Phe Asp Asn
465                 470                 475                 480
Tyr Thr Tyr Phe Lys Ala Asp Gly Ser Ile Glu Glu Lys Phe Ser Ser
                485                 490                 495
Ser Leu Ser Ala Gln Ala Phe Pro Arg Thr Thr Ser Ser Val Leu Ser
            500                 505                 510
Ser Thr Thr Thr Ser Arg Lys Ser Lys Asn Ala Ala Ile Ser Asn Lys
        515                 520                 525
Leu Thr Thr Ser Gln Leu Leu Pro Ile Lys Asn Met Ser Leu Thr Trp
    530                 535                 540
Lys Ala Ser Val Cys Ala Leu Ala Ile Thr Ile Ala Ala Leu Cys Ala
545                 550                 555                 560
Ser Leu
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