SEQUENCE LISTING

<110> Lonza Ltd

<120> CARBON-SOURCE REGULATED PROTEIN PRODUCTION IN A RECOMBINANT HOST CELL

<130> LO008P

<160> 86

<170> PatentIn version 3.5

<210> 1
<211> 806
<212> PRT
<213> Komagataella phaffii

<400> 1

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Lys Gln Glu Ser Gly Gly Pro Val Thr Ser Ser Thr Thr Pro Gly Thr
            20                  25                  30


Asn Thr Gly Leu Glu Asn Ser His Ser Met Gly Ala Asp Met Glu Pro
        35                  40                  45


Asp Val Gly Ala Thr Ser Pro Arg His Leu Leu Asn Gly Tyr Ile Tyr
    50                  55                  60


Asp Tyr Leu Val Lys Ser Asn Met Gln Asn Leu Ala Asp Gln Phe Ala
65                  70                  75                  80


Gln Glu Thr Glu Leu Leu Glu Thr Asp Leu Thr Val Pro Met Asp Thr
                85                  90                  95


Pro Ser Gly Tyr Leu Leu Glu Trp Trp Met Val Phe Trp Asp Leu Phe
            100                 105                 110


Asn Ala Arg Leu Lys Gln Arg Gly Ser Gln Lys Ala His Gln Tyr Ile
        115                 120                 125
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Gln Leu Asn Met Leu Arg Gln Gln Gln Gln Arg Thr Met Arg Asn Thr
    130                 135                 140

Ala Arg Val Gln Lys Val Pro Leu Arg Pro His Thr Gln Ser Ser Pro
145                 150                 155                 160

Ser Met Ser Gln Thr Phe Ile Pro Gln Gln Pro Gln Gln Gln Ala Gln
                165                 170                 175

Gly Gln Gln His Ala Gln Ala Gln Ala Gln Val Gln Ala His Gln Gln
            180                 185                 190

Ala Gln His His Ala Gln Ala Gln Val Pro Val Gln Pro Gln Gln His
        195                 200                 205

Gln Leu Gly Gly Gln Thr Gln Gln Gln Gln Ser Ile Asn Thr Gly Ser
    210                 215                 220

Pro Ala Gly Pro Asn Ala Ile Asn Ser Arg Val Gln His Leu Ala Gln
225                 230                 235                 240

Gln Gln Met Asn His Leu Arg Gln Gln Ala Thr Ala Thr Thr Gln Gln
                245                 250                 255

Pro Ile Pro Gln Gln Asn Ile Pro Ser Asn Gln Gln Gly Pro Thr Gly
            260                 265                 270

Pro Tyr Pro Thr Ser Pro Ser Arg Arg Pro Arg Leu Leu Ser Asn Glu
        275                 280                 285

Ser Gly Ala Ser Ala Pro Ser Val Met Thr Lys Ser Gln Leu Gln Gly
    290                 295                 300

Val Pro Pro Ser Gln Gln Pro His Gln Gln Gln Gly Gln Gln Val Gly
305                 310                 315                 320
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Pro Pro Asn Gln His Gln Gly Gln Ser Ser Ser Phe Tyr Ser Gly Met
                325                 330                 335

Pro Pro Gln Gly Val Val Val Pro His Gln Phe Asn Pro Gln Gln Tyr
            340                 345                 350

Ala Asn Met Leu Ala Arg Gln Gln His Val Gln Ala Gln Gln Gln Val
        355                 360                 365

Gln Leu Gln Gln Val Gln His Val Gln Gln Arg Gln Gln Gln Asp Gln
    370                 375                 380

Gln Gln His Arg Leu Ser Ala Gly Ser Pro Gly His Pro Ser Phe Gly
385                 390                 395                 400

Val Phe Gln Gln Pro Pro Pro Met Ser Asn His Asn Gln Val Met Ile
                405                 410                 415

Asn Gln Gln Gly Glu Thr Phe Phe Asp Pro His Ser Pro Tyr Ala Gln
            420                 425                 430

Pro Asn Gly Tyr Pro Gln Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln
        435                 440                 445

Gln Gln Gln Gln Gln Gln Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln
    450                 455                 460

Gln Lys Gln Gln Pro Pro Pro Pro Pro Arg Gln Pro Gln Arg Gln Gln
465                 470                 475                 480

Ala Met Ala Met Ala Pro Leu Pro His Ser Thr Ser Ala Ala Gly Thr
                485                 490                 495

Pro His Ser Ser Thr Thr Pro Arg Phe Ser Gln Pro Gly Pro Val Tyr
            500                 505                 510

Gln Gln Pro Leu Pro Ala Ser Gln Pro Gln His Ser Pro Pro Ser Ser
        515                 520                 525
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Ile Gln Gln Pro Glu Leu Val Pro Thr Pro Gly Ser Gln His Gln Gln
    530                 535                 540

Ile Ala Gln Pro Gln Ser Gln Ser Gln His Gln Gln Ser Gln Gln Ser
545                 550                 555                 560

Gln Ser Ser Ala Ser Lys Ile Val Gly Ile Gln Glu Tyr Gln Lys Glu
                565                 570                 575

Leu Met Met Leu Glu Lys Gln Asn Lys Gln Arg His Asp Met Ala Cys
            580                 585                 590

Lys Lys Gly Ser Gly His Phe Ser Asn Phe Asp Pro Ile Pro Glu His
        595                 600                 605

Thr Pro Pro Glu Pro Lys Phe Asn Val Asn Val Met Leu Pro Pro Gln
    610                 615                 620

Asn Ser Ala Val Val Thr Lys Asn Thr Pro Gly Thr Ser Pro Gly Thr
625                 630                 635                 640

Gln Thr Gln Asn Thr Ala His Ser Thr Gly Asn Thr Ser Ala Gly Ser
                645                 650                 655

Thr Pro Asn Asn Val Ala Pro Val Arg Lys Lys Lys Glu Pro Ala Lys
            660                 665                 670

Lys Lys Ala Lys Lys Ala Thr Glu Pro Pro Thr Pro Thr Thr Pro Gln
        675                 680                 685

Thr Pro Ile Ala Ala Arg Thr His Gln Asn Ser Thr Gly Gly Ile Pro
    690                 695                 700

Gly Asn Asn Ala Ala Thr Lys Arg Arg Lys Arg Glu Pro Leu Val Asp
705                 710                 715                 720
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Gln Thr Val Ser Pro Asn Leu Asn Glu Ala Ser Lys Ser Thr Lys Thr
                725                 730                 735

Gly Lys Ile Ser Ser Gln Thr Asp Phe Thr Gly Ser Asp Asn Gly Phe
            740                 745                 750

Leu Gln Asp Phe Gly Asp Gly Thr Gly Pro Pro Thr Gly Thr Asp Asp
        755                 760                 765

Met Glu Phe Asp Phe Asn Ser Phe Leu Asn Asn Glu Thr Gly Glu Pro
    770                 775                 780

Asn Ser Ser Thr Ile His Phe Asp Asn Val Phe Asn Trp Gly Glu Gly
785                 790                 795                 800

Thr Glu Ala Gly Asp Leu
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<212> DNA
<213> Komagataella phaffii

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gggtacattt acgattattt agtcaaatct aacatgcaaa atttggctga tcaatttgcc      240

caagagacgg agctcttaga aacagacttg acagtaccaa tggatacgcc ttcaggctat      300

cttctagaat ggtggatggt attctgggac cttttcaatg cccgcctaaa gcaacggggt      360

tcacagaagg cccaccagta tattcagttg aacatgctac gacaacagca acagaggacc      420

atgcgaaata cagcccgtgt tcaaaaagtc ccgttgaggc cacacaccca atcatctcct      480

tcaatgtcac agacttttat tccacagcag cctcaacagc aagcacaggg acaacagcac      540

gcccaggctc aagcccaagt gcaagcacat cagcaagccc aacaccacgc gcaggcacaa      600
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gtgccagtgc aaccgcaaca gcaccagcta ggaggccaaa ctcaacagca gcaatccatt 660

aacactgggt ctcctgcggg tccaaatgct atcaactcgc gtgttcaaca cttagcacaa 720

caacagatga atcaccttcg ccagcaggcg actgccacta cgcaacaacc tatcccgcaa 780

cagaatatcc catcaaacca acagggtcct acaggccctt atcctacttc cccttcaaga 840

agaccgagat tactgtctaa cgaatcgggt gcaagtgcac cctctgtaat gacaaagtca 900

cagctccaag gagtccctcc ctcacaacaa ccacaccagc agcaaggtca gcaggtaggc 960

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aactttgatc caattccaga gcacacaccg cccgaaccaa aatttaatgt gaatgtaatg 1860

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caaactgttt cacctaacct taacgaagct tccaagtcaa caaagaccgg aaaaatttca 2220

tctcaaactg actttacagg ttctgacaat ggattcttac aggattttgg cgatggaact 2280

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<213> Komagataella pastoris

<400> 3

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Lys Gln Asp Pro Gly Gly Pro Val Thr Ser Ser Thr Thr Pro Gly Thr
20 25 30

Asn Thr Gly Phe Glu Asn Ser His Ser Met Gly Ala Asp Val Glu Pro
35 40 45

Asp Val Gly Ala Ala Ser Pro Arg His Ile Leu Asn Gly Tyr Ile His
50 55 60

Asp Tyr Leu Val Lys Ser Asn Met Gln Asn Leu Ala Asp Gln Phe Ala
65 70 75 80

Gln Glu Ser Asp Leu Leu Glu Thr Asp Leu Thr Val Pro Met Asp Thr
85 90 95

Pro Thr Gly Tyr Leu Leu Glu Trp Trp Met Val Phe Trp Asp Leu Phe
100 105 110

Asn Ala Arg Leu Lys Gln Arg Gly Ser Gln Lys Ala His Gln Tyr Ile
115 120 125

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Gln Leu Asn Met Leu Arg Gln Gln Gln Gln Arg Thr Met Arg Asn Thr
    130                 135                 140

Ala Arg Val Gln Lys Val Pro Leu Arg Pro His Thr Gln Ser Ser Pro
145                 150                 155                 160

Ser Met Ser Gln Thr Phe Ile Pro Gln Gln Pro Gln Gln Gln Ala Gln
                165                 170                 175

Ala Gln Ala Gln Gln His Ala Gln Ala Gln Ala Gln Val Gln Ala His
            180                 185                 190

Gln Gln Ala Gln His His Ala Gln Ala Gln Val Pro Met Gln Ser Gln
        195                 200                 205

Pro His Gln Gln Gly Gly Gln Thr Gln Gln Gln Gln Pro Ile Asn Thr
    210                 215                 220

Gly Ser Pro Ala Gly Pro Asn Ala Ile Asn Ser Arg Val Gln His Leu
225                 230                 235                 240

Ala Gln Gln Gln Met Asn His Leu Arg Gln Gln Ala Thr Ala Thr Thr
                245                 250                 255

Gln Gln Pro Ile Pro Gln Gln Asn Ile Pro Ser Asn Gln Gln Gly Pro
            260                 265                 270

Ala Gly Pro Tyr Pro Thr Ser Pro Ser Arg Arg Pro Arg Leu Leu Ser
        275                 280                 285

Asn Glu Ser Gly Ala Ser Ala Pro Ser Val Met Thr Lys Ser Gln Leu
    290                 295                 300

Gln Gly Gly Pro Pro Ser Gln Gln Pro His Gln Gln Gln Ala Gln Gln
305                 310                 315                 320
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Val Gly Pro Pro Asn Gln His Gln Gly Gln Ser Ser Ser Phe Tyr Ser
                325                 330                 335

Gly Met Pro Pro Gln Gly Val Val Val Pro His Gln Phe Asn Pro Gln
            340                 345                 350

Gln Tyr Ala Asn Met Leu Ala Arg Gln Gln His Val Gln Ala Gln Gln
        355                 360                 365

Gln Val Gln Leu Gln Gln Val Pro His Val Gln Gln Arg Gln Gln Gln
    370                 375                 380

Asp Gln Gln Gln His Arg Leu Ser Ala Gly Ser Pro Gly His Pro Ser
385                 390                 395                 400

Phe Gly Val Phe Gln Gln Pro Pro Pro Met Ser Asn His Asn Gln Val
                405                 410                 415

Met Ile Asn Gln Gln Gly Glu Thr Phe Phe Asp Pro His Ser Pro Tyr
            420                 425                 430

Ala Gln Pro Asn Gly Tyr Pro Gln Pro Gln Gln Gln Gln Gln Gln Gln
        435                 440                 445

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
    450                 455                 460

Lys Gln Gln Gln Pro Pro Pro Arg Gln Pro Gln Arg Gln Gln Ala Met
465                 470                 475                 480

Ala Thr Ala Pro Leu Pro His Ser Thr Ser Ala Ser Gly Thr Pro His
                485                 490                 495

Thr Ala Thr Thr Pro Arg Phe Ser Gln Pro Gly Pro Val Tyr Gln Gln
            500                 505                 510

Pro Leu Pro Ala Ser Gln Pro Gln His Ser Pro Pro Thr Ser Ile Gln
        515                 520                 525
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Gln Gln Glu Pro Ile Pro Thr Pro Gly Ser Gln His Gln Gln Ile Ala
    530                 535                 540

Gln Pro Gln Ser Gln Asn Gln His Gln Gln Pro Gln Gln Pro Gln Ala
545                 550                 555                 560

Ser Ala Ser Lys Met Val Gly Ile Gln Glu Tyr Gln Lys Glu Leu Met
                565                 570                 575

Met Leu Glu Lys Gln Asn Lys Gln Arg His Asp Met Ala Ile Lys Lys
            580                 585                 590

Gly Ser Gly His Phe Ser Asn Phe Asp Pro Ile Pro Glu His Thr Gln
        595                 600                 605

Thr Glu Pro Lys Phe Asn Val Asn Val Met Leu Pro Pro Gln Asn Ser
    610                 615                 620

Ala Val Ala Thr Lys Asn Thr Pro Gly Thr Ser Pro Gly Thr Gln Thr
625                 630                 635                 640

Gln Asn Thr Ala His Ser Thr Gly Asn Thr Ser Ala Gly Ser Thr Pro
                645                 650                 655

Asn Asn Val Val Pro Val Arg Lys Lys Lys Glu Pro Ser Lys Lys Lys
            660                 665                 670

Ser Lys Lys Ala Thr Glu Pro Pro Thr Pro Thr Thr Pro Gln Thr Pro
        675                 680                 685

Ile Ala Ala Arg Ala His Gln Asn Ser Thr Gly Gly Ile Ser Gly Asn
    690                 695                 700

Asn Ala Ala Thr Lys Arg Arg Lys Arg Glu Pro Leu Val Asp Gln Thr
705                 710                 715                 720
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```
Val Ser Pro Asn Leu Asn Glu Ala Ser Lys Ser Thr Lys Pro Gly Lys
                725                 730                 735

Ile Ser Ser Gln Asn Asp Phe Thr Gly Ser Asp Asn Gly Phe Leu Gln
            740                 745                 750

Asp Phe Gly Asp Gly Thr Gly Pro Pro Thr Gly Thr Asp Asp Met Glu
        755                 760                 765

Phe Asp Phe Asn Ser Phe Leu Asn Asn Glu Thr Gly Glu Pro Asn Ser
    770                 775                 780

Ser Thr Ile His Phe Asp Asn Val Phe Asn Trp Gly Glu Gly Thr Glu
785                 790                 795                 800

Ala Gly Asp Leu
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<212> DNA
<213> Komagataella pastoris

<400> 4

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tccatgggag cggatgtgga gcctgatgtt ggtgccgcct ctcctcgcca tattcttaat      180

gggtacattc atgattactt agtcaaatct aatatgcaaa atttggccga tcaatttgct      240

caagagtcgg atctcttaga aacagaccta acggtaccaa tggatacacc tacaggctat      300

cttttagagt ggtggatggt attttgggac cttttcaatg cccgcctaaa gcaacgaggt      360

tcacagaagg ctcatcagta tattcagttg aacatgctac gacaacaaca gcagaggact      420

atgcgaaata cagcccgtgt tcagaaagtc ccgttgagac cacacaccca atcatctcct      480

tcaatgtcac agacctttat tccacagcag cctcaacagc aagcacaggc acaggcacag      540

cagcacgccc aagctcaagc gcaagtccag gctcatcagc aagcacagca tcatgcgcag      600
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gctcaagtgc caatgcaatc gcaaccacat cagcaaggag gccaaactca acaacagcaa 660

cccattaaca ctgggtctcc tgcggggcca aatgctatca actctcgtgt gcaacactta 720

gcgcaacaac agatgaatca tcttcgccag caggcaactg ccactaccca gcaacctatc 780

ccgcaacaga atattccatc aaaccagcag ggccctgcgg gcccttatcc tacatcgcct 840

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cctagattct cccagcctgg tcctgtttat cagcagcctt tacctgcatc tcaaccgcaa 1560

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gtttcaccta accttaacga agcttcgaaa tcaacaaagc ctgggaaaat ctcatctcaa 2220

aatgacttta caggttctga caatggattt ttacaggatt ttggcgatgg aacaggtccc 2280

cccactggaa ctgacgatat ggagtttgat tttaacagtt ttctcaacaa cgaaactggt 2340

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gccggggatc tatag 2415

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<211> 799
<212> PRT
<213> Saccharomyces cerevisiae

<400> 5

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20 25 30

Ile Ala Met Ala Thr Asn Ser Glu Gln Gln Arg Gln Gln Gln Gln Gln
35 40 45

Gln Gln Gln Gln Gln Gln Gln Trp Ile Asn Gln Pro Thr Ala Glu Asn
50 55 60

Ser Asp Leu Lys Glu Lys Met Asn Cys Lys Asn Thr Leu Asn Glu Tyr
65 70 75 80

Ile Phe Asp Phe Leu Thr Lys Ser Ser Leu Lys Asn Thr Ala Ala Ala
85 90 95

Phe Ala Gln Asp Ala His Leu Asp Arg Asp Lys Gly Gln Asn Pro Val
100 105 110

Asp Gly Pro Lys Ser Lys Glu Asn Asn Gly Asn Gln Asn Thr Phe Ser
115 120 125

```
Lys Val Val Asp Thr Pro Gln Gly Phe Leu Tyr Glu Trp Trp Gln Ile
    130                 135                 140

Phe Trp Asp Ile Phe Asn Thr Ser Ser Ser Arg Gly Gly Ser Glu Phe
145                 150                 155                 160

Ala Gln Gln Tyr Tyr Gln Leu Val Leu Gln Glu Gln Arg Gln Glu Gln
                165                 170                 175

Ile Tyr Arg Ser Leu Ala Val His Ala Ala Arg Leu Gln His Asp Ala
            180                 185                 190

Glu Arg Arg Gly Glu Tyr Ser Asn Glu Asp Ile Asp Pro Met His Leu
        195                 200                 205

Ala Ala Met Met Leu Gly Asn Pro Met Ala Pro Ala Val Gln Met Arg
    210                 215                 220

Asn Val Asn Met Asn Pro Ile Pro Ile Pro Met Val Gly Asn Pro Ile
225                 230                 235                 240

Val Asn Asn Phe Ser Ile Pro Pro Tyr Asn Asn Ala Asn Pro Thr Thr
                245                 250                 255

Gly Ala Thr Ala Val Ala Pro Thr Ala Pro Pro Ser Gly Asp Phe Thr
            260                 265                 270

Asn Val Gly Pro Thr Gln Asn Arg Ser Gln Asn Val Thr Gly Trp Pro
        275                 280                 285

Val Tyr Asn Tyr Pro Met Gln Pro Thr Thr Glu Asn Pro Val Gly Asn
    290                 295                 300

Pro Cys Asn Asn Asn Thr Thr Asn Asn Thr Thr Asn Asn Lys Ser Pro
305                 310                 315                 320
```

```
Val Asn Gln Pro Lys Ser Leu Lys Thr Met His Ser Thr Asp Lys Pro
                325                 330                 335

Asn Asn Val Pro Thr Ser Lys Ser Thr Arg Ser Arg Ser Ala Thr Ser
            340                 345                 350

Lys Ala Lys Gly Lys Val Lys Ala Gly Leu Val Ala Lys Arg Arg Arg
        355                 360                 365

Lys Asn Asn Thr Ala Thr Val Ser Ala Gly Ser Thr Asn Ala Cys Ser
    370                 375                 380

Pro Asn Ile Thr Thr Pro Gly Ser Thr Thr Ser Glu Pro Ala Met Val
385                 390                 395                 400

Gly Ser Arg Val Asn Lys Thr Pro Arg Ser Asp Ile Ala Thr Asn Phe
                405                 410                 415

Arg Asn Gln Ala Ile Ile Phe Gly Glu Glu Asp Ile Tyr Ser Asn Ser
            420                 425                 430

Lys Ser Ser Pro Ser Leu Asp Gly Ala Ser Pro Ser Ala Leu Ala Ser
        435                 440                 445

Lys Gln Pro Thr Lys Val Arg Lys Asn Thr Lys Lys Ala Ser Thr Ser
    450                 455                 460

Ala Phe Pro Val Glu Ser Thr Asn Lys Leu Gly Gly Asn Ser Val Val
465                 470                 475                 480

Thr Gly Lys Lys Arg Ser Pro Pro Asn Thr Arg Val Ser Arg Arg Lys
                485                 490                 495

Ser Thr Pro Ser Val Ile Leu Asn Ala Asp Ala Thr Lys Asp Glu Asn
            500                 505                 510

Asn Met Leu Arg Thr Phe Ser Asn Thr Ile Ala Pro Asn Ile His Ser
        515                 520                 525
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Ala Pro Pro Thr Lys Thr Ala Asn Ser Leu Pro Phe Pro Gly Ile Asn
    530                 535                 540

Leu Gly Ser Phe Asn Lys Pro Ala Val Ser Ser Pro Leu Ser Ser Val
545                 550                 555                 560

Thr Glu Ser Cys Phe Asp Pro Glu Ser Gly Lys Ile Ala Gly Lys Asn
                565                 570                 575

Gly Pro Lys Arg Ala Val Asn Ser Lys Val Ser Ala Ser Ser Pro Leu
            580                 585                 590

Ser Ile Ala Thr Pro Arg Ser Gly Asp Ala Gln Lys Gln Arg Ser Ser
        595                 600                 605

Lys Val Pro Gly Asn Val Val Ile Lys Pro Pro His Gly Phe Ser Thr
    610                 615                 620

Thr Asn Leu Asn Ile Thr Leu Lys Asn Ser Lys Ile Ile Thr Ser Gln
625                 630                 635                 640

Asn Asn Thr Val Ser Gln Glu Leu Pro Asn Gly Gly Asn Ile Leu Glu
                645                 650                 655

Ala Gln Val Gly Asn Asp Ser Arg Ser Ser Lys Gly Asn Arg Asn Thr
            660                 665                 670

Leu Ser Thr Pro Glu Glu Lys Lys Pro Ser Ser Asn Asn Gln Gly Tyr
        675                 680                 685

Asp Phe Asp Ala Leu Lys Asn Ser Ser Ser Leu Leu Phe Pro Asn Gln
    690                 695                 700

Ala Tyr Ala Ser Asn Asn Arg Thr Pro Asn Glu Asn Ser Asn Val Ala
705                 710                 715                 720
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Asp Glu Thr Ser Ala Ser Thr Asn Ser Gly Asp Asn Asp Asn Thr Leu
                725                 730                 735


Ile Gln Pro Ser Ser Asn Val Gly Thr Thr Leu Gly Pro Gln Gln Thr
            740                 745                 750


Ser Thr Asn Glu Asn Gln Asn Val His Ser Gln Asn Leu Lys Phe Gly
        755                 760                 765


Asn Ile Gly Met Val Glu Asp Gln Gly Pro Asp Tyr Asp Leu Asn Leu
    770                 775                 780


Leu Asp Thr Asn Glu Asn Asp Phe Asn Phe Ile Asn Trp Glu Gly
785                 790                 795


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1               5                   10                  15


Glu Gln Pro Tyr Met Ala Ser Gln Tyr Lys Gln Asp Leu Gln Ser Asn
            20                  25                  30


Ile Ala Met Ala Thr Asn Ser Glu Gln Gln Arg Gln Gln Gln Gln Trp
        35                  40                  45


Ile Asn Gln Pro Thr Ala Glu Asn Ser Asp Leu Lys Glu Lys Met Asn
    50                  55                  60


Cys Lys Asn Thr Leu Asn Glu Tyr Ile Phe Asp Phe Leu Thr Lys Ser
65                  70                  75                  80


Ser Leu Lys Asn Thr Ala Ala Ala Phe Ala Gln Asp Ala His Leu Asp
                85                  90                  95
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Arg Asp Lys Gly Gln Asn Pro Ile Asp Gly Pro Lys Ser Lys Glu Asn
            100                 105                 110

Asn Gly Asn Gln Asn Thr Phe Ser Lys Val Val Asp Thr Pro Gln Gly
        115                 120                 125

Phe Leu Tyr Glu Trp Trp Gln Ile Phe Trp Asp Ile Phe Asn Thr Ser
    130                 135                 140

Ser Ser Arg Gly Gly Ser Glu Phe Ala Gln Gln Tyr Tyr Gln Leu Val
145                 150                 155                 160

Leu Gln Glu Gln Arg Gln Glu Gln Ile Tyr Arg Ser Leu Ala Ala His
                165                 170                 175

Ala Ala Arg Leu Gln His Asp Ala Glu Arg Arg Gly Glu Tyr Ser Asn
            180                 185                 190

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

Met Ala Pro Ala Val Gln Met Arg Asn Val Asn Met Asn Pro Ile Pro
    210                 215                 220

Ile Pro Met Val Gly Asn Pro Ile Val Asn Asn Phe Ser Ile Pro Pro
225                 230                 235                 240

Tyr Asn Asn Ala Asn Pro Thr Thr Gly Ala Thr Ala Val Ala Pro Thr
                245                 250                 255

Ala Pro Pro Ser Gly Asp Phe Ala Asn Val Gly Pro Thr Gln Asn Arg
            260                 265                 270

Ser Gln Asn Val Thr Gly Trp Pro Val Tyr Asn Tyr Pro Met Gln Pro
        275                 280                 285

Thr Thr Glu Asn Pro Val Gly Asn Pro Cys Asn Asn Asn Thr Thr Asn
```

```
    290                 295                 300

Asn Thr Thr Asn Asn Lys Ser Pro Val Asn Gln Pro Lys Ser Leu Lys
305                 310                 315                 320

Thr Met His Ser Thr Asp Lys Pro Asn Asn Val Pro Thr Ser Lys Ser
                325                 330                 335

Thr Arg Ser Arg Ser Ala Thr Ser Lys Ala Lys Gly Lys Val Lys Ala
            340                 345                 350

Gly Leu Val Ala Lys Arg Arg Arg Lys Asn Asn Thr Ala Thr Val Ser
        355                 360                 365

Ala Gly Ser Thr Asn Ala Gly Ser Pro Asn Ile Thr Thr Pro Gly Ser
    370                 375                 380

Thr Thr Ser Glu Pro Ala Met Val Gly Ser Arg Val Asn Lys Thr Pro
385                 390                 395                 400

Arg Ser Asp Ile Ala Thr Asn Phe Arg Asn Gln Ala Ile Ile Phe Gly
                405                 410                 415

Glu Glu Asp Ile Tyr Ser Asn Ser Lys Ser Ser Pro Ser Leu Asp Gly
            420                 425                 430

Ala Ser Pro Ser Ala Leu Val Ser Lys Gln Pro Thr Lys Val Arg Lys
        435                 440                 445

Asn Thr Lys Lys Ala Ser Thr Ser Ala Phe Pro Val Glu Ser Ala Asn
    450                 455                 460

Lys Leu Gly Gly Asn Ser Val Val Thr Gly Lys Lys Arg Ser Pro Pro
465                 470                 475                 480

Asn Thr Arg Val Leu Arg Arg Lys Ser Thr Pro Ser Val Ile Leu Asn
                485                 490                 495
```

```
Ala Asp Ala Thr Lys Asp Glu Asn Asn Met Leu Arg Thr Phe Ser Asn
            500                 505                 510

Thr Thr Ala Pro Asn Ile His Ser Ala Pro Pro Thr Lys Thr Ala Asn
        515                 520                 525

Ser Leu Pro Phe Pro Gly Ile Asn Leu Gly Ser Phe Asn Lys Pro Ala
    530                 535                 540

Val Ser Ser Pro Leu Ser Ser Val Thr Glu Ser Cys Phe Asp Pro Glu
545                 550                 555                 560

Ser Gly Lys Ile Ala Gly Lys Asn Gly Pro Lys Arg Ala Val Asn Ser
                565                 570                 575

Lys Val Ser Ala Ser Ser Pro Leu Ser Ile Ala Thr Pro Pro Ser Gly
            580                 585                 590

Asp Ala Gln Glu Gln Arg Ser Ser Asn Val Pro Gly Asn Val Val Ile
        595                 600                 605

Lys Pro Pro His Gly Phe Ser Thr Thr Asn Leu Asn Ile Thr Leu Lys
    610                 615                 620

Ser Ser Lys Ile Ile Thr Ser Gln Asn Asn Thr Ala Phe Gln Glu Leu
625                 630                 635                 640

Pro Asn Gly Gly Asn Ile Leu Glu Ala Gln Val Gly Asn Asp Ser Arg
                645                 650                 655

Ser Ser Lys Gly Asn Arg Asp Thr Leu Ser Thr Pro Glu Glu Lys Lys
            660                 665                 670

Pro Ser Ser Asn Asn Gln Gly Tyr Asp Phe Asp Ala Leu Lys Asn Ser
        675                 680                 685

Ser Ser Leu Leu Phe Pro Asn Gln Ala Tyr Ala Ser Asn Asn Arg Thr
```

```
    690                 695                 700

Pro Asn Glu Asn Ser Asn Val Ala Asp Glu Thr Ser Ala Ser Thr Asn
705                 710                 715                 720

Asn Gly Asp Asn Asp Asn Thr Leu Ile Gln Pro Ser Ser Asn Val Gly
                725                 730                 735

Thr Thr Leu Gly Pro Gln Gln Thr Ser Thr Asn Glu Asn Gln Asn Val
            740                 745                 750

His Ser Gln Asn Leu Lys Phe Gly Asn Ile Gly Met Val Glu Asp Gln
        755                 760                 765

Gly Pro Asp Tyr Asp Leu Asn Leu Leu Asp Thr Asn Glu Asn Asp Phe
    770                 775                 780

Asn Phe Ile Asn Trp Glu Gly
785                 790


<210>  7
<211>  768
<212>  PRT
<213>  Yarrowia lipolytica

<400>  7

Met Pro Ala Lys Ser Asp Lys Glu Leu Leu Asn Ala Tyr Ile Tyr Asp
1               5                   10                  15

Tyr Leu Leu Lys His Asn Met His Asp Ser Ala Arg Thr Phe Gly Ala
            20                  25                  30

Glu Ala Lys Val Val Pro Asn Val Lys Lys Glu Asp Asp Lys Asp Leu
        35                  40                  45

Pro Lys Pro Leu Ile Pro Ile Asp Ala Pro Gln Gly Phe Leu Tyr Glu
    50                  55                  60
```

```
Trp Trp Ala Leu Phe Trp Asp Ile Tyr Ser Ala Arg Gly Ser Lys Gly
65                  70                  75                  80


Gly Gly Ser Val Pro Ala Gln Gln Tyr Val Gln Gly Thr Met Arg Leu
                85                  90                  95


Arg Gln Glu His Ala Ala Arg Ala Gln Leu Gln Gln Gln His Gln Ala
            100                 105                 110


Gln Gln His Ala Gln Ala Gln Ala Ala Ala Gln Val Gln Gly Gln Ala
        115                 120                 125


Gln Gly Gln Gly Gln Gly Gln Asn Pro Thr Gln Gly Pro Gln Pro Gln
    130                 135                 140


Gly His Met Gly Met Pro Gly Gln Gly Pro His Gln Pro Gly Gly Pro
145                 150                 155                 160


Phe Met Asn Gly Asn Met Met Phe Pro Pro Gly Gln Met Arg Met Gly
                165                 170                 175


Gln Leu Pro Gln His Leu Gln Gln Gln Gly Thr Gly Val Ala Gly Ala
            180                 185                 190


Asn Pro Ser Asp Asp Ser Ser Ser Pro Gly Gly Thr Ser Pro Ala Lys
        195                 200                 205


Arg Gln Arg Leu Ser Pro Asp Met Gly Gly Gln Ser His Pro Glu Gln
    210                 215                 220


Gln Gly Gln His Met Met Gly Thr Pro Asn Pro Asn Asn Pro Val Phe
225                 230                 235                 240


Asn Ser Gln Val Met Gln Gln Leu Lys Ala Ser Gln Gly Gln Met Pro
                245                 250                 255


Asn Leu Gln Gln Gln Gln Gln Ala Gln Leu Gln Gln Tyr Ser Asn Thr
            260                 265                 270
```

```
Leu Ser Leu Ala Gln Gln Arg Ala Met Met Asn Ala Lys Gly Gly Pro
        275                 280                 285

Asn Gly Gln Pro Gly Gln Pro Gly Gln Pro Gly Gln Pro Gly Gln Pro
    290                 295                 300

Gly Gln Pro Gly Gln Pro Gly Gln Pro Gly Gln Pro Leu Pro Met Gly
305                 310                 315                 320

Tyr Glu Gly Met Glu Pro Gly Phe Met Gly Gly Asn Gly Leu Ile Leu
                325                 330                 335

Asn Ala Gln Gln Met Arg Gln Gln Gln Ala Gly Ser Gly Gly Ala Ala
            340                 345                 350

Gly Ser Gly Gln Leu Asn Gly Asn Ser Asn Ala Leu His Asp Tyr Gln
        355                 360                 365

Met Gln Leu Met Leu Leu Glu Gln Gln Asn Lys Lys Arg Leu Met Val
    370                 375                 380

Ala Arg Gln Glu Gln Gln Glu Gly Gln Pro Arg Ala Glu Gly Gln Ala
385                 390                 395                 400

Ala Ala Ala Gly Ala Asn Pro Gly Ala Arg Met Ser Gly Gln Phe Lys
                405                 410                 415

Arg Pro Gly Ser Ser Pro Val Val Gly Asn Ile Gly Asp Gly Arg Arg
            420                 425                 430

Val Thr Pro Lys Leu Pro Asn Gln Pro Ser Pro Leu Ile Asp Ala Asn
        435                 440                 445

Arg Ala Ser Pro Leu Gln Ser Asn Phe Asn Gly Gln Gly Asp Phe Asn
    450                 455                 460
```

```
Val Val Val Gly Pro Ser Gly Gln Met Met Arg Met Gln Gln Pro Gln
465                 470                 475                 480


Gln Gln Gly Gly Pro Pro Gln Gln Gln Gly Gln Gln Gln Gly Gly Pro
                485                 490                 495


Gly Gln Gln Gln Gly Gly Pro Gly Gln Gln Pro Gln Gln Gly Gln Gln
            500                 505                 510


Gln Gly Gln Gln Gly Gly Pro Gln Gly Gly Gln His Arg Phe Asp Asp
        515                 520                 525


Pro Gln Gln Leu Pro Gln Ser Gln Asn Gly Gly Pro Gln Pro Gly Ser
    530                 535                 540


Ala Pro Gly Gln Leu Pro Gln Thr Gln Gly Gly Pro Gln Arg Pro Pro
545                 550                 555                 560


Ser Arg Val Ser Gln Met Pro Pro Pro Gly Val Gln Gly Gly Gln Arg
                565                 570                 575


Thr Gln Pro Ser Ser Pro Gly Gln Ala Ser Asn Pro Gly Ser Gly Gly
            580                 585                 590


Ser Ser Gly Ser Ala Pro Gly Gly Thr Thr Pro Thr Gln Ala Asn Lys
        595                 600                 605


Gln Leu Lys Gly Lys Lys Ala Glu Pro Lys Lys Arg Ala Lys Lys Gly
    610                 615                 620


Asn Gln Pro Val Thr Pro Lys Ala Val Ser Glu Ser Pro Thr Pro Thr
625                 630                 635                 640


Thr Pro Ala Thr Pro Ser Ala Ala Ser Asn Gln Ser Leu Leu Ser Lys
                645                 650                 655


Ala Thr Asn Phe Ala Ala Asn Asn Lys Gln Ala Gln Ala Ala Ala His
            660                 665                 670
```

```
Ala Gln Ala Gln Ala Gln Ala Ala Ala Gln Ala Gln Ser Gln Met His
        675                 680                 685

Met Gly Gly Met Gly Gly Ser Ser Ser Gly Leu Glu Leu Asp Val Asn
    690                 695                 700

Gly Gly Met Gly Leu Asp Asn Asp Ser Ser Ser Phe Leu Asn Asp Phe
705                 710                 715                 720

Ser Thr Gly Asn Glu Gly Asp Val Gly Asp Met Asp Phe Asp Phe Asn
                725                 730                 735

Ser Phe Leu Asn Thr Asp Asp Asn Ala Ala Gly Ala Leu Lys Phe Asp
            740                 745                 750

Ser Gly Ser Ala Phe Gly Trp Gly Glu Gly Val Glu Ala Met Asn Glu
        755                 760                 765
```

<210> 8
<211> 598
<212> PRT
<213> Ogataea polymorpha

<400> 8

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Met Ser Gln Asn Ala Thr Pro Gln Thr Thr Glu Gly His Met Ser Met
1               5                   10                  15

Asn Asp Gln Gln Ser Asn Ser Ser Ser Gly Thr Asn Asn Thr Glu His
            20                  25                  30

Pro Ser Ser Ser Ser Val Ser Ser Val Pro Thr Val Ser Asp Ser Thr
        35                  40                  45

Ala Val Asn Ser Arg Glu Leu Leu Asn Ala Tyr Val Tyr Asp Phe Ile
    50                  55                  60

Leu Lys Ser Gly Phe Thr Ala Thr Ala Ser Ala Phe Phe Lys Glu Ala
```

```
65                  70                  75                  80

Asn Ile Pro Val Ile His Ser Glu Lys Arg Pro Thr Asn Ser Pro Ser
                85                  90                  95

Ser Ser Ala Thr Gly Thr Ser Asp Leu Pro Ala Ser Phe Met Thr Met
            100                 105                 110

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

Val Phe Asn Ala Arg Thr Gln Arg Gly Gly Thr Thr Asn Ala Thr Gln
    130                 135                 140

Tyr Tyr His Tyr Val Asn Leu Lys Gln Lys Gln Asp His Leu Met Ser
145                 150                 155                 160

Gln Gln Ala Ala Ala Val Ala Ala Ala Ser Thr Val Met Asn Gly Asn
                165                 170                 175

Asn Thr Ser Met Ser Gly Ala Pro Val Thr Ser Ala Ala Gln Asp Ile
            180                 185                 190

Gly Val Leu Met Pro Gln Gln Gln Gln Gln Gln Gln Gln Ala Gln Met
        195                 200                 205

Ala His Pro Pro Gln Gln Val Pro Met Ala Gln Gln Gln Arg Val Asn
    210                 215                 220

Ala Arg Met Gln Gln Pro Gln Gln Gln Gln Ser Gln Ser Met Pro Met
225                 230                 235                 240

His Pro Gln Ala Ala Ala Gln Ala Gln Met Asn Thr Leu Arg Gln Gln
                245                 250                 255

Gln Ile Ala Gln Gln Ala Gln Ala Ala Gln Val Ala Ala Gln Ala Val
            260                 265                 270
```

```
Ser Gln Arg Gly Ser Pro Ser Lys Arg Gln Arg Met Asp Ala Ala Gly
        275                 280                 285

Asn Gly Ser Ala Thr Glu Ile Asn Gln Thr Ser Ser Pro Asn Ile Ala
    290                 295                 300

Met Asn Ser Gln Gln Gln Gln Gln Gln Gln Gln His Pro Pro Met Pro
305                 310                 315                 320

Met Pro Gln Gly Met Met Ile Pro Asn Gln Phe Gly Val Pro Gln Gln
                325                 330                 335

Tyr Ala Met Phe Ala Ala Ala Gln Ala Ala Gln Gln Gly Gln Ser Gln
            340                 345                 350

Gln Lys Phe Asn Gln Tyr Met Ile Pro Asn Phe Gln Asn Gln Pro Gln
        355                 360                 365

Gln Pro Gln Gln Gln Met Leu Met His Gln Gln Met His Gln Gln Ser
    370                 375                 380

Val His Met Gln His Asp Gln Gln His Pro Pro Pro Pro Pro Pro Asn
385                 390                 395                 400

Val Pro Gln His Ser Gln Thr Phe Ser Asn Pro Asn Asp Phe Phe His
                405                 410                 415

Glu Met Pro Lys Gln Asn Asn Pro Gly Thr Ala Arg Val Asn Asp Thr
            420                 425                 430

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

Arg Arg Arg Leu Asp Val His Arg Asn Val Ser Asp Ser Lys Asp Pro
    450                 455                 460

Asn Ser Pro Gly Ser Ala Gln Phe Thr Glu Tyr Ser Ala Met Leu Asn
```

```
465                 470                 475                 480

Gln Met Pro Pro Gln His Ala Ala Ala Ser Ile Met Gln Gln Arg Ala
                485                 490                 495

Ser Pro Ala Thr Lys Ala Ser Pro Thr Thr Lys Ser Pro Ala Asn Gly
            500                 505                 510

Ala Pro Pro Ala Asn Gly Lys Gln Lys Lys Ala Pro Arg Lys Ala Arg
        515                 520                 525

Lys Asn Ser Ser Ser Val Pro Ala Thr Pro Leu Thr Pro Ala Asn Asn
    530                 535                 540

Gln Pro Thr Pro Gln Thr Asn Ile Pro Pro Thr Pro Gln Asn Thr Thr
545                 550                 555                 560

Pro Gln Gln Thr Pro Gln Ser Ser Ala Ala Ala Ala Ser Gln Val Met
                565                 570                 575

Ala Gly Lys Lys Gly Ile Lys Arg Lys Asn Arg Gly Arg Ala Ile Tyr
            580                 585                 590

Pro Ile Glu Tyr Ser Arg
        595


<210>  9
<211>  771
<212>  PRT
<213>  Aspergillus niger

<400>  9

Met Asn Gln Met Asn Gln Met Asn Met Ala Gly Met Asn Pro Gly Ala
1               5                   10                  15

Gly Gly Pro Val Gly Gly Val Pro Met Ile Asn Asn Gly Ser Ala Ala
            20                  25                  30
```

```
Pro Arg Asn Glu Gln Asn Ile Asn Asn Ile Pro Glu Asn Met Ile Asn
        35                  40                  45

Asn Leu Asn Thr Tyr Ile Tyr Asp Tyr Phe Leu Lys Arg Gly Tyr His
    50                  55                  60

Asp Cys Ala Arg Ala Leu Val Lys Asp Glu Ser Ile Lys Leu Asn Thr
65                  70                  75                  80

Glu Pro Pro Ile Lys Thr Ser Pro Gly His Arg Arg Asp Ala Asp Val
                85                  90                  95

Asn Gly Val Asp Gly Asp Thr Met Met Thr Asp Gly Lys Asp Gly Asp
            100                 105                 110

Lys Leu Lys Ile Pro Asp Asp Leu Pro Arg Pro Asn Leu Pro Ser Glu
        115                 120                 125

Gly Gln Gln Ser Ser Phe Leu Leu Asp Trp Phe Ser Leu Phe Trp Asp
    130                 135                 140

Phe Phe Trp Ala Gln Arg Lys Lys Gly Asn Ser Asn Asp Val Arg Ser
145                 150                 155                 160

Tyr Leu Thr His Thr Gln Asn Met Met Arg Leu Arg Glu Gln His Gln
                165                 170                 175

Asn Gln Leu Leu Arg Gln Gln Pro Leu Met Asn Gly Gln Met Gly Gln
            180                 185                 190

Met Asn Ile Arg Arg Asn Gly Met Val Pro Pro Asn Leu Gln Lys Thr
        195                 200                 205

Val Leu Gln Asn Asn Thr Thr Gly Leu Ser Gln Gln Gln Leu Ala Gln
    210                 215                 220

Met His Lys Asn Gln Gln Val Gln Met Met Gln Gln Met Gln Arg Glu
225                 230                 235                 240
```

```
His Ser Asp Met Asp Met Asn Gly His Arg Pro Gln Ser Pro Ala Ser
               245                 250                 255

Ala Glu Asn Ala Pro Ser Pro Ser Lys Arg Pro Arg Leu Glu Gly Gly
            260                 265                 270

Pro Met Asn Gly Gln Gln Leu Ala Pro Asn Gly Arg Gly Gln Ala Gln
        275                 280                 285

Gly Ile Pro Gly Gln Pro Thr Pro Gln Ala Leu Leu Met Gln Asn Gly
    290                 295                 300

Leu Asn Arg Ala Met Asn Pro Asn Gln Phe Gln Ala Phe Gln Gln Ser
305                 310                 315                 320

Gly Pro Ala Ala Gln Gln Lys Gln Met Gln Gly Met Pro Asn Gly Met
               325                 330                 335

Met Asn Pro Ala Asn Val Met Ala Asn Pro Gln Thr Glu Met Val Ser
            340                 345                 350

Ile Pro Glu Gly Gln Val Tyr Pro Ile Asn Gly Asp Tyr Tyr Gly Ala
        355                 360                 365

Asn Gly Gln Met Ala Gln Val Arg Thr Gly Met Gln Thr Pro Gly Gly
    370                 375                 380

Gln His Gly Asn His Ala Leu Gln Asp Tyr Gln Met Gln Leu Met Leu
385                 390                 395                 400

Leu Glu Gln Gln Asn Lys Arg Arg Leu Met Met Ala Arg Gln Glu Gln
               405                 410                 415

Asp Ser Met Ala Arg Pro Asp Gly Gln Pro Gln Met Pro Gly Gln Gln
            420                 425                 430
```

```
Leu Pro Pro Gly Thr Ser Pro Gln Gly Ser Arg Ala Gly Thr Ser Pro
        435                 440                 445

Asn Pro Asn Asp Gln Met Lys Arg Gly Thr Pro Lys Met Pro Gln Thr
    450                 455                 460

Gly Leu Pro Gly Ser Pro Ser Ala Ala Asp Ala Met Ala Gln Gly Arg
465                 470                 475                 480

Gly Ser Pro Ala Ser Met Asn Phe Pro Gly Gly Gln Met Pro Pro Glu
                485                 490                 495

Met Ala Gly Pro Gln Phe Phe Val Lys Asn Met Ala Asp Gly Met Ala
            500                 505                 510

Ala Pro Asn Gly Met Arg Pro Pro Ser Ser Asn Pro Ala Phe Ser Thr
        515                 520                 525

Pro Gln Met Gly Gln Pro Ile Gln Ala Gly Ala Asn Arg Met Pro Asn
    530                 535                 540

Gly Gly Trp Gln Pro Gln Gln Gly Ala Gln Gly Gln Pro Met Ala Pro
545                 550                 555                 560

Gln Gln Ser Pro Ala Thr Gln Pro Gln Ser Thr Gly Thr Pro Gln Glu
                565                 570                 575

Arg Asn Ala Met Pro Pro Pro Gln Ala Pro Pro Ala Pro Gly Ala Asn
            580                 585                 590

Val Gly Arg Thr Gln Pro Pro Ser Pro Gln Thr Ala Ala Pro Pro Thr
        595                 600                 605

Pro Gln Gln Gly Asn Lys Pro Ala Pro Lys Lys Lys Glu Thr Lys Asp
    610                 615                 620

Ser Arg Lys Arg Pro Lys Lys Gly Ala Ala Ala Ala Ala Ala Ala Ala
625                 630                 635                 640
```

```
Gln Ala Asn Thr Ala Ala Thr Pro Ser Ser Glu Ala Glu His Pro Pro
                645                 650                 655

Thr Pro Thr Pro Ser Thr Pro Ile Thr Pro Gln His Pro Asn Ser Phe
            660                 665                 670

Asn Lys Thr Gly Ala Asn Ala Thr Thr Ser Ala Pro Gln Gln Pro Thr
        675                 680                 685

Ser Ala Pro Ala Pro Pro Pro Leu Val Gln Gln Pro Pro Asp Gln Thr
    690                 695                 700

Gln Gln Pro Phe Asn Glu Leu Ser Ile Pro Asp Ala Ser Ala Phe Asn
705                 710                 715                 720

Leu Asp Phe Ser Ala Leu Glu Asn Pro Asp Ile Leu Glu Asn Phe Asp
                725                 730                 735

Phe Asp Thr Phe Leu Asn Thr Asp Ala Asp Thr Ala Gly Phe Gly Phe
            740                 745                 750

Asp Pro Asn Thr Ser Tyr Pro Thr Asp Gly Val Glu Thr Gly Ala Gly
        755                 760                 765

Asp Gly Leu
    770
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<210> 10
<211> 1240
<212> DNA
<213> Artificial Sequence

<220>
<223> promoter

<400> 10
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taagacgctc agttgtcagg ataattacgt tcgactgtag taaaacagga atctgtattg 120

ttagaaagaa cgagagtttt ttacggcgcc gccatattgg gccgtgtgaa aacagcttga 180

aaccccacta ctttcaaagg ttctgttgct atacacgaac catgtttaac caacctcgct 240

tttgacttga ctgaagtcat cggttaacaa tcaagtaccc tagtctgtct gaatgctcct 300

ttccatattc agtaggtgtt tcttgcactt ttgcatgcac tgcggaagaa ttagccaata 360

gcgcgtttca tatgcgcttt taccccctct tttgtcaagc gcaaaatgcc tgtaagattt 420

ggtgggggtg tgagccgtta gctgaagtac aacaggctaa ttccctgaaa aaactgcagc 480

tcagggattc ccactatttg gtattctgat atgtttttcc tgatatgcat caaaactcta 540

atctaaaacc tgaatctccg ctatttttt ttttttttga tgaccccgtt ttcgtgacaa 600

attaatttcc aacggggtct tgtccggata agagaatttt gtttgattat ccgttcggat 660

aaatggacgc ctgctccata tttttccggt tattacccca cctggaagtg cccagaattt 720

tccggggatt acggataata cggtggtctg gattaattaa tacgagatct cagggattcc 780

cactatttgg tattctgata tgtttttcct gatatgcatc aaaactctaa tctaaaacct 840

gaatctccgc tatttttttt ttttttttgat gaccccgttt tcgtgacaaa ttaatttcca 900

acggggtctt gtccggataa gagaattttg tttgattatc cgttcggata aatggacgcc 960

tgctccatat ttttccggtt attaccccac ctggaagtgc ccagaatttt ccggggatta 1020

cggataatac ggtggtctgg attaattaat acgccaagtc ttacattttg ttgcagtctc 1080

gtgcgagtat gtgcaataat aaacaagatg agccaattta ttggattagt tgcagcttga 1140

ccccgccata gctaggcata gccaagtgct atgggtgtta gatgatgcac ttggatgcag 1200

tgagttttgg agtataaaag atccttaaaa ttccaccctt 1240

<210> 11
<211> 1425
<212> DNA
<213> Artificial Sequence

<220>
<223> promoter

<400> 11
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taagacgctc agttgtcagg ataattacgt tcgactgtag taaaacagga atctgtattg 120

ttagaaagaa cgagagtttt ttacggcgcc gccatattgg gccgtgtgaa aacagcttga 180

aaccccacta ctttcaaagg ttctgttgct atacacgaac catgtttaac caacctcgct 240

tttgacttga ctgaagtcat cggttaacaa tcaagtaccc tagtctgtct gaatgctcct 300

ttccatattc agtaggtgtt tcttgcactt ttgcatgcac tgcggaagaa ttagccaata 360

gcgcgtttca tatgcgcttt tacccccctct tttgtcaagc gcaaaatgcc tgtaagattt 420

ggtgggggtg tgagccgtta gctgaagtac aacaggctaa ttccctgaaa aaactgcagc 480

tcagggattc ccactatttg gtattctgat atgttttcc tgatatgcat caaaactcta 540

atctaaaacc tgaatctccg ctatttttt ttttttgat gaccccgttt tcgtgacaaa 600

ttaatttcca acggggtctt gtccggataa gagaattttg tttgattatc cgttcggata 660

aatggacgcc tgctccatat ttttccggtt attaccccac ctggaagtgc ccagaatttt 720

ccggggatta cggataatac ggtggtctgg attaattaat acgccaagtc ttacattttg 780

ttgcagtctc gtgcgagtat gtgcaataat aaacaagatg agccaattta ttggattagt 840

tgcagcttga ccccgccata gctaggcata gccaagtgct atgggtgtta gatgatgcac 900

ttggatgcag tgagttttgg agtataaaag atccttaaaa ttccaccctt agatctcagg 960

gattcccact atttggtatt ctgatatgtt tttcctgata tgcatcaaaa ctctaatcta 1020

aaacctgaat ctccgctatt ttttttttt ttgatgaccc cgttttcgtg acaaattaat 1080

ttccaacggg gtcttgtccg gataagagaa ttttgtttga ttatccgttc ggataaatgg 1140

acgcctgctc catatttttc cggttattac cccacctgga agtgcccaga attttccggg 1200

gattacggat aatacggtgg tctggattaa ttaatacgcc aagtcttaca ttttgttgca 1260

gtctcgtgcg agtatgtgca ataataaaca agatgagcca atttattgga ttagttgcag 1320

cttgaccccg ccatagctag gcatagccaa gtgctatggg tgttagatga tgcacttgga 1380

tgcagtgagt tttggagtat aaaagatcct taaaattcca ccctt 1425

<210> 12
<211> 966

<212> DNA
<213> Artificial Sequence

<220>
<223> promoter

<220>
<221> misc_feature
<222> (592)..(593)
<223> n is T or absent

<400> 12
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taagacgctc agttgtcagg ataattacgt tcgactgtag taaaacagga atctgtattg 120

ttagaaagaa cgagagtttt ttacggcgcc gccatattgg gccgtgtgaa aacagcttga 180

aaccccacta ctttcaaagg ttctgttgct atacacgaac catgtttaac caacctcgct 240

tttgacttga ctgaagtcat cggttaacaa tcaagtaccc tagtctgtct gaatgctcct 300

ttccatattc agtaggtgtt tcttgcactt ttgcatgcac tgcggaagaa ttagccaata 360

gcgcgtttca tatgcgcttt tacccccctct tttgtcaagc gcaaaatgcc tgtaagattt 420

ggtgggggtg tgagccgtta gctgaagtac aacaggctaa ttccctgaaa aaactgcaga 480

tagacttcaa gatctcaggg attcccacta tttggtattc tgatatgttt ttcctgatat 540

gcatcaaaac tctaatctaa aacctgaatc tccgctattt ttttttttnt tnngatgacc 600

ccgttttcgt gacaaattaa tttccaacgg ggtcttgtcc ggataagaga attttgtttg 660

attatccgtt cggataaatg gacgcctgct ccatattttt ccggttatta ccccacctgg 720

aagtgcccag aattttccgg ggattacgga taatacggtg gtctggatta attaatacgc 780

caagtcttac attttgttgc agtctcgtgc gagtatgtgc aataataaac aagatgagcc 840

aatttattgg attagttgca gcttgacccc gccatagcta ggcatagcca agtgctatgg 900

gtgttagatg atgcacttgg atgcagtgag ttttggagta taaaagatcc ttaaaattcc 960

accctt 966

<210> 13
<211> 1000

<212> DNA
<213> Artificial Sequence

<220>
<223> promoter

<400> 13
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ggccagggta aaaaattcga aatttgacac caaaaataaa gacttgtcgt tataagtctt 120

aacaaagtcc gcaattttgg agctaacggt ggcggttgct gggatattca ataatggtag 180

aatgttgctg cgggtatatg acagagcgtg aaacacactg aacaaggtaa atggaacaac 240

agcaattgca atatggggga ggatagtcaa gaacaaagca gcaatggcaa agtactgaat 300

attctccaaa gccaaaaggt ccagtggttt caacgacaaa gtcttgttgg tatagctttg 360

gaacaaaagg acaccgaaag actcgacagc gcccacaaat acagcgttgt agaagaacga 420

attgattgct ccagagcttc taatagtcag aagatacccc aaacctccga gcaacgttag 480

cacatgacct aagaaccagg cgaagtgaag agtctggaat aacgacaccc agtcagtttt 540

tcctgagctc ctggtgggat tggtagaagc atttgatttg cttggagtgg ttttatttga 600

agatggtgtt gaagccattg ttgctaaaga gtcggagttt tgcttttagg gtttgttaag 660

caaaggagga aaaactgcgc cgtttgaagt cccaggtagt ttcgcgtgtg aggccagcca 720

gggaaagctt ccttcggtac ttttttttct tttgcaggtt ccggacggat taagcttcgg 780

gttatgaggg gggcggtagc caattccgga cacaatattg cgtcgcagct agtcaccccg 840

ccataaatat acgcaggatt gaggtaataa catcgatagt cttagtaatt aatacaattc 900

agtggcgaat ttggcaacat gacgtaaggc ccactgttgt ctataaaagg ggatgaattt 960

tcatgttttt gaggcctccc ggacaattta ttgaactcaa 1000

<210> 14
<211> 1000
<212> DNA
<213> Artificial Sequence

<220>
<223> promoter

<400> 14
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tcatttgctg gttacactgg aaacgctact tttgttggcg gaaactctac cagtttggcc 120

gtccatgtaa acgatgtcgt tctgggccgt gaccgtttca acacgaacat aaccaatgac 180

aaatccactt acaggtctag ttcatatgga ggcaattggt accttacttc tttggatgtc 240

ccaagtgggg ctttaacgtc tggtactaac aatgtctcgt ttgtcactac aaactccgag 300

gtaaataaag gattcttgtg ggattctctc aagtttgttt ggaagttgta acaggtttat 360

aagcatatcg tgcgcttgtc cacaattgaa tcatttattg ttgcgagata catgaacaaa 420

gtgtgaactg ggacccatta ctacaattcc cacgcaaccg ttgtttcaaa gcccatattt 480

tttgacaatt gtttcgttac acccccagtt tgatgtacat cgcttgcaat gatgtgtgtc 540

ccggagtatt ttccatattc agcttgaatt cgtatactca accaatatct gggggtatac 600

ttttatgtaa cctatacaaa tcaactatac tatttcacct ttcgaccaat catctcccat 660

cttgttaagt tttgcttcct atatccctga ccctgacatc acccatgatt ccgctcaacg 720

gttctcctct acatcgtccc tcttttggag agggtgttca gtttgacatt caaattaccc 780

cccgccatca cgcgcaaccg agaccgcacc cccgaatttt cacaaattac cccacaccct 840

atactccacc actatgaggg ttattagaac tgatcacgta taaataccac cgcaagttcc 900

caagggatcg tgttcttctt ctccaattgc aatcatattt ctgactcttt ctagttcaga 960

ttaattcctt tacacttgct tttttccctt acctttatcc 1000

<210> 15
<211> 1001
<212> DNA
<213> Artificial Sequence

<220>
<223> promoter

<400> 15
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taccacgacg tcaaggaatg gaaacgacga cttggaggaa gacttcgtca acctcttgcg 120

gagtacccga ggctaagaca ataagaagaa aaaaaaaaga aaagcggtgg gggagggatt 180

attaaataag gattatgtaa ccccagggta ccgttctata catatttaag gattatttag 240

gacaatcgat gaaatcggca tcaaactgga tgggagtata gtgtccggat aatcggataa 300

atcatcttgc gaggagccgc ttggttggtt ggtgagagga gtgaaatatg tgtctcctca 360

cccaagaatc gcgatatcag caccctgtgg gggacactat tggcctccct cccaaacctt 420

cgatgtggta gtgctttatt atattgatta cattgattac atagctaaac cctgcctggt 480

tgcaagttga gctccgaatt ccaatattag taaaatgcct gcaagataac ctcggtatgg 540

cgtccgaccc cgcttaatta ttttaactcc tttccaacga ggacttcgta atttttgatt 600

agggagttga gaaacggggg gtcttgatac ctcctcgatt tcagatccca ccccctctca 660

gtcccaagtg ggacccccct cggccgtgaa atgcgcgcac tttagttttt ttcgcatgta 720

aacgccggtg tccgtcaatt aaaagtcgca gactagggtg aactttacca tttttgtcgc 780

actccgtctc ctcggaatag gggtgtagta attctgcagt agtgcaattt ttaccccgcc 840

aaggggggggc gaaaagagac gacctcatca cgcattctcc agtcgctctc tacgcctaca 900

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aacctctgct ttttcttgat ttttccttgc ccaaagaaaa g 1001

<210> 16
<211> 1000
<212> DNA
<213> Artificial Sequence

<220>
<223> promoter

<400> 16
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agtgaacttt aacacattga tcgggaaatt gaccaccaag ggaatgctgg ttgaggctgg 180

aagcgttgcc agtgtcctga gggaactgga ccgaaagttt agtaatgcat aagaggatat 240

atataggaat gcagtaataa tattagtacc cattaagtgg gctaagccat tggaaggccg 300

tctgactgat ggtggtgttc ttctcattta gatagtgcat ttgcaactac cgtctgagat 360

tgagtttgat gtgaagctcc agcgccaaaa cagtataaga accttatctc cgcattattg 420

ttcttgcgta aaagtttgtg tgaagaaaca ggggtagttg cgcagattag ttgtaatatg 480

cgcataggat gggtcattga cttctttcct cgaaagagcc acaccgttag ctaaaaaagg 540

acgcgcatct accccaaaat agaatgtggg gaaataggac gcgcaacttc ctctcaatca 600

ctggacgtca gaaaaacaaa tgcgcaatcg agtcaccctc cgtgataccc tccgtgatac 660

cccctctccg tctattctga cagcgtctcc ccatgacgtt tcaatctact tagaaaagat 720

ttcgtttttt tttccttcaa ttacacgatc tcatcttctg caagggtctg gaggacatca 780

ccaatctgcg actccataac ttagtcctga gtttatattt acgcttcatc tgatgagtag 840

gaagaaaaag tttcacgaaa ttcccccgcc aacttgccct tcggaataag cagccactct 900

ccttctgccc atagtaagct tgcgcgaggc cccaacttgg ccagaaactt taaatatgcc 960

aaacaatctc ccccaatcta agttctccct cttctaaaaa 1000

<210> 17
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> regulatory region

<400> 17
ataaatgga 9

<210> 18
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> regulatory region

<400> 18
catatttttc cggtt 15

<210> 19
<211> 15

<212> DNA
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<220>
<223> motif

<400> 19
tatttttttt ttttt 15

<210> 20
<211> 15
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<220>
<223> motif

<400> 20
ttttttttt ttttt 15

<210> 21
<211> 16
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<220>
<223> motif

<400> 21
tatttttttt tttttt 16

<210> 22
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> motif

<400> 22
ttttttttt tttttt 16

<210> 23
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> motif

<400> 23
tatttttttt ttttttt 17

<210> 24
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> motif

<400> 24
ttttttttttt ttttttt 17

<210> 25
<211> 18
<212> DNA
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<220>
<223> motif

<400> 25
tatttttttt tttttttt 18

<210> 26
<211> 18
<212> DNA
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<220>
<223> motif

<400> 26
ttttttttttt tttttttt 18

<210> 27
<211> 19
<212> DNA
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<220>

<223> motif

<400> 27
tatttttttt ttttttttt 19

<210> 28
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> motif

<400> 28
ttttttttt ttttttttt 19

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> motif

<400> 29
tatttttttt ttttttttt 20

<210> 30
<211> 20
<212> DNA
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<220>
<223> motif

<400> 30
ttttttttt ttttttttt 20

<210> 31
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> motif

<400> 31
tatttttttt ttttttttt t 21

<210> 32
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> motif

<400> 32
ttttttttt ttttttttt t 21

<210> 33
<211> 22
<212> DNA
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<220>
<223> motif

<400> 33
tatttttttt ttttttttt tt 22

<210> 34
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> motif

<400> 34
ttttttttt ttttttttt tt 22

<210> 35
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> main regulatory region

<400> 35
ataaatggac gcctgctcca tatttttccg gtt 33

<210> 36
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> spacer core region

<400> 36
cgcctgctc 9

<210> 37
<211> 255
<212> DNA
<213> Artificial Sequence

<220>
<223> spacer main region

<400> 37
attaccccac ctggaagtgc ccagaatttt ccggggatta cggataatac ggtggtctgg 60

attaattaat acgagatctc agggattccc actatttggt attctgatat gtttttcctg 120

atatgcatca aaactctaat ctaaaacctg aatctccgct ttttttttt tttttgatga 180

ccccgttttc gtgacaaatt aatttccaac ggggtcttgt ccggataaga gaattttgtt 240

tgattatccg ttcgg 255

<210> 38
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> translation initiation site

<400> 38
ttccaccctt 10

<210> 39
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> translation initiation site

<400> 39
ttcgaaacg 9

<210> 40
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> translation initiation site

<220>
<221> misc_feature
<222> (7)..(7)
<223> R at position 7 is A or G, preferably A

<400> 40
gccgccrcc 9

<210> 41
<211> 859
<212> DNA
<213> Artificial Sequence

<220>
<223> promoter

<400> 41
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gaaaacagct tgaaacccca ctactttcaa aggttctgtt gctatacacg aaccatgttt 120

aaccaacctc gcttttgact tgactgaagt catcggttaa caatcaagta ccctagtctg 180

tctgaatgct cctttccata ttcagtaggt gtttcttgca cttttgcatg cactgcggaa 240

gaattagcca atagcgcgtt tcatatgcgc ttttaccccc tcttttgtca agcgcaaaat 300

gcctgtaaga tttggtgggg gtgtgagccg ttagctgaag tacaacaggc taattccctg 360

aaaaaactgc agatagactt caagatctca gggattccca ctatttggta ttctgatatg 420

tttttcctga tatgcatcaa aactctaatc taaaacctga atctccgcta ttttttttt 480

tttttgatg accccgtttt cgtgacaaat taatttccaa cggggtcttg tccggataag 540

agaattttgt ttgattatcc gttcggataa atggacgcct gctccatatt tttccggtta 600

ttaccccacc tggaagtgcc cagaattttc cggggattac ggataatacg gtggtctgga 660

ttaattaata cgccaagtct tacattttgt tgcagtctcg tgcgagtatg tgcaataata 720

aacaagatga gccaatttat tggattagtt gcagcttgac cccgccatag ctaggcatag 780

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tccttaaaat tccaccctt 859

<210> 42
<211> 664
<212> DNA
<213> Artificial Sequence

<220>
<223> promoter

<400> 42
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tgggggtgtg agccgttagc tgaagtacaa caggctaatt ccctgaaaaa actgcagata 180

gacttcaaga tctcagggat tcccactatt tggtattctg atatgttttt cctgatatgc 240

atcaaaactc taatctaaaa cctgaatctc cgctattttt ttttttttt tgatgacccc 300

gttttcgtga caaattaatt tccaacgggg tcttgtccgg ataagagaat tttgtttgat 360

tatccgttcg gataaatgga cgcctgctcc atatttttcc ggttattacc ccacctggaa 420

gtgcccagaa ttttccgggg attacggata atacggtggt ctggattaat taatacgcca 480

agtcttacat tttgttgcag tctcgtgcga gtatgtgcaa taataaacaa gatgagccaa 540

tttattggat tagttgcagc ttgaccccgc catagctagg catagccaag tgctatgggt 600

gttagatgat gcacttggat gcagtgagtt ttggagtata aaagatcctt aaaattccac 660

cctt 664

<210> 43
<211> 493
<212> DNA
<213> Artificial Sequence

<220>
<223> promoter

<400> 43
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gatgaccccg ttttcgtgac aaattaattt ccaacggggt cttgtccgga taagagaatt 180

ttgtttgatt atccgttcgg ataaatggac gcctgctcca tatttttccg gttattaccc 240

cacctggaag tgcccagaat tttccgggga ttacggataa tacggtggtc tggattaatt 300

aatacgccaa gtcttacatt ttgttgcagt ctcgtgcgag tatgtgcaat aataaacaag 360

atgagccaat ttattggatt agttgcagct tgaccccgcc atagctaggc atagccaagt 420

gctatgggtg ttagatgatg cacttggatg cagtgagttt tggagtataa aagatcctta 480

aaattccacc ctt 493

<210> 44
<211> 370
<212> DNA
<213> Artificial Sequence

<220>
<223> promoter

<400> 44
gaccccgttt tcgtgacaaa ttaatttcca acggggtctt gtccggataa gagaattttg 60

tttgattatc cgttcggata aatggacgcc tgctccatat ttttccggtt attaccccac 120

ctggaagtgc ccagaatttt ccggggatta cggataatac ggtggtctgg attaattaat 180

acgccaagtc ttacattttg ttgcagtctc gtgcgagtat gtgcaataat aaacaagatg 240

agccaattta ttggattagt tgcagcttga ccccgccata gctaggcata gccaagtgct 300

atgggtgtta gatgatgcac ttggatgcag tgagttttgg agtataaaag atccttaaaa 360

ttccaccctt 370

<210> 45
<211> 328
<212> DNA
<213> Artificial Sequence

<220>
<223> promoter

<400> 45
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ttccggttat taccccacct ggaagtgccc agaattttcc ggggattacg gataatacgg 120

tggtctggat taattaatac gccaagtctt acattttgtt gcagtctcgt gcgagtatgt 180

gcaataataa acaagatgag ccaatttatt ggattagttg cagcttgacc ccgccatagc 240

taggcatagc caagtgctat gggtgttaga tgatgcactt ggatgcagtg agttttggag 300

tataaaagat ccttaaaatt ccaccctt 328

<210> 46
<211> 1000
<212> DNA
<213> Pichia pastoris

<400> 46
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caaacctaaa cgcttaatgc ctcagacgtt ttaatgcctc tcaacacctc caaggttgct 120

ttcttgagca tgcctactag gaactttaac gaactgtggg gttgcagaca gtttcaggcg 180

tgtcccgacc aatatggcct actagactct ctgaaaaatc acagttttcc agtagttccg 240

atcaaattac catcgaaatg gtcccataaa cggacatttg acatccgttc ctgaattata 300

gtcttccacc gtggatcatg gtgttccttt ttttcccaaa gaatatcagc atcccttaac 360

tacgttaggt cagtgatgac aatggaccaa attgttgcaa ggtttttctt tttctttcat 420

cggcacattt cagcctcaca tgcgactatt atcgatcaat gaaatccatc aagattgaaa 480

tcttaaaatt gccccttca cttgacagga tccttttttg tagaaatgtc ttggtgtcct 540

cgtccaatca ggtagccatc tctgaaatat ctggctccgt tgcaactccg aacgacctgc 600

tggcaacgta aaattctccg gggtaaaact taaatgtgga gtaatggaac cagaaacgtc 660

tcttcccttc tctctccttc caccgcccgt taccgtccct aggaaatttt actctgctgg 720

agagcttctt ctacggcccc cttgcagcaa tgctcttccc agcattacgt tgcgggtaaa 780

acggaggtcg tgtacccgac ctagcagccc agggatggaa aagtcccggc cgtcgctggc 840

aataatagcg ggcggacgca tgtcatgaga ttattggaaa ccaccagaat cgaatataaa 900

aggcgaacac ctttcccaat tttggtttct cctgacccaa agactttaaa tttaatttat 960

ttgtccctat ttcaatcaat tgaacaacta tcaaaacaca 1000

<210> 47
<211> 756
<212> PRT
<213> Pichia pastoris

<400> 47

Met Ile Pro Thr Ile Asp Pro Lys Asp Pro Glu Leu Val Ser Glu Asp
1 5 10 15

Thr Ala Gln Ser Ala Ser Ala Arg Lys Arg Ser Lys Val Ser Arg Ala
20 25 30

Cys Asp Glu Cys Arg Arg Lys Lys Ile Lys Cys Asp Ala Thr Phe Leu
35 40 45

Ala Asn Ser Asn Thr Leu Leu Lys Pro Cys Thr Asn Cys Tyr Lys Tyr
50 55 60

Asn Cys Ser Cys Ser Phe Thr Arg Val Pro Leu Lys Arg Gly Pro Ser
65 70 75 80

Lys Gly Phe Ala Arg Asp Gly Ser Gly Tyr Glu Arg Arg Arg Ser Ser
85 90 95

Ser Val His Ser Val Ser Ser Ser Gln Ser Val Thr Ser Pro Val Pro
100 105 110

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Ser His Ala Ser Leu Pro Ile Pro Pro Ala Asn Pro Val Ser Leu Pro
        115                 120                 125

Arg Leu Asn Val Pro Gly Asp Gly Leu Leu Ser Pro Lys Ala Val Pro
    130                 135                 140

Pro Thr Asn Leu Phe Trp Lys Val Pro Tyr Glu Leu Pro Ser Phe Ser
145                 150                 155                 160

Asp Arg Arg Ser Ser Val Ala Ser Ala Asp Ser Phe Arg Arg Pro Ser
                165                 170                 175

Ile Tyr Gln Ser Asp Ser Glu Asp Asp Phe Tyr Ser Ala Thr Gly Ser
            180                 185                 190

Gln Arg Asn Ser Ile Ser Gln Ala Pro Arg Gln Arg Asn Leu Ser Pro
        195                 200                 205

Ala Leu Ser Val Ser Ser Thr Ser Ser Leu Asn Asn Arg Ile Lys Ser
    210                 215                 220

Leu Asn Met Val Ala Ser Thr Leu Glu Ser Asn Ile His Asn Tyr Tyr
225                 230                 235                 240

Ser Gln Gly Phe Asn Ser Ser Leu Pro Ile Leu Pro Leu Asp Glu Arg
                245                 250                 255

Ile Leu Ser Thr Leu Leu Ser Asn Val Ser Asn Gly Ser Ser Ser Ala
            260                 265                 270

Ser Trp Asp Ala Ile Arg Ser Pro Ile Leu Glu Leu Phe Asp Lys Ser
        275                 280                 285

Ile Leu Met Leu Leu Arg Ser Tyr Glu Ser Gln Phe Asn Phe Asn Asp
    290                 295                 300

Leu Leu Asp His Val Thr Glu Met Gln Ser Ile Tyr Pro Arg Ile Arg
305                 310                 315                 320
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Ser His Leu Leu Ser Asp Glu Leu Leu Lys Leu Ile Phe Leu Met Ser
                325                 330                 335

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

Thr Gly Leu Ser Ile Thr Val Ser Val Phe Asn Asp Trp Lys Thr Tyr
        355                 360                 365

Glu Asn Val Gln Arg Val Leu Val Ile Asn Arg Ala Gly Ser Leu Asp
    370                 375                 380

Leu Asp Tyr Asp Ser Leu Pro Phe Leu Phe Ala Arg Cys Tyr Leu Ser
385                 390                 395                 400

Leu Ala Thr Leu Asp Leu Ile Tyr Ser Leu Ser Phe Ser Ser Pro Arg
                405                 410                 415

Leu Ile Ser Ser Phe Ala Asn Leu Pro Ile Leu Asp Ile Val Gln Lys
            420                 425                 430

Cys Gly Ile Thr Lys Asp Ala Lys Leu Asp Glu Thr Pro Leu Pro Val
        435                 440                 445

Leu Asp Gln Phe Leu Asn Cys Phe Leu Pro Gly Asp Thr Tyr Pro Thr
    450                 455                 460

Ala Leu Asn Thr Leu Lys Thr Gly Leu Val Leu Leu Asp Phe Thr Asn
465                 470                 475                 480

Asn Arg Ser Thr Thr Leu Arg Phe Pro Phe Ile Asn Ile His Asp Asp
                485                 490                 495

Asn His Met Thr Gly Leu Ser His Leu Leu Ser Asn Val Ser Asp Phe
            500                 505                 510
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Met Ser Gln Phe Thr Glu Val His Ser Asp Ser Lys Asp Ser Gln Leu
        515                 520                 525

Leu Phe Leu Arg Cys Ile Trp Ala Phe Trp Glu Ile Gly Ser Val Leu
    530                 535                 540

Ser Glu Leu Ile Asp His Phe Ile Ser Ser Ser Ala Asn Ser Gln Val
545                 550                 555                 560

Gly Asp Lys Asp Ala Ser Phe Phe Tyr Glu His Gln Leu Lys Val Thr
                565                 570                 575

Thr Leu Leu Gly Thr Phe Ser Asn Ile Ala Ser Ala Phe Leu Thr Ser
            580                 585                 590

Ser Thr Thr Ala Ala Ser His Pro Pro Pro Ser Ile Ser Pro Phe His
        595                 600                 605

Ile Ile Ser Met Val Glu Ser Phe Lys Met Val Gln Phe Leu Asn Lys
    610                 615                 620

Leu Ile Ala Ser Phe Ile Ser Leu Asn Glu Lys Leu Glu Lys Arg Glu
625                 630                 635                 640

Leu Glu Asp Glu Leu Ser Lys Cys Lys Glu Glu Leu Asn Asn Leu Asn
                645                 650                 655

Glu Arg Phe Gln Ala Val Ser Ser Val Gln Thr Leu Pro Val Val His
            660                 665                 670

Val Leu Phe Arg Asp Leu Val Phe Ser Ser Asn Arg Leu Asp Thr Gln
        675                 680                 685

Arg Asp Arg Ala Ser Ser Val Val Ser Ala Thr Thr Thr Thr Ser Thr
    690                 695                 700

Ala Thr Thr Thr Ala Thr Thr Lys Lys Ser Ser Phe Gly Asn Leu Leu
705                 710                 715                 720
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His Ser Asp Glu Glu Asn Ile Leu Pro Thr Val Ile Asp Trp Cys Lys
                725                 730                 735


Glu Gln Lys His Ser Ala Glu Met Phe Leu Asn Lys Asn Asp Leu Asn
            740                 745                 750


Gly Trp Leu Tyr
        755


<210>  48
<211>  1036
<212>  PRT
<213>  Pichia pastoris

<400>  48

Met Met Pro Glu Glu Gln Val Thr Ser Pro Gln Arg Lys His Gln Lys
1               5                   10                  15


Ser Lys Ala Lys Thr Ile Arg Ala Pro Gly Ser Ser Ile Glu Arg Val
            20                  25                  30


Ala Gln Ala Cys Asp Arg Cys Arg Ser Lys Lys Thr Arg Cys Asp Gly
        35                  40                  45


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


Ile Ser Asp Lys Leu Ser Arg Arg Ala Phe Pro Arg Gly Tyr Thr Glu
65                  70                  75                  80


Thr Leu Glu Glu Arg Ile Arg Glu Leu Glu Phe Glu Asn Lys Lys Leu
                85                  90                  95


His Lys Leu Ile Asp Leu Lys Asn Glu Gln Val Glu Ile Lys Asn Arg
            100                 105                 110


Ile Asp Gln Glu Ser Thr Leu Thr Asn Glu Asn Leu Thr Leu Leu Asn
```

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        115                 120                 125

Lys Glu Gln Glu Val Ser His Ser Gly Asn Ile His His His Ala Asp
    130                 135                 140

Gly Glu Pro Cys Asn Cys Ala Asn Ser Val Ser Ala Arg Pro Val Ser
145                 150                 155                 160

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

Asp Ser Leu Tyr Ser Ala Ala Ser Tyr Asn Ala Lys Tyr His Gln Thr
            180                 185                 190

Gly Thr Ser Gly Pro Glu Met Val Arg Leu Ser Gln Arg Tyr Ser Ser
        195                 200                 205

Gly Asn Phe Asn Asp Pro Leu Ser Phe Glu Gln Ser Asn Ala Pro Gly
    210                 215                 220

Ala Ala Ala Ala Ile Ser Ile Gln Asn Lys Met Arg Thr Gln Thr Phe
225                 230                 235                 240

Val Asn Leu Ala Asn Leu Val Ala Met Ser Ile Pro Arg Thr Thr Glu
                245                 250                 255

Glu Thr Leu Phe Ile Ala Ser Leu Leu Ala Lys Ile Cys Asn Val His
            260                 265                 270

Gly Phe Gln Ser Lys Ala Pro Ile Leu Thr Ala Lys Ser Ile Ala Leu
        275                 280                 285

Leu Lys Asp Lys Tyr Asn Tyr Gly Asn Asp Glu Val Phe Ala Asn Ile
    290                 295                 300

Thr Leu Lys Asn Val Asn Phe Asn Lys Leu Thr Ser Gln Gln Ser Gln
305                 310                 315                 320
```

```
Gln Phe Phe Gln Ser Leu Asn Leu Pro Asn Gln Val Asn Leu Asp Leu
                325                 330                 335

Phe Ile Thr Thr Phe Phe Asn Thr Trp Asn Asn Phe Ile Pro Ile Ile
            340                 345                 350

Asn Arg His Ile Phe Met Ser Ser Tyr Ile Lys Phe Asn Lys Ser Arg
        355                 360                 365

Glu Thr Met Phe Thr Asp Asn Ser Met Phe Gly Asn Glu Lys Phe Gly
    370                 375                 380

Glu Ile Leu Leu Leu Ile Thr Thr Met Val Met Leu Ser Gln Glu Arg
385                 390                 395                 400

Asn Asn Asn Arg Glu Ala Val Pro Ser Ser Ser Tyr Lys Lys Asp Ser
                405                 410                 415

Thr Pro His Pro His Arg Pro Asp Ala Ser Ser Gln Ser Asn Val Glu
            420                 425                 430

Ile Leu Gln Tyr Tyr Asp His Leu Ile His Glu Phe Ile Lys Ser Asn
        435                 440                 445

Ile Ser Asp Asp Cys Ser Leu Pro Thr Leu Glu Ser Leu Ser Leu Gln
    450                 455                 460

Leu Leu Tyr Cys Leu Ala Ile Gly Asp Leu Thr Thr Ser Tyr Glu Leu
465                 470                 475                 480

Arg Gly Lys Ile Ile Thr Met Gly Gln Gln Leu Arg Leu His Arg Cys
                485                 490                 495

Pro Ser Ala Val Leu Gly Thr Asn Gly Ser Lys Val Ser Gln Met Gln
            500                 505                 510

Gln Gly Glu Arg Arg Ile Leu Phe Trp Cys Ile Tyr Ile Leu Asp Thr
```

```
        515                 520                 525

Phe Ser Ala Leu Ile Leu Gly Val Pro Arg Leu Leu Lys Asp Tyr Glu
    530                 535                 540

Ile Glu Cys Ala Leu Pro Phe Ser Asn Glu Ser Asn Asn Ala Asn Val
545                 550                 555                 560

Lys Gly Ser Ile Glu Asn Thr Thr Asn Thr Val Ile Ile Asn Asn Ile
                565                 570                 575

Lys Leu Ser Leu Ala Gly Lys Val Ser Asp Cys Ala Leu Ala Val Met
            580                 585                 590

Arg Tyr Ser Lys Val Leu Gly Asn Ile Leu Asp Ser Ile Phe Gln Arg
        595                 600                 605

Ser Ser Ile Asn Asn Pro Ser Val Val Ser Lys Ser Thr Asn Ile Thr
    610                 615                 620

Glu Glu Thr Cys Leu Leu His Glu His Ala Leu Asp Leu Trp Arg Arg
625                 630                 635                 640

Glu Leu Ser Pro His Ile Asn Val Asp Leu Asp Lys Ser Pro Gly Gly
                645                 650                 655

Val Glu Tyr Glu Arg Leu Ser Asp Asn Gln Leu Thr Ile Leu Phe Leu
            660                 665                 670

Tyr Tyr His Ala Lys Ile Leu Ile Tyr Leu Pro Leu Met Ala Asn Glu
        675                 680                 685

Ser Ser Gln Ser Arg Ser Ser Ala Ser Tyr Ile Asn Ile Gln Gln Ser
    690                 695                 700

Thr Thr Ser Ile Leu Ala Ile Ala Asn Thr Leu Ala Thr Lys Glu Arg
705                 710                 715                 720
```

```
Asn Phe Tyr Phe Leu Pro Leu Pro Val Asn Leu Ser Arg Glu Lys Val
                725                 730                 735

Arg Leu Ala Phe Leu Ser Ala Lys Gly Ser Leu Glu Tyr Ala Arg Gly
            740                 745                 750

Gly Ala Leu Phe Gln Glu Ser Lys Ile Leu Leu Ala Ser Val Ile Asn
        755                 760                 765

Glu Leu Lys Ile Glu Thr Ser Ile Gly Met Leu Gly Cys Leu Ser Val
    770                 775                 780

Pro Cys Met Glu Ala Val Asp Asn Ala Met Glu Gln Ile Met Ala Leu
785                 790                 795                 800

Pro Gly Lys Val Ser Ser Val Asn Gly Ser Asn Ser Glu Met Lys Arg
                805                 810                 815

Ser Ser Ser Lys Arg Lys Ser Ser Pro Leu Arg Gln Asp Ile Ser Gly
            820                 825                 830

Asp Glu Arg Lys Ser His Asn Ile Glu Val Ser Asp Ser Arg Thr Pro
        835                 840                 845

Ser Val Gln Ser Ser Leu Tyr Pro Gln Pro Asn Gln Met His His Pro
    850                 855                 860

Asn Ile Ile Lys Ser Glu Asn Asn Glu Gln Met Ile Pro Glu Asn Asp
865                 870                 875                 880

Thr Pro Gly Ala Ile Asn Asp Ile Phe Thr Ser His Ser Pro Pro Gly
                885                 890                 895

Thr Val Thr Ser Met Lys Glu Glu Asp Leu Pro Ile Lys Val Pro Ile
            900                 905                 910

Leu Leu Gln Thr Gln Gln Arg Gln Ile Tyr Asn Asn Asn Pro Asn His
```

```
        915                 920                 925

Ser Leu Phe Ser Gln Gln Pro Gly Thr Gln Val Leu Ser Gly Gln Gln
    930                 935                 940

Met Pro Gly Pro Ser Ser Thr Asp Gln Gln Phe Lys Arg Ile Thr Thr
945                 950                 955                 960

Pro Asp Gly Leu Asp Ser Leu Met Met Gln Asp Phe Gly Val Asp Ala
                965                 970                 975

Ser Leu Gly Leu Pro Met Leu Asp Phe Asp Phe Asn Phe Asp Phe Glu
            980                 985                 990

Asn Val Gln Asn Asn Tyr Ser Gln  Ser Asn Val Ser Pro  Pro Asn Ser
        995                 1000                1005

Glu Ser  Val Pro Ser Ser Ile  Gln Gly Thr His Ser  Asn Asp Pro
    1010                1015                1020

Lys Asp  Ser Gln Val Ser Ala  Gly Ser Leu Phe Gly  Leu
    1025                1030                1035
```

<210> 49
<211> 887
<212> PRT
<213> Pichia pastoris

<400> 49

```
Met Lys Glu Asn Gln Ala Ser Asn Lys Phe Asn Leu Ile Lys Asn Pro
1               5                   10                  15

Ile Thr Gly Lys Pro Arg Ile Ser Gln Ala Cys Asp Arg Cys Arg Ile
            20                  25                  30

Lys Lys Ile Lys Cys Asp Gly Thr Leu Pro Ser Cys Thr Asn Cys Ser
        35                  40                  45
```

```
Lys Ile Gly Phe Val Cys Lys Ile Ser Asp Arg Leu Thr Arg Ser Ser
    50                  55                  60

Phe Pro Lys Gly Tyr Thr Lys Asn Leu Glu Gln Lys Leu Ile Asp Met
65                  70                  75                  80

Glu Leu Asp Arg Asn Arg Leu Met Leu Glu Leu Asn Arg Ile Lys Lys
                85                  90                  95

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

Ser Ser Ser Glu Asn Leu Lys Ser Asp Asp Ser Ser Glu Cys Gln Ser
        115                 120                 125

Val Thr Val Ser Leu Ser Ser Thr Ser Gly Pro Ser Leu Ser Pro Glu
    130                 135                 140

Pro Lys Gln Asp Asp Phe Arg Phe Arg Val Gly Met Asp Gly Ser Phe
145                 150                 155                 160

Val Leu Asn Gln Phe Leu Gln Ser Pro Leu Met Asp Tyr Ile Lys Ser
                165                 170                 175

Leu Asn Val Leu Gln Phe Asn Gly Cys Ala Asn Phe Asp Gln Ser Phe
            180                 185                 190

Asn Asp Asp Pro Leu Val Leu Asn Lys Tyr His Met Asn Leu Asn Arg
        195                 200                 205

Phe Leu Asn Leu Ile Phe Tyr Lys Leu Leu Leu Pro Leu Ile His Arg
    210                 215                 220

Asn Ser Asn Thr Leu Asn Glu Lys Phe Ala Glu Asp Asn Asn Ser Leu
225                 230                 235                 240

Asp Ser Leu Ile Trp Lys Phe Phe Thr Asn Tyr Asn Lys Leu Ile Pro
                245                 250                 255
```

```
Ile Leu Glu Phe Asp Ser Phe Tyr Lys Asp Tyr Leu Gln Phe Ile His
            260                 265                 270

Lys Tyr Tyr Ser Asn Asn Gln Val Phe Val Asp Gly Phe Arg Lys Tyr
        275                 280                 285

Phe Glu Phe Ser Glu Phe Glu Gln Cys Phe Ile Val Lys Leu Ile Leu
    290                 295                 300

Ile Leu Lys Phe Thr Leu Pro Val Ile His Asp Thr Ser Val Pro Ser
305                 310                 315                 320

Glu Ile Tyr Arg Leu Ile Ser Met Asp Ser Leu Gln Arg Leu Phe Gly
                325                 330                 335

Asn Ile Asp Phe Leu Lys Pro Ser Thr Asp Lys Val Ser Ile Leu Leu
            340                 345                 350

Leu Val Leu His Tyr Met Val Leu Tyr Glu Ser Pro Lys Ser Leu Leu
        355                 360                 365

Asp Thr Gln Asp Glu Ala Gln Lys Tyr Asp Glu Phe Ile Gly Asn Leu
    370                 375                 380

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

Pro Arg Lys Leu Gln Phe Pro Arg Pro Leu Pro Ser Asn Gly Asn Arg
                405                 410                 415

Leu Arg Ile Lys Leu Ser Trp Cys Tyr Lys Leu Ile Ser Lys Leu Phe
            420                 425                 430

Arg Val Ile Tyr Asn Ile Asp Asn Asp Ser Leu Tyr Ser Leu Asp Asp
        435                 440                 445
```

```
Ser His Leu Pro Glu Leu Gln Ser Ile Ser Ile Leu His Glu Glu Leu
    450                 455                 460

Asp Val Thr Ile Gln Phe Asn Asn Leu Leu Asn Leu Ile Pro Asn Asn
465                 470                 475                 480

Phe His Ser Leu Arg Asp Lys Gln Ser Leu Ser Lys Ile Lys Thr Gln
                485                 490                 495

Leu Leu Glu Trp His Lys Asn Phe Asn Thr Glu Phe Val Glu His Phe
            500                 505                 510

Asn Leu Asn Asp Thr Asp Ser Asp Glu Leu Ser Ala Glu Lys Ile Asn
        515                 520                 525

Val Leu Arg Ser Lys Leu Ile Ser Leu Asn Arg Leu Asn Cys Tyr Asn
    530                 535                 540

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

Ser Val Val Ser Gly Ile Phe Gly Leu Ser Asn Glu Met Leu Ile Asp
                565                 570                 575

Asn Lys Ser Ser Thr Glu Leu Leu Asn Thr Leu Gln Gln Thr Pro Ile
            580                 585                 590

Ile His Gln Ser Ser Ile Leu Val Ser Leu Cys Tyr Arg Ile Gln Thr
        595                 600                 605

Gly Asn Leu Gln Asp Glu Ile Cys Ser Ile Leu Val Asn Asn Tyr Glu
    610                 615                 620

Lys Leu Leu Gln Cys Asn Asp Ala Gly Leu Pro Ile Lys Ile Leu Pro
625                 630                 635                 640

Gln Leu Val His Tyr Phe Lys Gly Lys Ile Ser Thr Asn Leu Ser Asn
                645                 650                 655
```

```
Ser Ala Ala His Glu Asp Leu Met Asn Met Phe Thr Leu Asn Asp Asn
            660                 665                 670

Leu Ser Thr Thr Thr Thr Asp Leu Asp Ser Phe Ile Ile Pro Pro Lys
        675                 680                 685

Arg Lys Gln Asp Gln Thr Leu Pro Ile Gly Thr Lys Arg Ser Lys Ser
    690                 695                 700

Ala Ser Thr Ser Ser Val Ile Ser Ser Asp Asp Cys Ser Leu Phe Ser
705                 710                 715                 720

Asn Ser Leu Ser Val Pro Thr Thr Phe Ser Gly Ser Ser Ile Ser Val
                725                 730                 735

Gly Met Asp Asn Pro Pro Ser Ser Leu Phe Gly Ser Tyr Lys Arg Pro
            740                 745                 750

Ser Ser Ile Val Lys Gln Glu Pro Thr Ile Asn Pro Arg Ser Asn Gly
        755                 760                 765

Thr Asn Thr Asp Ser Asn Leu Phe Asp Thr Phe Asn Asp Ser Ile Lys
    770                 775                 780

Gly Ser Leu Asn Asn Gly Leu Lys Lys Leu Lys Asp Ile Arg Cys Asn
785                 790                 795                 800

Ser Val Val Glu Arg Ser His Ser Ser Gln Arg Asn Asp Phe Leu Met
                805                 810                 815

Asp Gln Glu Asp Ser Ile Thr Lys Glu Thr Ile Asn Phe Ser Glu Leu
            820                 825                 830

Phe Thr Cys Gly Thr Pro Thr Ala Ser Gln Ser Ile Asp Arg Ser Pro
        835                 840                 845
```

```
Lys Ser Leu Leu Leu Asn Asp Leu Ala Ile Ala Pro Asp Thr Leu Val
    850                 855                 860

Ile Lys Pro Asp Ala Glu Asp Leu Asp Arg Leu Lys Asn Lys Ile Arg
865                 870                 875                 880

Ser Val Lys Ser Thr Val His
                885
```

<210> 50
<211> 26
<212> PRT
<213> Komagataella phaffii

<400> 50

```
Leu Leu Asn Gly Tyr Ile Tyr Asp Tyr Leu Val Lys Ser Asn Met Gln
1               5                   10                  15

Asn Leu Ala Asp Gln Phe Ala Gln Glu Thr
            20                  25
```

<210> 51
<211> 25
<212> PRT
<213> Komagatella pastoris

<400> 51

```
Leu Asn Gly Tyr Ile His Asp Tyr Leu Val Lys Ser Asn Met Gln Asn
1               5                   10                  15

Leu Ala Asp Gln Phe Ala Gln Glu Ser
            20                  25
```

<210> 52
<211> 25
<212> PRT
<213> Saccharomyces cerevisiae

<400> 52

```
Leu Asn Glu Tyr Ile Phe Asp Phe Leu Thr Lys Ser Ser Leu Lys Asn
```

1 5 10 15

Thr Ala Ala Ala Phe Ala Gln Asp Ala
20 25

<210> 53
<211> 25
<212> PRT
<213> Saccharomyces cerevisiae

<400> 53

Leu Asn Glu Tyr Ile Phe Asp Phe Leu Thr Lys Ser Ser Leu Lys Asn
1 5 10 15

Thr Ala Ala Ala Phe Ala Gln Asp Ala
20 25

<210> 54
<211> 27
<212> PRT
<213> Yarrowia lipolytica

<400> 54

Glu Leu Leu Asn Ala Tyr Ile Tyr Asp Tyr Leu Leu Lys His Asn Met
1 5 10 15

His Asp Ser Ala Arg Thr Phe Gly Ala Glu Ala
20 25

<210> 55
<211> 27
<212> PRT
<213> Ogataea polymorpha

<400> 55

Glu Leu Leu Asn Ala Tyr Val Tyr Asp Phe Ile Leu Lys Ser Gly Phe
1 5 10 15

Thr Ala Thr Ala Ser Ala Phe Phe Lys Glu Ala
20 25

<210> 56
<211> 26
<212> PRT
<213> Aspergillus niger

<400> 56

Asn Asn Leu Asn Thr Tyr Ile Tyr Asp Tyr Phe Leu Lys Arg Gly Tyr
1 5 10 15

His Asp Cys Ala Arg Ala Leu Val Lys Asp
20 25

<210> 57
<211> 774
<212> DNA
<213> Artificial Sequence

<220>
<223> scR sequence

<400> 57
caggaacaac taatggagtc tgggggtggt ttggttaccc tgggtggttc tcttaagctt 60

tcatgtaagg cctctggtat tgatttttcg cactacggta tctcctgggt tagacaagct 120

cctggaaaag gtctggaatg gatcgcttac atttacccaa attacggttc tgttgactat 180

gcctcctggg tcaatggtag gttcactatt tcccttgaca acgctcagaa cacggtattc 240

ctacagatga tctccctaac cgctgctgat actgcaacct acttctgtgc tcgtgacaga 300

ggttactact ctggctctcg tggaactaga cttgacttat ggggacaagg tactctcgtt 360

accatctcta gtggtggagg tggttctgga ggaggaggtt ccggcggagg tggtagcgag 420

ctggtcatga ctcaaacccc tccatcccta tctgcatcag tcggtgaaac cgttagaatt 480

agatgccttg catctgagtt cttgttcaac ggtgtgtcct ggtatcaaca aaagcctggt 540

aagcctccaa agtttctcat ttctggtgcc tcaaacctcg aatctggagt gccaccaaga 600

ttttccggat ctggctctgg tactgactac actctgacaa ttggtggtgt tcaagctgag 660

gatgttgcta cctactattg tctcggtggt tactcaggat cttccggcct aactttcggt 720

gccggtacaa acgtcgagat caaaggtgga catcaccacc accatcacta atag 774

<210> 58
<211> 837
<212> DNA
<213> Artificial Sequence

<220>
<223> vHH sequence

<400> 58
caggttcagc tgcaggagtc cggtggtggt ctggttcaag ccggtggttc attaagattg 60

tcctgtgctg cctctggtag aactttcact tctttcgcaa tgggttggtt tagacaagca 120

cctggaaaag agagagagtt tgttgcttct atctccagat ccggtacttt aactagatac 180

gctgactctg ccaagggtag attcactatt tctgttgaca acgccaagaa cactgtttct 240

ttgcaaatgg acaaccttaa cccagatgac accgcagtct attactgtgc cgctgacttg 300

cacagaccat acggtccagg aacccaaaga tccgatgagt acgattcttg gggtcaggga 360

actcaagtca ctgtctcttc aggtggtgga tctggtggtg gaggttcagg tggtggagga 420

tccggtggtg gtggttctgg tggtggtgga tctggtggag gtgaagttca acttgtcgaa 480

tccggtggtg cacttgtcca acctggtgga tctcttagac tttcttgtgc cgcctccggt 540

tttcctgtta accgttactc tatgcgttgg tacagacaag cccctggaaa agaacgtgaa 600

tgggttgccg gaatgtcctc agctggtgac agatcctcct acgaagattc tgtgaaggga 660

cgtttcacca tctccagaga tgacgcccgt aacaccgttt accttcaaat gaactccctt 720

aagcctgagg atactgccgt ctactattgt aacgtgaatg tcggatttga atactgggga 780

cagggaaccc aagttactgt ctcttccggt ggacatcacc accaccatca ctaatag 837

<210> 59
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> signal sequence

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> X at position 3 is either F or L

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> X at position 16 is either A or T

<400> 59

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

Val Val Ser Ala
            20

<210> 60
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> leader sequence

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> X at position 3 is either F or L

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> X at position 16 is either A or T

<400> 60

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

Val Val Ser Ala Ala Pro Val Ala Pro Ala Glu Glu Ala Ala Asn His
            20   25   30

Leu His Lys Arg

35

<210> 61
<211> 85
<212> PRT
<213> Saccharomyces cerevisiae

<400> 61

Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1 5 10 15

Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
20 25 30

Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
35 40 45

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
50 55 60

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65 70 75 80

Ser Leu Glu Lys Arg
85

<210> 62
<211> 274
<212> PRT
<213> Komagataella pastoris

<400> 62

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

Phe Asp Arg Phe Asp Pro Ser Thr Gln Ser Thr Ile Arg Ile Ala Arg
20 25 30

Ser Pro Lys Pro Ile Pro Val Lys Val Val Ile Val Gly Asp Gly Gly

```
        35                  40                  45

Cys Gly Lys Thr Cys Leu Leu Asn Val Phe Ala Thr Gly Thr Phe Pro
    50                  55                  60

Glu Ala Tyr Val Pro Thr Ile Ile Glu Asn Val Val Ile Thr Leu Val
65                  70                  75                  80

Thr Pro Thr Gly Gln Ile Ala Ala Val Thr Leu Trp Asp Thr Ala Gly
                85                  90                  95

Gln Glu Glu Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Ser Asp Val Asp
            100                 105                 110

Val Val Leu Leu Cys Tyr Ser Ile Asp Asn Leu Ser Thr Phe His Asn
        115                 120                 125

Val Ala Asp Lys Trp Tyr Pro Glu Val Ala His Phe Cys Pro Asn Thr
    130                 135                 140

Pro Ile Ile Leu Val Gly Thr Lys Ser Asp Met Arg Arg His Gln Lys
145                 150                 155                 160

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

Gln Met Gly Ala Val Met Asn Ile Glu Cys Ser Ala Lys Glu Val Ser
            180                 185                 190

Asn Val Asn Ile Val Phe Asp Ala Ala Val Ser Tyr Cys Leu Ser Asn
        195                 200                 205

Ser Arg Pro Lys Thr Arg Gly Asp Asn Asp Asn Asn Arg Ser Asn Arg
    210                 215                 220

Arg Leu Ser Arg Ala Lys Arg Ala Ser Met Phe Ile Arg Gly Lys Asp
225                 230                 235                 240
```

```
Val Ser Ser Thr Ser Gly Asn Ser Arg Glu Glu Leu Val Glu Tyr Asp
                245                 250                 255


Gln Asp Gly Leu Ala Ile Ile Pro Asp Arg Lys Lys Arg Lys Cys Ser
            260                 265                 270


Ile Ile
```

<210> 63
<211> 95
<212> PRT
<213> Komagataella pastoris

<400> 63

```
Met Leu Asn Lys Leu Phe Ile Ala Ile Leu Ile Val Ile Thr Ala Val
1               5                   10                  15


Ile Gly Glu Thr Thr Thr Ser Ser Thr Thr Ala Ser Leu Ser Glu Ser
            20                  25                  30


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


Thr Thr Gln Ser Ala Tyr Thr Gln Gln Phe Ser Gln Leu Tyr Ser Ser
    50                  55                  60


Ile Ala Ser Pro Ser Ser Gly Ser Ile Gly Leu Gly Thr Ile Gln Gly
65                  70                  75                  80


Thr Val Gly Ile Val Arg Thr Tyr Glu Thr Ile Thr Leu Ala Ser
                85                  90                  95
```

<210> 64
<211> 86
<212> PRT
<213> Komagataella pastoris

<400> 64

```
Met Ser Thr Ala Ile Pro Gly Gly Gln Arg Thr Leu Ala Lys Arg Arg
1               5                   10                  15


Ala Ala Asn Leu Asp Lys Lys Gln Asp Glu Pro Thr Ser Ala Arg Ser
            20                  25                  30


Ala Gly Ala Gly Gly Ser Ser Ser Thr Met Leu Lys Leu Tyr Thr Asp
        35                  40                  45


Glu Ala Gln Gly Leu Lys Val Asp Pro Leu Ile Val Leu Val Leu Ala
    50                  55                  60


Val Gly Phe Ile Phe Ser Val Ile Gly Leu His Val Val Ala Lys Leu
65                  70                  75                  80


Thr Gly Lys Leu Ile Asn
                85
```

<210> 65
<211> 361
<212> PRT
<213> Komagataella pastoris

<400> 65

```
Met Thr Pro Arg Ser His Ile Phe Phe Asp Ile Ser Ile Asn Asn Gln
1               5                   10                  15


Pro Ala Gly Arg Ile Ile Phe Glu Leu Phe Asn Asp Ile Val Pro Lys
            20                  25                  30


Thr Ala Glu Asn Phe Arg Ala Leu Ser Thr Gly Glu Lys Gly Ile Gly
        35                  40                  45


Lys Ser Gly Lys Pro Leu His Tyr Lys Gly Ser Thr Phe His Arg Ile
    50                  55                  60


Ile Lys Asp Phe Met Val Gln Gly Gly Asp Phe Thr Asn Gly Asn Gly
65                  70                  75                  80
```

```
Thr Gly Gly Glu Ser Ile Tyr Gly Glu Lys Phe Glu Asp Glu Asn Phe
                85                  90                  95

Gln Leu Thr His Asp Lys Pro Phe Leu Leu Ser Met Ala Asn Ala Gly
            100                 105                 110

Pro Gly Thr Asn Gly Ser Gln Phe Phe Ile Thr Thr Val Pro Thr Pro
        115                 120                 125

His Leu Asp Asn Lys His Val Val Phe Gly Lys Val Ile Ala Gly Lys
    130                 135                 140

Ala Thr Val Arg Lys Ile Glu Arg Asn Ser Glu Gly Glu Ala Pro Ile
145                 150                 155                 160

Glu Pro Val Val Ile Glu Asp Cys Gly Glu Leu Pro Glu Asp Ala Asp
                165                 170                 175

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

Asp Asn Glu Asn Ile Asp Ile Asp Asp Phe Glu Gln Val Tyr Gln Ala
        195                 200                 205

Ile Thr Glu Ile Lys Glu Leu Gly Thr Lys Tyr Phe Lys Asn Gly Asp
    210                 215                 220

Thr Lys Ile Ala Phe Glu Lys Tyr Gln Lys Ala Ala Asn Tyr Leu Leu
225                 230                 235                 240

Glu Tyr Ile Pro Ser Asp Leu Ser Glu Glu Gln Ser Ser Lys Leu Glu
                245                 250                 255

Leu Leu Lys Thr Ser Val Phe Ser Asn Val Ala Leu Ala Gly Leu Lys
            260                 265                 270
```

```
Val Ser Lys Phe Lys Asp Thr Ile Lys Tyr Ala Thr Leu Val Ile Glu
        275                 280                 285

Asp Glu Ser Ala Asp Ala Lys Ala Lys Ser Lys Gly Tyr Tyr Arg Arg
    290                 295                 300

Gly Ser Ala Tyr Ser Ser Leu Lys Asp Glu Asp Ser Ala Ile Ser Asp
305                 310                 315                 320

Phe Gln Lys Ala Leu Glu Leu Ser Pro Gly Asp Pro Ala Ile Ser Gln
                325                 330                 335

Ser Leu Gln Arg Thr Thr Lys Ala Arg Lys Asp Arg Leu Ala Lys Glu
            340                 345                 350

Lys Ala Ala Leu Ser Lys Phe Phe Glu
        355                 360
```

<210> 66
<211> 127
<212> PRT
<213> Komagataella pastoris

<400> 66

```
Met Thr Asn Trp Lys Ala Ile Leu Thr Pro Ala Gln Tyr Gln Val Leu
1               5                   10                  15

Arg Leu Gly Gly Thr Glu Arg Pro Tyr Thr Gly Gln Tyr Val Asn Phe
            20                  25                  30

Lys Lys Asn Gly Thr Tyr Leu Cys Ser Gly Cys Gln Thr Pro Leu Tyr
        35                  40                  45

Lys Ser Gly Thr Lys Phe Asp Ser Ser Cys Gly Trp Pro Ala Phe Tyr
    50                  55                  60

Glu Ala Leu Pro Gly Ala Val Lys Arg Ile Glu Asp Asn Ser Leu Gly
65                  70                  75                  80
```

```
Met Arg Arg Ile Glu Ile Arg Cys Ser Lys Cys Asp Gly His Leu Gly
                85                  90                  95


His Val Phe Glu Gly Glu Gly Phe Asp Thr Pro Thr Asp Ser Arg His
            100                 105                 110


Cys Val Asn Ser Ile Ser Leu Lys Phe Gln Gly Glu Glu Glu Asn
        115                 120                 125
```

<210> 67
<211> 546
<212> PRT
<213> Komagataella pastoris

<400> 67

```
Met Ser His Leu Leu Leu Arg Asp Ser Phe Trp Gly Arg Thr Ile Tyr
1               5                   10                  15


His Leu Ser Lys His Arg Tyr Phe Ser Phe Pro Glu Glu Lys Asp Gly
            20                  25                  30


Phe Ile Ala Pro Glu Lys Tyr Tyr Leu Asn Met Asp Gln Val Ser Ile
        35                  40                  45


His Ala Glu Ser Glu Lys Asn Ile Val Glu Gly Leu Val Asp Thr Ser
    50                  55                  60


Asn Ser Ser Leu Glu Glu Val Lys Thr Thr Arg Val Ile Val Asp Trp
65                  70                  75                  80


Asp Glu Tyr Asp Gln Lys Glu Asn Pro Gln Asn Trp Ser Ser Leu Leu
                85                  90                  95


Lys Cys Phe Val Val Phe Glu Val Gly Ile Leu Thr Val Ala Val Tyr
            100                 105                 110


Met Gly Ser Ala Ile Tyr Thr Pro Gly Ile Glu Asp Ile Met Arg Asp
        115                 120                 125
```

```
Leu Asn Val Ser Arg Thr Val Ala Thr Leu Pro Leu Thr Leu Phe Val
    130                 135                 140

Ile Gly Tyr Ala Val Gly Pro Met Ile Phe Ser Pro Met Ser Glu His
145                 150                 155                 160

Pro Ala Ile Gly Arg Thr Thr Ile Tyr Val Trp Thr Leu Phe Ile Phe
                165                 170                 175

Ala Ile Leu Gln Ile Pro Thr Ala Leu Thr Thr Asn Ile Ala Gly Phe
            180                 185                 190

Cys Ile Leu Arg Phe Ile Gly Gly Phe Phe Ala Ser Pro Ala Leu Ala
        195                 200                 205

Thr Gly Pro Ala Ser Val Gly Asp Val Ile Ala Ile Pro His Leu Pro
    210                 215                 220

Val Gly Leu Gly Leu Trp Ser Ile Cys Ala Val Cys Gly Pro Ser Leu
225                 230                 235                 240

Gly Pro Leu Phe Gly Ala Ile Phe Ser Gln Leu Val Ser Trp Arg Trp
                245                 250                 255

Cys Phe Trp Phe Leu Leu Ile Thr Ser Gly Thr Leu Phe Ile Val Leu
            260                 265                 270

Gly Phe Thr Leu Pro Glu Thr Tyr Val Pro Thr Leu Leu Tyr Arg Lys
        275                 280                 285

Ala Arg Arg Leu Arg Ala Leu Thr Lys Asn Glu Leu Ile Ile Ser Lys
    290                 295                 300

Gly Glu Leu Asp Ile Gln Asp Arg Thr Ala Lys Glu Val Leu Ile Glu
305                 310                 315                 320
```

```
Cys Leu Trp Arg Pro Val Asp Ile Ser Phe Arg Asp Pro Val Val Leu
                325                 330                 335

Met Ile Asn Leu Tyr Ile Ser Met Val Tyr Ser Ile Trp Tyr Ile Trp
            340                 345                 350

Phe Glu Ala Phe Pro Ile Val Phe Leu Glu Ile Tyr Gly Phe Ser Leu
        355                 360                 365

Ile Gly Met Gly Ala Ser Phe Ala Gly Ile Leu Ile Gly Val Leu Ile
    370                 375                 380

Cys Ser Ala Cys Tyr Cys Tyr Ala Cys His Val Thr Phe Ala Arg Arg
385                 390                 395                 400

Ile Ile Ala Asn Glu Thr Ile His Pro Glu Phe Phe Val Pro Gly Ala
                405                 410                 415

Ile Ile Gly Gly Cys Ile Met Pro Thr Gly Ile Phe Ile Leu Gly Trp
            420                 425                 430

Thr Ala Thr Lys Ser Val His Trp Ile Val Pro Ile Ile Gly Ser Gly
        435                 440                 445

Leu Phe Ala Ala Gly Gly Tyr Leu Ile Phe Gln Thr Leu Phe Asn Tyr
    450                 455                 460

Leu Ala Met Ser Phe Pro Arg Tyr Met Ala Ser Ala Phe Ala Gly Asn
465                 470                 475                 480

Asp Leu Phe Arg Ser Phe Ser Ala Ser Val Phe Pro Leu Phe Gly His
                485                 490                 495

Ala Leu Tyr Ala Asn Leu Gly Ser Glu Lys Phe Pro Val Gly Trp Gly
            500                 505                 510

Ser Ser Val Leu Gly Phe Ile Thr Val Ala Met Ile Ala Ile Pro Val
        515                 520                 525
```

Thr Phe Met Arg Tyr Gly Pro Arg Leu Arg Ala Asn Ser Arg Tyr Ala
    530   535   540

Gly Pro
545

<210> 68
<211> 355
<212> PRT
<213> Komagataella pastoris

<400> 68

Met Thr Asp Tyr Val Thr Ser Lys Arg Pro Asp Asn Val Leu Asn Trp
1   5   10   15

Thr Ser Ile His Val Ser Ser Trp Ile Gly Glu Thr Ile Pro Glu Ile
            20   25   30

Asp Pro Ser Leu Leu Gln Asn Phe Leu Glu His Asp Ile Ala Gly Asp
        35   40   45

Val Leu Pro Tyr Leu Lys Ser Glu Asp Leu Lys Glu Ile Gly Ile Asn
    50   55   60

Glu Leu Lys His Arg Ile Ser Ile Lys Lys Asn Ile His Glu Leu Leu
65   70   75   80

Val Ser Asn Glu Lys His Ile Asp Thr Ser Ile Leu Ser Asp Thr Ala
                85   90   95

Thr Glu Leu Gly Thr Leu Ile Leu Thr Asn Lys Phe Ile Thr Gln Met
            100   105   110

Ala Asn Arg Lys Asn Val Val Asp Asp Ser Thr His His Ser Asn Asn
        115   120   125

Arg Arg Leu Thr Glu Gln Phe Asn Lys Leu Arg Lys Asp Leu Leu Pro

```
    130                 135                 140

Ile Phe Lys Trp Ile Lys Glu Thr Gln Pro Leu Pro Thr Pro Glu Asn
145                 150                 155                 160

Thr His Phe Ala Asn Met Gly Ser Val Pro Ala Ser Pro Val Glu His
                165                 170                 175

Thr Ser Gly Glu Ser Thr Leu Ser Asn Pro Ser Leu Ser Thr Ile Asn
            180                 185                 190

Ala Gly Glu Gly Val Asn Ser Ala Val Ala Gly Gln Ser Leu Gly Arg
        195                 200                 205

Lys Pro Thr Leu Ser Ser Arg Arg Gln Ser His Ala Leu Ser Pro Thr
    210                 215                 220

Gly Glu His Leu Asn Val Ser Ser Ser Ser Pro Ser Thr Gly Asn Phe
225                 230                 235                 240

Glu Thr Leu Asn Gly Glu Arg Pro Asn Leu Arg Ser Ala Ser Ser Gly
                245                 250                 255

Ser Gln Glu His Thr Glu Asn Glu Leu Leu Lys Pro Leu Arg Val Lys
            260                 265                 270

Ala Asp Glu Pro Cys Tyr Lys Val Ile Gln Asn Ala Met Lys Arg His
        275                 280                 285

Gly Leu Ser Val Asp Asp Trp Arg Lys Tyr Ala Leu Val Ile Cys Tyr
    290                 295                 300

Gly Asp Glu Glu Arg Val Leu Gly Leu His Glu Lys Pro Gly Ser Ile
305                 310                 315                 320

Phe Lys Glu Leu Lys Asp Gln Lys Gln Asn Pro Ala Ile Met Leu Arg
                325                 330                 335
```

Gln Ile Asp Thr Asn Asn Asp Asp Gln Asn His Ile Glu Thr Pro Gly
340 345 350

Gly Arg Leu
355

<210> 69
<211> 1027
<212> PRT
<213> Komagataella pastoris

<400> 69

Met Thr Thr Asn Gly Gln Lys Arg Gln Lys Thr Arg Lys Pro Leu Leu
1 5 10 15

Ile Asn Ala Phe Val Met Gly Cys Ala Gly Leu Gln Asn Pro Gly Leu
20 25 30

Trp Lys His Pro Lys Asp Ser Ser His Arg Phe Asn Gln Ile Asp His
35 40 45

Trp Thr Tyr Leu Ala Lys Leu Ala Glu Lys Gly Lys Phe Asn Ala Leu
50 55 60

Phe Ile Ala Asp Val Leu Gly Gly Tyr Asp Val Tyr Lys Gly Pro Glu
65 70 75 80

Asn Leu Ala Thr Pro Ala Val Ala Gly Ala Gln Trp Pro Val Thr Glu
85 90 95

Pro Ser Ala Val Val Ser Ala Met Ala Ala Val Thr Thr Asn Leu Ala
100 105 110

Phe Gly Val Thr Phe Ser Thr Ile Ser Glu Ala Pro Tyr His Phe Ala
115 120 125

Arg Arg Leu Ser Thr Leu Asp His Leu Thr Lys Gly Arg Ile Gly Trp
130 135 140

```
Asn Val Val Ser Ser Tyr Leu Glu Ser Ala Ala Arg Asn Leu Leu Asn
145                 150                 155                 160

Gly Glu Lys Leu Asp Glu His Asp Gln Arg Tyr Leu Lys Ala Glu Glu
                165                 170                 175

Tyr Ile Gln Ile Val Tyr Glu Leu Leu Leu Ser Ser Trp Arg Asp Asp
            180                 185                 190

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

Phe Arg Lys Ile Asn Phe Glu Gly Lys Phe Phe Lys Val Pro Gly Pro
    210                 215                 220

His Ile Val Asp Pro Thr Pro Gln Arg Leu Pro Val Ile Leu Gln Ala
225                 230                 235                 240

Gly Thr Ser Lys Val Gly Lys Glu Phe Ala Ala Lys His Ala Glu Ile
                245                 250                 255

Val Phe Val Ile Ser Phe Ser Pro Asp Asp Leu Lys Pro Lys Ile Ala
            260                 265                 270

Glu Val Arg Gln Leu Ala Lys Glu Lys Phe Gly Arg Asn His Asp Asp
        275                 280                 285

Ile Lys Phe Val Ala Leu Ala Thr Pro Val Ile Gly Ala Thr His Glu
    290                 295                 300

Leu Ala Glu Glu Lys Tyr Gln Glu Leu Leu Ser Tyr Gly Asp Ile Glu
305                 310                 315                 320

Gly Ala Gln Ala Leu Phe Gly Gly Trp Thr Gly Ile Asp Leu Ser Gln
                325                 330                 335
```

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

Gly Ala Val Gln Asn Trp Thr Lys Ala Ile Pro Asn Glu Lys Arg Trp
        355                 360                 365

Thr Arg Lys Val Ile Ala Lys Gln Ile Thr Val Gly Gly Leu Gly Pro
    370                 375                 380

Ala Phe Val Gly Thr Pro Glu Glu Ile Ala Asp Glu Leu Glu His Trp
385                 390                 395                 400

Ser Asp His Ala Gly Leu Asp Gly Phe Asn Phe Thr Tyr Ala Val Asn
                405                 410                 415

Pro Leu Ser Phe Glu Glu Ile Val Glu Asp Leu Ile Pro Val Leu Gln
            420                 425                 430

Arg Arg Gly Leu Ala Gln Lys Glu Tyr Pro Asn Pro Glu Thr Gly Ser
        435                 440                 445

Thr Phe Arg Lys Asn Leu Phe Gly Thr Asp Phe Val Pro Ser Thr His
    450                 455                 460

Pro Ala Tyr Asn Leu Arg Trp Arg Ala Gly Val Ser Lys Glu Glu Phe
465                 470                 475                 480

Glu Lys Ser Leu Asn Ala Thr Thr Asn Trp Tyr Ser Ser Phe Ala Arg
                485                 490                 495

Ser Gly Ala Leu Gly Glu Leu His Asn Thr Cys Arg Ile Leu Tyr Leu
            500                 505                 510

Gln Ile Val Lys Tyr Lys Tyr Arg Leu Arg Val Arg Ser Glu Gly Asn
        515                 520                 525

Ser Ile Pro Phe Ala Lys Met Thr Lys Glu Asn Glu Ala Lys Arg Gln
    530                 535                 540
```

```
Lys Thr Ser Gln Pro Lys Ala Lys Lys Gln Leu Ile Ile Asn Ala Phe
545                 550                 555                 560

Met Ser Gly Ser Ser Gly Asn Gln Ser Pro Gly Leu Trp Ser Tyr Pro
                565                 570                 575

Gly Asp Lys Ser Thr Glu Tyr Thr Thr Leu Asp Tyr Trp Val Glu Leu
            580                 585                 590

Ala Gln Lys Leu Glu Lys Ala Lys Phe His Ser Ile Phe Ile Ala Asp
        595                 600                 605

Val Leu Gly Gly Tyr Asp Val Tyr Asn Gly Pro Gly Asn Tyr Ser Ala
    610                 615                 620

Ala Ala Lys Ser Gly Ala Gln Phe Pro Met Ile Glu Pro Ser Ala Ala
625                 630                 635                 640

Val Thr Ala Met Ala Ala Ala Thr Lys Ser Ile Thr Phe Gly Val Thr
                645                 650                 655

Phe Ser Thr Ile Ser Glu Ala Pro Tyr His Phe Ala Arg Arg Leu Gly
            660                 665                 670

Thr Leu Asp Leu Leu Thr Asn Gly Arg Val Gly Trp Asn Ile Val Ser
        675                 680                 685

Ser Tyr Leu Asp Ser Ala Ala Arg Asn Leu Leu Asn Gly Glu Pro Leu
    690                 695                 700

Pro Leu His Ala Asp Arg Tyr Lys Arg Ala Glu Glu Phe Leu Gln Val
705                 710                 715                 720

Val Tyr Arg Leu Phe Leu Ser Ser Trp Arg Asp Asp Ala Tyr Lys Leu
                725                 730                 735
```

```
Asp Lys Lys Thr Arg Thr Phe Ala Asp Pro Lys Leu Ile Arg Thr Ile
            740                 745                 750

Asp His Val Gly Glu Phe Phe Asn Val Pro Gly Pro Gln Phe Leu Pro
        755                 760                 765

Pro Thr Pro Gln Arg Leu Pro Leu Ile Leu Gln Ala Gly Thr Ser Lys
    770                 775                 780

Val Gly Met Asp Tyr Ala Ala Lys His Ala Glu Val Val Phe Leu Ala
785                 790                 795                 800

Ser Phe Asp Pro Glu Ser Leu Gln Glu Lys Ile Lys Thr Val Arg Asp
                805                 810                 815

Ile Ala Glu Thr Lys Tyr Asn Arg Pro Arg Asp Ser Ile Lys Phe Leu
            820                 825                 830

Ile Leu Ile Thr Val Val Ile Ala Asp Thr His Glu Asp Ala Val Lys
        835                 840                 845

Arg Tyr Glu Asp Leu Ala Ser Tyr Ala Asp Leu Glu Gly Ala Gln Ala
    850                 855                 860

Leu Phe Ser Gly Trp Thr Gly Ile Asp Ile Gly Lys Tyr Gly Glu Asp
865                 870                 875                 880

Glu Pro Leu Glu His Val Glu Ser Asn Ala Ile Lys Ser His Val Lys
                885                 890                 895

Asn Trp Thr Lys Phe Lys Asp Asn Lys Pro Arg Ala Arg Lys Asp Ile
            900                 905                 910

Ala Lys Gln Ile Gly Val Gly Gly Ser Gly Pro Leu Leu Val Gly Ser
        915                 920                 925

Val Gln Glu Ile Ala Asp Glu Leu Glu Arg Trp Ala Glu Val Ser Asp
    930                 935                 940
```

```
Leu Asp Gly Phe Asn Phe Ala Tyr Ala Asp Tyr Pro Gln Thr Phe Asp
945                 950                 955                 960


Asp Ile Ile Glu Lys Leu Leu Pro Glu Leu Asn Lys Arg Gly Val Phe
                965                 970                 975


Trp Asp Asp Tyr Lys Ile Pro Gly Gly Thr Phe Arg Glu Ser Val Phe
            980                 985                 990


Gly Arg Lys Phe Val Asp Lys Asp  His Pro Ala Tyr Asp  Leu Arg Trp
        995                 1000                1005


Arg Ser  Asp Gln Thr Arg Glu  Glu Phe Glu Lys Lys  Leu Ala Glu
    1010                1015                1020


Leu Glu  Lys Lys
    1025
```

<210> 70
<211> 194
<212> PRT
<213> Komagataella pastoris

<400> 70

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


Gln Ala Asp Glu Ala Leu Tyr Thr Val Phe Tyr Asn Asp Val Thr Glu
            20                  25                  30


Asn Ala Gln Glu Tyr Leu Ser Tyr Ile Gln Ala Asn Thr Ala Ala Gly
        35                  40                  45


Phe Thr Asp Leu Leu Ser Leu Tyr Thr Glu Leu Ala Thr Tyr Thr Asp
    50                  55                  60


Asp Ser Tyr Thr Ser Ile Phe Thr Glu Glu Asp Phe Pro Ala Ser Glu
```

65 70 75 80

Leu Ser Ser Phe Val Val Asn Leu Pro Trp Tyr Ser Ser Arg Ile Glu
85 90 95

Pro Gln Val Ala Ala Ala Glu Thr Gly Glu Ser Glu Glu Glu Ser Glu
100 105 110

Thr Gly Glu Ser Glu Glu Glu Ser Glu Thr Gly Glu Glu Thr Glu Thr
115 120 125

Glu Thr Gly Ser Glu Ser Glu Ser Glu Ser Glu Ser Glu Ser Glu Thr Ser Ala
130 135 140

Thr Gly Thr Gly Thr Gly Thr Ser Ala Ser Glu Ser Ala Glu Thr Glu
145 150 155 160

Thr Ser Thr Asp Ala Ala Val Ser Ile Asp His Pro Lys Ser Thr Leu
165 170 175

Leu Met Gly Leu Thr Ala Ala Val Val Ser Ile Thr Phe Gly Val Phe
180 185 190

Ala Leu

<210> 71
<211> 478
<212> PRT
<213> Komagataella pastoris

<400> 71

Met Ser Ser Phe Arg Val Leu Asp Leu Val Lys Pro Phe Thr Pro Phe
1 5 10 15

Leu Pro Glu Val Ile Ser Pro Glu Arg Lys Val Pro Phe Gln Gln Lys
20 25 30

```
Leu Met Trp Thr Gly Val Thr Leu Leu Ile Phe Leu Val Met Ser Glu
        35                  40                  45

Ile Pro Leu Tyr Gly Ile Thr Ser Ser Asp Ser Ser Asp Pro Leu Phe
    50                  55                  60

Trp Leu Arg Met Met Leu Ala Ser Asn Arg Gly Thr Leu Met Glu Leu
65                  70                  75                  80

Gly Ile Ser Pro Ile Val Thr Ser Gly Met Val Phe Gln Leu Leu Gln
                85                  90                  95

Gly Ile Gln Ile Leu Asp Val Asn Met Glu Asn Lys Ala Asp Arg Glu
            100                 105                 110

Leu Phe Gln Thr Ala Gln Lys Val Phe Ala Ile Leu Leu Ser Ile Gly
        115                 120                 125

Gln Ala Thr Val Tyr Val Leu Thr Gly Met Tyr Gly Pro Pro Gly Glu
    130                 135                 140

Leu Gly Val Gly Val Cys Leu Leu Leu Val Leu Gln Leu Val Phe Ala
145                 150                 155                 160

Gly Ile Val Val Ile Leu Leu Asp Glu Leu Leu Gln Lys Gly Tyr Gly
                165                 170                 175

Leu Gly Ser Gly Ile Ser Leu Phe Met Ala Thr Asn Ile Cys Glu Gln
            180                 185                 190

Ile Phe Trp Lys Thr Phe Ala Pro Thr Thr Val Asn Arg Gly Arg Gly
        195                 200                 205

Lys Glu Phe Glu Gly Ala Phe Ile Ser Phe Phe His Leu Ile Leu Thr
    210                 215                 220

Lys Lys Asp Lys Lys Arg Ala Leu Leu Glu Ser Phe Tyr Arg Asp Asn
225                 230                 235                 240
```

```
Ala Pro Asn Met Phe Gln Val Ile Ala Thr Leu Val Val Phe Phe Thr
                245                 250                 255

Val Val Tyr Leu Gln Gly Phe Arg Leu Glu Ile Pro Val Lys Ser Thr
            260                 265                 270

Arg Gln Arg Gly Pro Tyr Gly Thr Tyr Pro Ile Arg Leu Phe Tyr Thr
        275                 280                 285

Ser Asn Met Pro Ile Met Leu Gln Ser Ala Leu Thr Ser Asn Ile Phe
    290                 295                 300

Ile Ile Ser Gln Met Leu Tyr Ser His Phe Pro Asp Asn Ala Phe Val
305                 310                 315                 320

Lys Leu Ile Gly Thr Trp Glu Ala Gln Pro Gly Ser Ala Gln Leu Phe
                325                 330                 335

Ala Ala Ser Gly Leu Ala Tyr Tyr Met Gln Pro Pro Met Ser Leu Ser
            340                 345                 350

Gln Ala Leu Leu Asp Pro Ile Lys Thr Val Val Tyr Val Val Phe Val
        355                 360                 365

Leu Thr Thr Cys Ala Ile Phe Ser Lys Thr Trp Ile Glu Ile Ser Gly
    370                 375                 380

Ser Ser Pro Arg Asp Val Ala Lys Gln Phe Lys Asp Gln Gly Leu Val
385                 390                 395                 400

Ile Ala Gly His Arg Asp Ala Thr Val Tyr Lys Glu Leu Lys Lys Ile
                405                 410                 415

Ile Pro Thr Ala Ala Ala Phe Gly Gly Ala Thr Ile Gly Ala Leu Ser
            420                 425                 430
```

Val Val Ser Asp Leu Leu Gly Thr Leu Gly Ser Gly Thr Ser Ile Leu
435 440 445

Leu Ala Val Thr Thr Ile Tyr Gly Tyr Tyr Glu Leu Ala Val Lys Glu
450 455 460

Gly Gly Phe Ser Lys Gly Gly Pro Ser Gly Phe Val Asp Leu
465 470 475

<210> 72
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 72
cgaacatcca tcaccaaaac ac 22

<210> 73
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 73
gttgtcgacc tgcagcgtac ggtgttgccg cgaaatg 37

<210> 74
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 74
taggtgatat cagatccact gatcaatttg cccaagagac g 41

<210> 75
<211> 20

<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 75
gactgttgcg attgctggtg 20

<210> 76
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 76
catttcgcgg caacaccgta cgctgcaggt cgacaac 37

<210> 77
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 77
cggtgagaat ggcaaaagct tat 23

<210> 78
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 78
aagcccgatg cgccagagtt g 21

<210> 79
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 79
cgtctcttgg gcaaattgat cagtggatct gatatcacct a 41

<210> 80
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 80
atccaggaca cgctcatcaa g 21

<210> 81
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 81
tgtaacgtga atgtcggatt tg 22

<210> 82
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 82
tagtgatggt ggtggtgatg 20

<210> 83
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<400> 83
cctgaggctt tgttccaccc act 23

<210> 84
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 84
ggaacatagt agcaccggca taacga 26

<210> 85
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> translation initiation site

<400> 85
cctgcaggcc 10

<210> 86
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> translation initiation site

<220>
<221> misc_feature
<222> (1)..(6)
<223> n at positions 1-6 is any nucleic acid, preferably A

<220>
<221> misc_feature
<222> (8)..(9)
<223> n at positions 8-9 is any nucleic acid, preferably A

<400> 86