SEQUENCE LISTING

<110> PALLEON PHARMACEUTICALS INC.

<120> SIALIDASE-PD-1-ANTIBODY FUSION PROTEINS AND METHODS OF USE THEREOF

<130> PAL-025WO

<140> PCT/US2022/011487
<141> 2022-01-06

<150> 63/134,415
<151> 2021-01-06

<160> 150

<170> PatentIn version 3.5

<210> 1
<211> 380
<212> PRT
<213> Homo sapiens

<400> 1

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Met Ala Ser Leu Pro Val Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1               5                  10                  15


Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20                  25                  30


Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
        35                  40                  45


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


Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80


Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
                85                  90                  95


Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110


Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
```

```
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Ile Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Cys Ala Tyr Ser Asp
                325                 330                 335
```

```
Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
    370                 375                 380
```

<210> 2
<211> 385
<212> PRT
<213> Mus musculus

<400> 2

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Met Glu Asp Leu Arg Pro Met Ala Thr Cys Pro Val Leu Gln Lys Glu
1               5                   10                  15

Thr Leu Phe Arg Thr Gly Val His Ala Tyr Arg Ile Pro Ala Leu Leu
            20                  25                  30

Tyr Leu Lys Lys Gln Lys Thr Leu Leu Ala Phe Ala Glu Lys Arg Ala
        35                  40                  45

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

Tyr Asn Glu Ala Thr Asn Arg Val Lys Trp Gln Pro Glu Glu Val Val
65                  70                  75                  80

Thr Gln Ala Gln Leu Glu Gly His Arg Ser Met Asn Pro Cys Pro Leu
                85                  90                  95

Tyr Asp Lys Gln Thr Lys Thr Leu Phe Leu Phe Phe Ile Ala Val Pro
            100                 105                 110

Gly Arg Val Ser Glu His His Gln Leu His Thr Lys Val Asn Val Thr
        115                 120                 125

Arg Leu Cys Cys Val Ser Ser Thr Asp His Gly Arg Thr Trp Ser Pro
    130                 135                 140
```

```
Ile Gln Asp Leu Thr Glu Thr Thr Ile Gly Ser Thr His Gln Glu Trp
145                 150                 155                 160

Ala Thr Phe Ala Val Gly Pro Gly His Cys Leu Gln Leu Arg Asn Pro
                165                 170                 175

Ala Gly Ser Leu Leu Val Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro
            180                 185                 190

Ala Gln Lys Pro Thr Pro Phe Ala Phe Cys Phe Ile Ser Leu Asp His
        195                 200                 205

Gly His Thr Trp Lys Leu Gly Asn Phe Val Ala Glu Asn Ser Leu Glu
    210                 215                 220

Cys Gln Val Ala Glu Val Gly Thr Gly Ala Gln Arg Met Val Tyr Leu
225                 230                 235                 240

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

Asp Gly Leu Asp Phe Gln Asp Asn Arg Val Val Ser Lys Leu Val Glu
            260                 265                 270

Pro Pro His Gly Cys His Gly Ser Val Val Ala Phe His Asn Pro Ile
        275                 280                 285

Ser Lys Pro His Ala Leu Asp Thr Trp Leu Leu Tyr Thr His Pro Thr
    290                 295                 300

Asp Ser Arg Asn Arg Thr Asn Leu Gly Val Tyr Leu Asn Gln Met Pro
305                 310                 315                 320

Leu Asp Pro Thr Ala Trp Ser Glu Pro Thr Leu Leu Ala Met Gly Ile
                325                 330                 335

Cys Ala Tyr Ser Asp Leu Gln Asn Met Gly Gln Gly Pro Asp Gly Ser
            340                 345                 350

Pro Gln Phe Gly Cys Leu Tyr Glu Ser Gly Asn Tyr Glu Glu Ile Ile
```

355 360 365

Phe Leu Ile Phe Thr Leu Lys Gln Ala Phe Pro Thr Val Phe Asp Ala
370 375 380

Gln
385

<210> 3
<211> 5
<212> PRT
<213> Mus musculus

<400> 3
Glu Asp Leu Arg Pro
1 5

<210> 4
<211> 6
<212> PRT
<213> Mus musculus

<400> 4
Met Glu Asp Leu Arg Pro
1 5

<210> 5
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 5
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

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

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Lys
225

<210> 6
<211> 1143
<212> DNA
<213> Salmonella typhimurium

<400> 6
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aataccatcg tcggctctgg cagcggcggc accaccaagt actttagaat ccccgccatg 120

tgcaccacca gcaagggcac cattgtggtg ttcgccgacg ccagacacaa caccgccagc 180

gatcagagct tcatcgatac cgctgccgcc agatctaccg atggcggcaa gacctggaac 240

aagaagatcg ccatctacaa cgaccgcgtg aacagcaagc tgagcagagt gatggaccct 300

acctgcatcg tggccaacat ccagggcaga gaaaccatcc tggtcatggt cggaaagtgg 360

aacaacaacg ataagacctg gggcgcctac agagacaagg cccctgatac cgattgggac 420

ctcgtgctgt acaagagcac cgatgacggc gtgaccttca gcaaggtgga aacaaacatc 480

cacgacatcg tgaccaagaa cggcaccatc tctgccatgc tcggcggcgt tggatctggc 540

ctgcaactga atgatggcaa gctggtgttc cccgtgcaga tggtccgaac aaagaatatc 600

accaccgtgc tgaataccag cttcatctac agcaccgacg gcatcacatg gtccctgcct 660

agcggctact gtgaaggctt tggcagcgag aacaacatca tcgagttcaa cgccagcctg 720

gtcaacaaca tccggaacag cggcctgcgg agaagcttcg agacaaagga cttcggaaag 780

acgtggaccg agtttcctcc aatggacaag aaggtggaca accggaacca cggcgtgcag 840

ggcagcacaa tcacaatccc tagcggcaac aaactggtgg ccgctcactc tagcgcccag 900

aacaagaaca acgactacac cagaagcgac atcagcctgt acgcccacaa cctgtacagc 960

ggcgaagtga agctgatcga cgacttctac cccaaagtgg gcaatgccag cggagccggc 1020

tacagctgtc tgagctaccg gaaaaatgtg gacaaagaaa ccctgtacgt ggtgtacgag 1080

gccaacggca gcatcgagtt tcaggacctg agcagacatc tgcccgtgat caagagctac 1140

aac 1143

<210> 7
<211> 364
<212> PRT
<213> Homo sapiens

<400> 7
Glu Asn Asp Phe Gly Leu Val Gln Pro Leu Val Thr Met Glu Gln Leu
1 5 10 15

Leu Trp Val Ser Gly Arg Gln Ile Gly Ser Val Asp Thr Phe Arg Ile
20 25 30

```
Pro Leu Ile Thr Ala Thr Pro Arg Gly Thr Leu Leu Ala Phe Ala Glu
        35                  40                  45

Ala Arg Lys Met Ser Ser Ser Asp Glu Gly Ala Lys Phe Ile Ala Leu
    50                  55                  60

Arg Arg Ser Met Asp Gln Gly Ser Thr Trp Ser Pro Thr Ala Phe Ile
65                  70                  75                  80

Val Asn Asp Gly Asp Val Pro Asp Gly Leu Asn Leu Gly Ala Val Val
                85                  90                  95

Ser Asp Val Glu Thr Gly Val Val Phe Leu Phe Tyr Ser Leu Cys Ala
            100                 105                 110

His Lys Ala Gly Cys Gln Val Ala Ser Thr Met Leu Val Trp Ser Lys
        115                 120                 125

Asp Asp Gly Val Ser Trp Ser Thr Pro Arg Asn Leu Ser Leu Asp Ile
    130                 135                 140

Gly Thr Glu Val Phe Ala Pro Gly Pro Gly Ser Gly Ile Gln Lys Gln
145                 150                 155                 160

Arg Glu Pro Arg Lys Gly Arg Leu Ile Val Cys Gly His Gly Thr Leu
                165                 170                 175

Glu Arg Asp Gly Val Phe Cys Leu Leu Ser Asp Asp His Gly Ala Ser
            180                 185                 190

Trp Arg Tyr Gly Ser Gly Val Ser Gly Ile Pro Tyr Gly Gln Pro Lys
        195                 200                 205

Gln Glu Asn Asp Phe Asn Pro Asp Glu Cys Gln Pro Tyr Glu Leu Pro
    210                 215                 220

Asp Gly Ser Val Val Ile Asn Ala Arg Asn Gln Asn Asn Tyr His Cys
225                 230                 235                 240

His Cys Arg Ile Val Leu Arg Ser Tyr Asp Ala Cys Asp Thr Leu Arg
                245                 250                 255
```

```
Pro Arg Asp Val Thr Phe Asp Pro Glu Leu Val Asp Pro Val Val Ala
            260                 265                 270

Ala Gly Ala Val Val Thr Ser Ser Gly Ile Val Phe Phe Ser Asn Pro
        275                 280                 285

Ala His Pro Glu Phe Arg Val Asn Leu Thr Leu Arg Trp Ser Phe Ser
    290                 295                 300

Asn Gly Thr Ser Trp Arg Lys Glu Thr Val Gln Leu Trp Pro Gly Pro
305                 310                 315                 320

Ser Gly Tyr Ser Ser Leu Ala Thr Leu Glu Gly Ser Met Asp Gly Glu
                325                 330                 335

Glu Gln Ala Pro Gln Leu Tyr Val Leu Tyr Glu Lys Gly Arg Asn His
            340                 345                 350

Tyr Thr Glu Ser Ile Ser Val Ala Lys Ile Ser Val
        355                 360
```

<210> 8
<211> 428
<212> PRT
<213> Homo sapiens

<400> 8

```
Met Glu Glu Val Thr Thr Cys Ser Phe Asn Ser Pro Leu Phe Arg Gln
1               5                   10                  15

Glu Asp Asp Arg Gly Ile Thr Tyr Arg Ile Pro Ala Leu Leu Tyr Ile
            20                  25                  30

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

Arg Asp Glu Asp Ala Leu His Leu Val Leu Arg Arg Gly Leu Arg Ile
    50                  55                  60

Gly Gln Leu Val Gln Trp Gly Pro Leu Lys Pro Leu Met Glu Ala Thr
65                  70                  75                  80
```

```
Leu Pro Gly His Arg Thr Met Asn Pro Cys Pro Val Trp Glu Gln Lys
                85                  90                  95

Ser Gly Cys Val Phe Leu Phe Phe Ile Cys Val Arg Gly His Val Thr
            100                 105                 110

Glu Arg Gln Gln Ile Val Ser Gly Arg Asn Ala Ala Arg Leu Cys Phe
        115                 120                 125

Ile Tyr Ser Gln Asp Ala Gly Cys Ser Trp Ser Glu Val Arg Asp Leu
    130                 135                 140

Thr Glu Glu Val Ile Gly Ser Glu Leu Lys His Trp Ala Thr Phe Ala
145                 150                 155                 160

Val Gly Pro Gly His Gly Ile Gln Leu Gln Ser Gly Arg Leu Val Ile
                165                 170                 175

Pro Ala Tyr Thr Tyr Tyr Ile Pro Ser Trp Phe Phe Cys Phe Gln Leu
            180                 185                 190

Pro Cys Lys Thr Arg Pro His Ser Leu Met Ile Tyr Ser Asp Asp Leu
        195                 200                 205

Gly Val Thr Trp His His Gly Arg Leu Ile Arg Pro Met Val Thr Val
    210                 215                 220

Glu Cys Glu Val Ala Glu Val Thr Gly Arg Ala Gly His Pro Val Leu
225                 230                 235                 240

Tyr Cys Ser Ala Arg Thr Pro Asn Arg Cys Arg Ala Glu Ala Leu Ser
                245                 250                 255

Thr Asp His Gly Glu Gly Phe Gln Arg Leu Ala Leu Ser Arg Gln Leu
            260                 265                 270

Cys Glu Pro Pro His Gly Cys Gln Gly Ser Val Val Ser Phe Arg Pro
        275                 280                 285
```

```
Leu Glu Ile Pro His Arg Cys Gln Asp Ser Ser Ser Lys Asp Ala Pro
    290                 295                 300

Thr Ile Gln Gln Ser Ser Pro Gly Ser Ser Leu Arg Leu Glu Glu Glu
305                 310                 315                 320

Ala Gly Thr Pro Ser Glu Ser Trp Leu Leu Tyr Ser His Pro Thr Ser
                325                 330                 335

Arg Lys Gln Arg Val Asp Leu Gly Ile Tyr Leu Asn Gln Thr Pro Leu
            340                 345                 350

Glu Ala Ala Cys Trp Ser Arg Pro Trp Ile Leu His Cys Gly Pro Cys
        355                 360                 365

Gly Tyr Ser Asp Leu Ala Ala Leu Glu Glu Glu Gly Leu Phe Gly Cys
    370                 375                 380

Leu Phe Glu Cys Gly Thr Lys Gln Glu Cys Glu Gln Ile Ala Phe Arg
385                 390                 395                 400

Leu Phe Thr His Arg Glu Ile Leu Ser His Leu Gln Gly Asp Cys Thr
                405                 410                 415

Ser Pro Gly Arg Asn Pro Ser Gln Phe Lys Ser Asn
            420                 425
```

<210> 9
<211> 461
<212> PRT
<213> Homo sapiens

<400> 9

```
Met Arg Pro Ala Asp Leu Pro Pro Arg Pro Met Glu Glu Ser Pro Ala
1               5                   10                  15

Ser Ser Ser Ala Pro Thr Glu Thr Glu Glu Pro Gly Ser Ser Ala Glu
            20                  25                  30

Val Met Glu Glu Val Thr Thr Cys Ser Phe Asn Ser Pro Leu Phe Arg
        35                  40                  45
```

```
Gln Glu Asp Asp Arg Gly Ile Thr Tyr Arg Ile Pro Ala Leu Leu Tyr
    50                  55                  60

Ile Pro Pro Thr His Thr Phe Leu Ala Phe Ala Glu Lys Arg Ser Thr
65                  70                  75                  80

Arg Arg Asp Glu Asp Ala Leu His Leu Val Leu Arg Arg Gly Leu Arg
                85                  90                  95

Ile Gly Gln Leu Val Gln Trp Gly Pro Leu Lys Pro Leu Met Glu Ala
            100                 105                 110

Thr Leu Pro Gly His Arg Thr Met Asn Pro Cys Pro Val Trp Glu Gln
        115                 120                 125

Lys Ser Gly Cys Val Phe Leu Phe Phe Ile Cys Val Arg Gly His Val
    130                 135                 140

Thr Glu Arg Gln Gln Ile Val Ser Gly Arg Asn Ala Ala Arg Leu Cys
145                 150                 155                 160

Phe Ile Tyr Ser Gln Asp Ala Gly Cys Ser Trp Ser Glu Val Arg Asp
                165                 170                 175

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

Ala Val Gly Pro Gly His Gly Ile Gln Leu Gln Ser Gly Arg Leu Val
        195                 200                 205

Ile Pro Ala Tyr Thr Tyr Tyr Ile Pro Ser Trp Phe Phe Cys Phe Gln
    210                 215                 220

Leu Pro Cys Lys Thr Arg Pro His Ser Leu Met Ile Tyr Ser Asp Asp
225                 230                 235                 240

Leu Gly Val Thr Trp His His Gly Arg Leu Ile Arg Pro Met Val Thr
                245                 250                 255

Val Glu Cys Glu Val Ala Glu Val Thr Gly Arg Ala Gly His Pro Val
            260                 265                 270
```

```
Leu Tyr Cys Ser Ala Arg Thr Pro Asn Arg Cys Arg Ala Glu Ala Leu
        275                 280                 285

Ser Thr Asp His Gly Glu Gly Phe Gln Arg Leu Ala Leu Ser Arg Gln
    290                 295                 300

Leu Cys Glu Pro Pro His Gly Cys Gln Gly Ser Val Val Ser Phe Arg
305                 310                 315                 320

Pro Leu Glu Ile Pro His Arg Cys Gln Asp Ser Ser Ser Lys Asp Ala
                325                 330                 335

Pro Thr Ile Gln Gln Ser Ser Pro Gly Ser Ser Leu Arg Leu Glu Glu
            340                 345                 350

Glu Ala Gly Thr Pro Ser Glu Ser Trp Leu Leu Tyr Ser His Pro Thr
        355                 360                 365

Ser Arg Lys Gln Arg Val Asp Leu Gly Ile Tyr Leu Asn Gln Thr Pro
    370                 375                 380

Leu Glu Ala Ala Cys Trp Ser Arg Pro Trp Ile Leu His Cys Gly Pro
385                 390                 395                 400

Cys Gly Tyr Ser Asp Leu Ala Ala Leu Glu Glu Glu Gly Leu Phe Gly
                405                 410                 415

Cys Leu Phe Glu Cys Gly Thr Lys Gln Glu Cys Glu Gln Ile Ala Phe
            420                 425                 430

Arg Leu Phe Thr His Arg Glu Ile Leu Ser His Leu Gln Gly Asp Cys
        435                 440                 445

Thr Ser Pro Gly Arg Asn Pro Ser Gln Phe Lys Ser Asn
    450                 455                 460
```

<210> 10
<211> 484
<212> PRT
<213> Homo sapiens

<400> 10
Met Gly Val Pro Arg Thr Pro Ser Arg Thr Val Leu Phe Glu Arg Glu
1 5 10 15

Arg Thr Gly Leu Thr Tyr Arg Val Pro Ser Leu Leu Pro Val Pro Pro
20 25 30

Gly Pro Thr Leu Leu Ala Phe Val Glu Gln Arg Leu Ser Pro Asp Asp
35 40 45

Ser His Ala His Arg Leu Val Leu Arg Arg Gly Thr Leu Ala Gly Gly
50 55 60

Ser Val Arg Trp Gly Ala Leu His Val Leu Gly Thr Ala Ala Leu Ala
65 70 75 80

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

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

Val Gln Ile Ala Thr Gly Arg Asn Ala Ala Arg Leu Cys Cys Val Ala
115 120 125

Ser Arg Asp Ala Gly Leu Ser Trp Gly Ser Ala Arg Asp Leu Thr Glu
130 135 140

Glu Ala Ile Gly Gly Ala Val Gln Asp Trp Ala Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Gly Val Gln Leu Pro Ser Gly Arg Leu Leu Val Pro Ala
165 170 175

Tyr Thr Tyr Arg Val Asp Arg Arg Glu Cys Phe Gly Lys Ile Cys Arg
180 185 190

Thr Ser Pro His Ser Phe Ala Phe Tyr Ser Asp Asp His Gly Arg Thr
195 200 205

```
Trp Arg Cys Gly Gly Leu Val Pro Asn Leu Arg Ser Gly Glu Cys Gln
    210                 215                 220

Leu Ala Ala Val Asp Gly Gly Gln Ala Gly Ser Phe Leu Tyr Cys Asn
225                 230                 235                 240

Ala Arg Ser Pro Leu Gly Ser Arg Val Gln Ala Leu Ser Thr Asp Glu
                245                 250                 255

Gly Thr Ser Phe Leu Pro Ala Glu Arg Val Ala Ser Leu Pro Glu Thr
            260                 265                 270

Ala Trp Gly Cys Gln Gly Ser Ile Val Gly Phe Pro Ala Pro Ala Pro
        275                 280                 285

Asn Arg Pro Arg Asp Asp Ser Trp Ser Val Gly Pro Gly Ser Pro Leu
    290                 295                 300

Gln Pro Pro Leu Leu Gly Pro Gly Val His Glu Pro Pro Glu Glu Ala
305                 310                 315                 320

Ala Val Asp Pro Arg Gly Gly Gln Val Pro Gly Gly Pro Phe Ser Arg
                325                 330                 335

Leu Gln Pro Arg Gly Asp Gly Pro Arg Gln Pro Gly Pro Arg Pro Gly
            340                 345                 350

Val Ser Gly Asp Val Gly Ser Trp Thr Leu Ala Leu Pro Met Pro Phe
        355                 360                 365

Ala Ala Pro Pro Gln Ser Pro Thr Trp Leu Leu Tyr Ser His Pro Val
    370                 375                 380

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

Leu Asp Pro Arg Ser Trp Thr Glu Pro Trp Val Ile Tyr Glu Gly Pro
                405                 410                 415

Ser Gly Tyr Ser Asp Leu Ala Ser Ile Gly Pro Ala Pro Glu Gly Gly
            420                 425                 430
```

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

Glu Ile Ser Phe Cys Thr Phe Ser Leu Arg Glu Val Leu Glu Asn Val
450 455 460

Pro Ala Ser Pro Lys Pro Pro Asn Leu Gly Asp Lys Pro Arg Gly Cys
465 470 475 480

Cys Trp Pro Ser

<210> 11
<211> 496
<212> PRT
<213> Homo sapiens

<400> 11
Met Met Ser Ser Ala Ala Phe Pro Arg Trp Leu Ser Met Gly Val Pro
1 5 10 15

Arg Thr Pro Ser Arg Thr Val Leu Phe Glu Arg Glu Arg Thr Gly Leu
20 25 30

Thr Tyr Arg Val Pro Ser Leu Leu Pro Val Pro Pro Gly Pro Thr Leu
35 40 45

Leu Ala Phe Val Glu Gln Arg Leu Ser Pro Asp Asp Ser His Ala His
50 55 60

Arg Leu Val Leu Arg Arg Gly Thr Leu Ala Gly Gly Ser Val Arg Trp
65 70 75 80

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

Met Asn Pro Cys Pro Val His Asp Ala Gly Thr Gly Thr Val Phe Leu
100 105 110

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

```
Thr Gly Arg Asn Ala Ala Arg Leu Cys Cys Val Ala Ser Arg Asp Ala
    130                 135                 140

Gly Leu Ser Trp Gly Ser Ala Arg Asp Leu Thr Glu Glu Ala Ile Gly
145                 150                 155                 160

Gly Ala Val Gln Asp Trp Ala Thr Phe Ala Val Gly Pro Gly His Gly
                165                 170                 175

Val Gln Leu Pro Ser Gly Arg Leu Leu Val Pro Ala Tyr Thr Tyr Arg
            180                 185                 190

Val Asp Arg Arg Glu Cys Phe Gly Lys Ile Cys Arg Thr Ser Pro His
        195                 200                 205

Ser Phe Ala Phe Tyr Ser Asp Asp His Gly Arg Thr Trp Arg Cys Gly
    210                 215                 220

Gly Leu Val Pro Asn Leu Arg Ser Gly Glu Cys Gln Leu Ala Ala Val
225                 230                 235                 240

Asp Gly Gly Gln Ala Gly Ser Phe Leu Tyr Cys Asn Ala Arg Ser Pro
                245                 250                 255

Leu Gly Ser Arg Val Gln Ala Leu Ser Thr Asp Glu Gly Thr Ser Phe
            260                 265                 270

Leu Pro Ala Glu Arg Val Ala Ser Leu Pro Glu Thr Ala Trp Gly Cys
        275                 280                 285

Gln Gly Ser Ile Val Gly Phe Pro Ala Pro Ala Pro Asn Arg Pro Arg
    290                 295                 300

Asp Asp Ser Trp Ser Val Gly Pro Gly Ser Pro Leu Gln Pro Pro Leu
305                 310                 315                 320

Leu Gly Pro Gly Val His Glu Pro Pro Glu Glu Ala Ala Val Asp Pro
                325                 330                 335
```

```
Arg Gly Gly Gln Val Pro Gly Gly Pro Phe Ser Arg Leu Gln Pro Arg
            340                 345                 350

Gly Asp Gly Pro Arg Gln Pro Gly Pro Arg Pro Gly Val Ser Gly Asp
        355                 360                 365

Val Gly Ser Trp Thr Leu Ala Leu Pro Met Pro Phe Ala Ala Pro Pro
    370                 375                 380

Gln Ser Pro Thr Trp Leu Leu Tyr Ser His Pro Val Gly Arg Arg Ala
385                 390                 395                 400

Arg Leu His Met Gly Ile Arg Leu Ser Gln Ser Pro Leu Asp Pro Arg
                405                 410                 415

Ser Trp Thr Glu Pro Trp Val Ile Tyr Glu Gly Pro Ser Gly Tyr Ser
            420                 425                 430

Asp Leu Ala Ser Ile Gly Pro Ala Pro Glu Gly Gly Leu Val Phe Ala
        435                 440                 445

Cys Leu Tyr Glu Ser Gly Ala Arg Thr Ser Tyr Asp Glu Ile Ser Phe
    450                 455                 460

Cys Thr Phe Ser Leu Arg Glu Val Leu Glu Asn Val Pro Ala Ser Pro
465                 470                 475                 480

Lys Pro Pro Asn Leu Gly Asp Lys Pro Arg Gly Cys Cys Trp Pro Ser
                485                 490                 495
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<210> 12
<211> 5
<212> PRT
<213> Homo sapiens

<400> 12
Met Ala Ser Leu Pro
1   5

<210> 13
<211> 4
<212> PRT
<213> Homo sapiens

<400> 13
Ala Ser Leu Pro
1

<210> 14
<211> 8
<212> PRT
<213> Salmonella typhimurium

<400> 14
Thr Val Glu Lys Ser Val Val Phe
1 5

<210> 15
<211> 12
<212> PRT
<213> Homo sapiens

<400> 15
Gly Asp Tyr Asp Ala Pro Thr His Gln Val Gln Trp
1 5 10

<210> 16
<211> 8
<212> PRT
<213> Homo sapiens

<400> 16
Ser Met Asp Gln Gly Ser Thr Trp
1 5

<210> 17
<211> 8
<212> PRT
<213> Salmonella typhimurium

<400> 17
Ser Thr Asp Gly Gly Lys Thr Trp
1 5

<210> 18
<211> 8
<212> PRT
<213> Homo sapiens

<400> 18
Pro Arg Pro Pro Ala Pro Glu Ala
1 5

<210> 19
<211> 8
<212> PRT
<213> Homo sapiens

<400> 19
Gln Thr Pro Leu Glu Ala Ala Cys
1 5

<210> 20
<211> 9
<212> PRT
<213> Homo sapiens

<400> 20
Asn Pro Arg Pro Pro Ala Pro Glu Ala
1 5

<210> 21
<211> 7
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Recombinant mutant human sialidase substitution sequence

<400> 21
Ser Gln Asn Asp Gly Glu Ser
1 5

<210> 22
<211> 7
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Recombinant mutant human sialidase substitution sequence

<400> 22
Leu Ser His Ser Leu Ser Thr
1 5

<210> 23
<211> 1092
<212> DNA
<213> Homo sapiens

<400> 23
gagaacgact ttggactggt gcagcctctg gtcaccatgg aacagctgct gtgggtttcc 60

ggcagacaga tcggcagcgt ggacaccttc agaatccctc tgatcaccgc cacacctaga 120

ggcaccctgc tggcctttgc cgaggccaga aagatgagca gctctgacga gggcgccaag 180

tttattgccc tgaggcggtc tatggaccag ggctctacat ggtcccctac cgccttcatc 240

gtgaacgatg gcgacgtgcc cgatggcctg aatctgggag ctgtggtgtc cgatgtggaa 300

accggcgtgg tgttcctgtt ctacagcctg tgtgcccaca aggccggttg tcaggtggcc 360

agcacaatgc tcgtgtggtc caaggacgac ggcgtgtcct ggtctacccc tagaaacctg 420

agcctggaca tcggcaccga agtgtttgct ccaggacctg gctctggcat ccagaagcag 480

agagagccca gaaagggcag actgatcgtg tgtggccacg gcacccttga gagagatggc 540

gttttctgcc tgctgagcga cgatcatggc gcctcttgga gatacggcag cggagtgtct 600

ggaatccctt acggccagcc taagcaagag aacgatttca accccgacga gtgccagcct 660

tacgagctgc ctgatggcag cgtcgtgatc aacgcccgga accagaacaa ctaccactgc 720

cactgccgga tcgtgctgag aagctacgac gcctgcgata ccctgcggcc tagagatgtg 780

accttcgatc ctgagctggt ggaccctgtt gttgccgctg gtgccgtcgt gacatctagc 840

ggcatcgtgt tcttcagcaa ccctgctcac cccgagttca gagtgaatct gaccctgcgg 900

tggtccttca gcaatggcac aagctggcgg aaagaaaccg tgcagctttg gcctggacct 960

agcggctact cttctctggc tacactggaa ggcagcatgg acggcgaaga acaggcccct 1020

cagctgtacg tgctgtacga gaagggcaga aaccactaca ccgagagcat cagcgtggcc 1080

aagatcagcg tt 1092

<210> 24
<211> 1140
<212> DNA
<213> Homo sapiens

<400> 24
atggccagcc tgcctgtgct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gcccctacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgccc agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgtcaagt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccat ccagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agagccagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccacag ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960

tggagcgaac ctgttctgct ggccaagggc agctgtgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

gagatcgtgt tcctgatgtt caccctgaag caggcctttc agccgagta cctgcctcaa 1140

<210> 25
<211> 1284
<212> DNA
<213> Homo sapiens

<400> 25
atggaggaag tgaccacctg tagcttcaac agccctctgt tccggcaaga ggacgaccgg 60

ggcatcacct acagaatccc tgctctgctg tacatccctc ctacacacac ctttctggcc 120

ttcgccgaga agcggagcac cagacgagat gaagatgccc tgcacctggt gctgagaaga 180

ggcctgagaa tcggacagct ggtgcagtgg ggacctctga agcctctgat ggaagccaca 240

ctgcccggcc acagaaccat gaatccttgt cctgtgtggg agcagaaaag cggctgcgtg 300

ttcctgttct tcatctgcgt gcggggccac gtgaccgaga gacagcaaat cgtgtccggc 360

agaaacgccg ccagactgtg cttcatctac agccaggatg ccggctgctc ttggagcgaa 420

gttcgggatc tgaccgaaga agtgatcggc agcgagctga agcactgggc cacatttgct 480

gttggccctg gccacggaat ccagctgcaa tctggcagac tggtcatccc cgcctacacc 540

tactatatcc ccagctggtt cttctgcttc caactgcctt gcaagacccg gcctcacagc 600

ctgatgatct acagcgacga tctgggcgtg acatggcacc acggcagact gatcagaccc 660

atggtcaccg tggaatgcga ggtggccgaa gtgacaggca gagctggaca ccctgtgctg 720

tactgctctg ccagaacacc caaccggtgt agagccgagg ctctgtctac agatcacggc 780

gagggctttc agagactggc cctctctaga cagctgtgcg aacctcctca tggctgtcag 840

ggcagcgtgg tgtccttcag acctctggaa atccctcacc ggtgccagga cagcagctct 900

aaggatgccc ctaccatcca gcagtctagc cctggcagca gcctgagact ggaagaggaa 960

gccggaacac ctagcgagag ctggctgctg tactctcacc ccaccagcag aaagcagaga 1020

gtggacctgg gcatctacct gaatcagacc cctctggaag ccgcctgttg gagcagacct 1080

tggattctgc actgtggccc ttgcggctac tctgatctgg ccgctctgga agaagagggc 1140

ctgttcggct gcctgtttga gtgcggcaca aagcaagagt gcgagcagat cgccttccgg 1200

ctgttcaccc acagagagat cctgagccat ctgcagggcg actgcacaag cccaggcaga 1260

aatcccagcc agttcaagag caac 1284

<210> 26
<211> 1452
<212> DNA
<213> Homo sapiens

<400> 26
atgggcgtgc ccagaacacc cagcagaacc gtgctgttcg agagagagag gaccggcctg 60

acctacagag tgccttctct gctgcctgtg cctcctggac ctacactgct ggccttcgtg 120

gaacagagac tgagccccga tgattctcac gcccacagac tggtgctgag aagaggaaca 180

ctggctggcg gctctgttag atggggagca ctgcatgtgc tgggcacagc tgctcttgcc 240

gagcacagat ccatgaatcc ctgtcctgtg cacgacgccg gaaccggcac agtgtttctg 300

ttctttatcg ccgtgctggg ccacacacct gaggccgttc aaattgccac cggcagaaat 360

gccgccagac tgtgttgtgt ggcctccaga gatgccggcc tgtcttgggg atctgccaga 420

gatctgaccg aggaagccat tggcggagcc gttcaggatt gggccacatt tgctgttgga 480

cctggacacg gcgtgcagct gccaagtggt agactgctgg tgcctgccta cacatacaga 540

gtggatcgga gagagtgctt cggaaagatc tgccggacaa gccctcacag cttcgccttc 600

tactccgacg atcacggccg gacttggaga tgtggtggcc tggtgcctaa tctgagaagc 660

ggcgaatgtc aactggccgc cgttgatggt ggacaggctg gcagcttcct gtactgcaac 720

gccagatctc ctctgggctc tagagtgcag gccctgtcta ccgatgaggg caccagtttt 780

ctgcccgccg aaagagttgc ctctctgcct gaaacagcct ggggctgtca gggctctatc 840

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ctggacccca gaagctggac agagccttgg gtcatctatg agggccctag cggctacagc 1260

gatctggcct ctattggccc agctcctgaa ggcggactgg tgttcgcttg tctgtatgag 1320

agcggcgcca gaaccagcta cgacgagatc agcttctgca ccttcagcct gcgcgaggtg 1380

ctggaaaatg tgcccgcctc tcctaagcct cctaacctgg gcgataagcc tagaggctgt 1440

tgctggccat ct 1452

<210> 27
<211> 47
<212> PRT
<213> Homo sapiens

<400> 27
Met Thr Gly Glu Arg Pro Ser Thr Ala Leu Pro Asp Arg Arg Trp Gly
1 5 10 15

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

Ala Ile Phe Leu Leu Leu Ser Leu Ala Ala Ser Trp Ser Lys Ala
35 40 45

<210> 28
<211> 22
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
N-terminal signal peptide sequence

<400> 28
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Pro Gly Ala Arg Cys
20

<210> 29
<211> 4
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
C-terminal lysosomal signal motif sequence

<400> 29
Tyr Gly Thr Leu
1

<210> 30
<211> 382
<212> PRT
<213> Salmonella typhimurium

<400> 30
Met Thr Val Glu Lys Ser Val Val Phe Lys Ala Glu Gly Glu His Phe
1 5 10 15

Thr Asp Gln Lys Gly Asn Thr Ile Val Gly Ser Gly Ser Gly Gly Thr
20 25 30

Thr Lys Tyr Phe Arg Ile Pro Ala Met Cys Thr Thr Ser Lys Gly Thr
35 40 45

Ile Val Val Phe Ala Asp Ala Arg His Asn Thr Ala Ser Asp Gln Ser
50 55 60

Phe Ile Asp Thr Ala Ala Ala Arg Ser Thr Asp Gly Gly Lys Thr Trp
65 70 75 80

```
Asn Lys Lys Ile Ala Ile Tyr Asn Asp Arg Val Asn Ser Lys Leu Ser
                85                  90                  95

Arg Val Met Asp Pro Thr Cys Ile Val Ala Asn Ile Gln Gly Arg Glu
            100                 105                 110

Thr Ile Leu Val Met Val Gly Lys Trp Asn Asn Asn Asp Lys Thr Trp
        115                 120                 125

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

Tyr Lys Ser Thr Asp Asp Gly Val Thr Phe Ser Lys Val Glu Thr Asn
145                 150                 155                 160

Ile His Asp Ile Val Thr Lys Asn Gly Thr Ile Ser Ala Met Leu Gly
                165                 170                 175

Gly Val Gly Ser Gly Leu Gln Leu Asn Asp Gly Lys Leu Val Phe Pro
            180                 185                 190

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

Phe Ile Tyr Ser Thr Asp Gly Ile Thr Trp Ser Leu Pro Ser Gly Tyr
    210                 215                 220

Cys Glu Gly Phe Gly Ser Glu Asn Asn Ile Ile Glu Phe Asn Ala Ser
225                 230                 235                 240

Leu Val Asn Asn Ile Arg Asn Ser Gly Leu Arg Arg Ser Phe Glu Thr
                245                 250                 255

Lys Asp Phe Gly Lys Thr Trp Thr Glu Phe Pro Pro Met Asp Lys Lys
            260                 265                 270

Val Asp Asn Arg Asn His Gly Val Gln Gly Ser Thr Ile Thr Ile Pro
        275                 280                 285

Ser Gly Asn Lys Leu Val Ala Ala His Ser Ser Ala Gln Asn Lys Asn
    290                 295                 300
```

```
Asn Asp Tyr Thr Arg Ser Asp Ile Ser Leu Tyr Ala His Asn Leu Tyr
305                 310                 315                 320

Ser Gly Glu Val Lys Leu Ile Asp Asp Phe Tyr Pro Lys Val Gly Asn
                325                 330                 335

Ala Ser Gly Ala Gly Tyr Ser Cys Leu Ser Tyr Arg Lys Asn Val Asp
            340                 345                 350

Lys Glu Thr Leu Tyr Val Val Tyr Glu Ala Asn Gly Ser Ile Glu Phe
        355                 360                 365

Gln Asp Leu Ser Arg His Leu Pro Val Ile Lys Ser Tyr Asn
    370                 375                 380
```

<210> 31
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 31

```
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                   10                  15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95
```

```
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Lys
225                 230
```

<210> 32
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 32

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1               5                   10                  15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
```

```
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    130                 135                 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225
```

<210> 33
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 33

```
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                  10                  15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175
```

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 34
<211> 1383
<212> DNA
<213> Homo sapiens

<400> 34
atgagacctg cggacctgcc cccgcgcccc atggaagaat ccccggcgtc agctctgcc 60

ccgacagaga cggaggagcc ggggtccagt gcagaggtca tggaagaagt gacaacatgc 120

tccttcaaca gccctctgtt ccggcaggaa gatgacagag ggattaccta ccggatccca 180

gccctgctct acataccccc cacccacacc ttcctggcct ttgcagagaa gcgttctacg 240

aggagagatg aggatgctct ccacctggtg ctgaggcgag ggttgaggat tgggcagttg 300

gtacagtggg ggcccctgaa gccactgatg gaagccacac taccggggca tcggaccatg 360

aacccctgtc ctgtatggga gcagaagagt ggttgtgtgt tcctgttctt catctgtgtg 420

cggggccatg tcacagagcg tcaacagatt gtgtcaggca ggaatgctgc ccgcctttgc 480

ttcatctaca gtcaggatgc tggatgttca tggagtgagg tgagggactt gactgaggag 540

gtcattggct cagagctgaa gcactgggcc acatttgctg tgggcccagg tcatggcatc 600

cagctgcagt cagggagact ggtcatccct gcgtatacct actacatccc ttcctggttc 660

ttttgcttcc agctaccatg taaaaccagg cctcattctc tgatgatcta cagtgatgac 720

ctaggggtca catggcacca tggtagactc attaggccca tggttacagt agaatgtgaa 780

gtggcagagg tgactgggag ggctggccac cctgtgctat attgcagtgc ccggacacca 840

aacaggtgcc gggcagaggc gctcagcact gaccatggtg aaggctttca gagactggcc 900

ctgagtcgac agctctgtga gcccccacat ggttgccaag ggagtgtggt aagtttccgg 960

cccctggaga tcccacatag gtgccaggac tctagcagca aagatgcacc caccattcag 1020

cagagctctc caggcagttc actgaggctg gaggaggaag ctggaacacc gtcagaatca 1080

tggctcttgt actcacaccc aaccagtagg aaacagaggg ttgacctagg tatctatctc 1140

aaccagaccc ccttggaggc tgcctgctgg tcccgcccct ggatcttgca ctgtgggccc 1200

tgtggctact ctgatctggc tgctctggag gaggagggct tgtttgggtg tttgtttgaa 1260

tgtgggacca agcaagagtg tgagcagatt gccttccgcc tgtttacaca ccgggagatc 1320

ctgagtcacc tgcaggggga ctgcaccagc cctggtagga acccaagcca attcaaaagc 1380

aat 1383

<210> 35
<211> 1488
<212> DNA
<213> Homo sapiens

<400> 35
atgatgagct ctgcagcctt cccaaggtgg ctgagcatgg gggtccctcg tacccccttca 60

cggacagtgc tcttcgagcg ggagaggacg ggcctgacct accgcgtgcc ctcgctgctc 120

cccgtgcccc ccgggcccac cctgctggcc tttgtggagc agcggctcag ccctgacgac 180

tcccacgccc accgcctggt gctgaggagg ggcacgctgg ccgggggctc cgtgcggtgg 240

ggtgccctgc acgtgctggg gacagcagcc ctggcggagc accggtccat gaacccctgc 300

cctgtgcacg atgctggcac gggcaccgtc ttcctcttct tcatcgcggt gctgggccac 360

acgcctgagg ccgtgcagat cgccacggga aggaacgccg cgcgcctctg ctgtgtggcc 420

agccgtgacg ccggcctctc gtggggcagc gcccgggacc tcaccgagga ggccatcggt 480

ggtgccgtgc aggactgggc cacattcgct gtgggtcccg gccacggtgt gcagctgccc 540

tcaggccgcc tgctggtacc cgcctacacc taccgcgtgg accgccgaga gtgttttggc 600

aagatctgcc ggaccagccc tcactccttc gccttctaca gcgatgacca cggccgcacc 660

tggcgctgtg gaggcctcgt gcccaacctg cgctcaggcg agtgccagct ggcagcggtg 720

gacggtgggc aggccggcag cttcctctac tgcaatgccc ggagcccact gggcagccgt 780

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gagatttcct tttgtacatt ctccctgcgt gaggtcctgg agaacgtgcc cgccagcccc 1440

aaaccgccca accttgggga caagcctcgg gggtgctgct ggccctcc 1488

<210> 36
<211> 781
<212> PRT
<213> Vibrio cholerae

<400> 36
Met Arg Phe Lys Asn Val Lys Lys Thr Ala Leu Met Leu Ala Met Phe
1 5 10 15

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

Gly Asp Thr Glu Phe Asp Ser Pro Ala Lys Gln Gly Trp Met Gln Asp
35 40 45

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

Ala Trp Leu Val Gln Gly Ile Gly Gly Arg Ala Gln Trp Thr Tyr Ser
65 70 75 80

Leu Ser Thr Asn Gln His Ala Gln Ala Ser Ser Phe Gly Trp Arg Met
85 90 95

Thr Thr Glu Met Lys Val Leu Ser Gly Gly Met Ile Thr Asn Tyr Tyr
100 105 110

```
Ala Asn Gly Thr Gln Arg Val Leu Pro Ile Ile Ser Leu Asp Ser Ser
        115                 120                 125

Gly Asn Leu Val Val Glu Phe Glu Gly Gln Thr Gly Arg Thr Val Leu
    130                 135                 140

Ala Thr Gly Thr Ala Ala Thr Glu Tyr His Lys Phe Glu Leu Val Phe
145                 150                 155                 160

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

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

Trp Gly Asn Gly Ser Ser Asn Thr Asp Gly Val Ala Ala Tyr Arg Asp
        195                 200                 205

Ile Lys Phe Glu Ile Gln Gly Asp Val Ile Phe Arg Gly Pro Asp Arg
    210                 215                 220

Ile Pro Ser Ile Val Ala Ser Ser Val Thr Pro Gly Val Val Thr Ala
225                 230                 235                 240

Phe Ala Glu Lys Arg Val Gly Gly Gly Asp Pro Gly Ala Leu Ser Asn
                245                 250                 255

Thr Asn Asp Ile Ile Thr Arg Thr Ser Arg Asp Gly Gly Ile Thr Trp
            260                 265                 270

Asp Thr Glu Leu Asn Leu Thr Glu Gln Ile Asn Val Ser Asp Glu Phe
        275                 280                 285

Asp Phe Ser Asp Pro Arg Pro Ile Tyr Asp Pro Ser Ser Asn Thr Val
    290                 295                 300

Leu Val Ser Tyr Ala Arg Trp Pro Thr Asp Ala Ala Gln Asn Gly Asp
305                 310                 315                 320

Arg Ile Lys Pro Trp Met Pro Asn Gly Ile Phe Tyr Ser Val Tyr Asp
                325                 330                 335
```

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Val Ala Ser Gly Asn Trp Gln Ala Pro Ile Asp Val Thr Asp Gln Val
            340                 345                 350

Lys Glu Arg Ser Phe Gln Ile Ala Gly Trp Gly Gly Ser Glu Leu Tyr
        355                 360                 365

Arg Arg Asn Thr Ser Leu Asn Ser Gln Gln Asp Trp Gln Ser Asn Ala
    370                 375                 380

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

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

Leu Val Ala Asn Leu Asn Gly Val Ser Ala Pro Ile Ile Leu Gln Ser
            420                 425                 430

Glu His Ala Lys Val His Ser Phe His Asp Tyr Glu Leu Gln Tyr Ser
        435                 440                 445

Ala Leu Asn His Thr Thr Thr Leu Phe Val Asp Gly Gln Gln Ile Thr
    450                 455                 460

Thr Trp Ala Gly Glu Val Ser Gln Glu Asn Asn Ile Gln Phe Gly Asn
465                 470                 475                 480

Ala Asp Ala Gln Ile Asp Gly Arg Leu His Val Gln Lys Ile Val Leu
                485                 490                 495

Thr Gln Gln Gly His Asn Leu Val Glu Phe Asp Ala Phe Tyr Leu Ala
            500                 505                 510

Gln Gln Thr Pro Glu Val Glu Lys Asp Leu Glu Lys Leu Gly Trp Thr
        515                 520                 525

Lys Ile Lys Thr Gly Asn Thr Met Ser Leu Tyr Gly Asn Ala Ser Val
    530                 535                 540
```

```
Asn Pro Gly Pro Gly His Gly Ile Thr Leu Thr Arg Gln Gln Asn Ile
545                 550                 555                 560

Ser Gly Ser Gln Asn Gly Arg Leu Ile Tyr Pro Ala Ile Val Leu Asp
                565                 570                 575

Arg Phe Phe Leu Asn Val Met Ser Ile Tyr Ser Asp Asp Gly Gly Ser
            580                 585                 590

Asn Trp Gln Thr Gly Ser Thr Leu Pro Ile Pro Phe Arg Trp Lys Ser
        595                 600                 605

Ser Ser Ile Leu Glu Thr Leu Glu Pro Ser Glu Ala Asp Met Val Glu
    610                 615                 620

Leu Gln Asn Gly Asp Leu Leu Leu Thr Ala Arg Leu Asp Phe Asn Gln
625                 630                 635                 640

Ile Val Asn Gly Val Asn Tyr Ser Pro Arg Gln Gln Phe Leu Ser Lys
                645                 650                 655

Asp Gly Gly Ile Thr Trp Ser Leu Leu Glu Ala Asn Asn Ala Asn Val
            660                 665                 670

Phe Ser Asn Ile Ser Thr Gly Thr Val Asp Ala Ser Ile Thr Arg Phe
        675                 680                 685

Glu Gln Ser Asp Gly Ser His Phe Leu Leu Phe Thr Asn Pro Gln Gly
    690                 695                 700

Asn Pro Ala Gly Thr Asn Gly Arg Gln Asn Leu Gly Leu Trp Phe Ser
705                 710                 715                 720

Phe Asp Glu Gly Val Thr Trp Lys Gly Pro Ile Gln Leu Val Asn Gly
                725                 730                 735

Ala Ser Ala Tyr Ser Asp Ile Tyr Gln Leu Asp Ser Glu Asn Ala Ile
            740                 745                 750

Val Ile Val Glu Thr Asp Asn Ser Asn Met Arg Ile Leu Arg Met Pro
        755                 760                 765
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Ile Thr Leu Leu Lys Gln Lys Leu Thr Leu Ser Gln Asn
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<211> 2424
<212> DNA
<213> Vibrio cholerae

<400> 37
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atgttcggta tggcgacaag ctcaaacgcc gcacttttg actataacgc aacgggtgac 180

actgagtttg acagtccagc caaacaggga tggatgcaag acaacacgaa taatggcagc 240

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gctcaatgga catattctct ctctactaat caacatgccc aagcatcaag tttcggttgg 360

cgaatgacga cagaaatgaa agtgctcagt ggtggaatga tcacaaacta ctacgccaac 420

ggcactcagc gtgtcttacc catcatttca ttagatagca gtggtaactt agttgttgag 480

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<211> 409
<212> PRT
<213> Mus musculus

<400> 38
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Ala Gly Arg Arg Gly Gln Gly Leu Ala Ala Ile Phe Leu Leu Leu Val
20 25 30

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Ser Ala Ala Glu Ser Glu Ala Arg Ala Glu Asp Asp Phe Ser Leu Val
        35                  40                  45

Gln Pro Leu Val Thr Met Glu Gln Leu Leu Trp Val Ser Gly Lys Gln
    50                  55                  60

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

Arg Gly Thr Leu Leu Ala Phe Ala Glu Ala Arg Lys Lys Ser Ala Ser
                85                  90                  95

Asp Glu Gly Ala Lys Phe Ile Ala Met Arg Arg Ser Thr Asp Gln Gly
            100                 105                 110

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

Asp Gly Leu Asn Leu Gly Ala Val Val Asn Asp Val Asp Thr Gly Ile
    130                 135                 140

Val Phe Leu Ile Tyr Thr Leu Cys Ala His Lys Val Asn Cys Gln Val
145                 150                 155                 160

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

Pro Pro Arg Asn Leu Ser Val Asp Ile Gly Thr Glu Met Phe Ala Pro
            180                 185                 190

Gly Pro Gly Ser Gly Ile Gln Lys Gln Arg Glu Pro Gly Lys Gly Arg
        195                 200                 205

Leu Ile Val Cys Gly His Gly Thr Leu Glu Arg Asp Gly Val Phe Cys
    210                 215                 220

Leu Leu Ser Asp Asp His Gly Ala Ser Trp His Tyr Gly Thr Gly Val
225                 230                 235                 240

Ser Gly Ile Pro Phe Gly Gln Pro Lys His Asp His Asp Phe Asn Pro
```

```
                245                 250                 255

Asp Glu Cys Gln Pro Tyr Glu Leu Pro Asp Gly Ser Val Ile Ile Asn
            260                 265                 270

Ala Arg Asn Gln Asn Asn Tyr His Cys Arg Cys Arg Ile Val Leu Arg
        275                 280                 285

Ser Tyr Asp Ala Cys Asp Thr Leu Arg Pro Arg Asp Val Thr Phe Asp
    290                 295                 300

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

Ser Gly Ile Val Phe Phe Ser Asn Pro Ala His Pro Glu Phe Arg Val
                325                 330                 335

Asn Leu Thr Leu Arg Trp Ser Phe Ser Asn Gly Thr Ser Trp Leu Lys
            340                 345                 350

Glu Arg Val Gln Val Trp Pro Gly Pro Ser Gly Tyr Ser Ser Leu Thr
        355                 360                 365

Ala Leu Glu Asn Ser Thr Asp Gly Lys Lys Gln Pro Pro Gln Leu Phe
    370                 375                 380

Val Leu Tyr Glu Lys Gly Leu Asn Arg Tyr Thr Glu Ser Ile Ser Met
385                 390                 395                 400

Val Lys Ile Ser Val Tyr Gly Thr Leu
                405
```

<210> 39
<211> 393
<212> PRT
<213> Mus musculus

<400> 39

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Met Thr Val Gln Pro Ser Pro Trp Phe Ser Asp Leu Arg Pro Met Ala
1               5                   10                  15

Thr Cys Pro Val Leu Gln Lys Glu Thr Leu Phe Arg Thr Gly Val His
```

```
            20                  25                  30

Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Lys Lys Gln Lys Thr Leu
        35                  40                  45

Leu Ala Phe Ala Glu Lys Arg Ala Ser Lys Thr Asp Glu His Ala Glu
    50                  55                  60

Leu Ile Val Leu Arg Arg Gly Ser Tyr Asn Glu Ala Thr Asn Arg Val
65                  70                  75                  80

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

Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Lys Gln Thr Lys Thr Leu
            100                 105                 110

Phe Leu Phe Phe Ile Ala Val Pro Gly Arg Val Ser Glu His His Gln
        115                 120                 125

Leu His Thr Lys Val Asn Val Thr Arg Leu Cys Cys Val Ser Ser Thr
    130                 135                 140

Asp His Gly Arg Thr Trp Ser Pro Ile Gln Asp Leu Thr Glu Thr Thr
145                 150                 155                 160

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

His Cys Leu Gln Leu Arg Asn Pro Ala Gly Ser Leu Leu Val Pro Ala
            180                 185                 190

Tyr Ala Tyr Arg Lys Leu His Pro Ala Gln Lys Pro Thr Pro Phe Ala
        195                 200                 205

Phe Cys Phe Ile Ser Leu Asp His Gly His Thr Trp Lys Leu Gly Asn
    210                 215                 220

Phe Val Ala Glu Asn Ser Leu Glu Cys Gln Val Ala Glu Val Gly Thr
225                 230                 235                 240
```

```
Gly Ala Gln Arg Met Val Tyr Leu Asn Ala Arg Ser Phe Leu Gly Ala
                245                 250                 255

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

Arg Val Val Ser Lys Leu Val Glu Pro Pro His Gly Cys His Gly Ser
        275                 280                 285

Val Val Ala Phe His Asn Pro Ile Ser Lys Pro His Ala Leu Asp Thr
    290                 295                 300

Trp Leu Leu Tyr Thr His Pro Thr Asp Ser Arg Asn Arg Thr Asn Leu
305                 310                 315                 320

Gly Val Tyr Leu Asn Gln Met Pro Leu Asp Pro Thr Ala Trp Ser Glu
                325                 330                 335

Pro Thr Leu Leu Ala Met Gly Ile Cys Ala Tyr Ser Asp Leu Gln Asn
            340                 345                 350

Met Gly Gln Gly Pro Asp Gly Ser Pro Gln Phe Gly Cys Leu Tyr Glu
        355                 360                 365

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

Ala Phe Pro Thr Val Phe Asp Ala Gln
385                 390
```

<210> 40
<211> 418
<212> PRT
<213> Mus musculus

<400> 40

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Met Glu Glu Val Pro Pro Tyr Ser Leu Ser Ser Thr Leu Phe Gln Gln
1               5                   10                  15

Glu Glu Gln Ser Gly Val Thr Tyr Arg Ile Pro Ala Leu Leu Tyr Leu
            20                  25                  30
```

```
Pro Pro Thr His Thr Phe Leu Ala Phe Ala Glu Lys Arg Thr Ser Val
        35                  40                  45

Arg Asp Glu Asp Ala Ala Cys Leu Val Leu Arg Arg Gly Leu Met Lys
    50                  55                  60

Gly Arg Ser Val Gln Trp Gly Pro Gln Arg Leu Leu Met Glu Ala Thr
65                  70                  75                  80

Leu Pro Gly His Arg Thr Met Asn Pro Cys Pro Val Trp Glu Lys Asn
                85                  90                  95

Thr Gly Arg Val Tyr Leu Phe Phe Ile Cys Val Arg Gly His Val Thr
            100                 105                 110

Glu Arg Cys Gln Ile Val Trp Gly Lys Asn Ala Ala Arg Leu Cys Phe
        115                 120                 125

Leu Cys Ser Glu Asp Ala Gly Cys Ser Trp Gly Glu Val Lys Asp Leu
    130                 135                 140

Thr Glu Glu Val Ile Gly Ser Glu Val Lys Arg Trp Ala Thr Phe Ala
145                 150                 155                 160

Val Gly Pro Gly His Gly Ile Gln Leu His Ser Gly Arg Leu Ile Ile
                165                 170                 175

Pro Ala Tyr Ala Tyr Tyr Val Ser Arg Trp Phe Leu Cys Phe Ala Cys
            180                 185                 190

Ser Val Lys Pro His Ser Leu Met Ile Tyr Ser Asp Asp Phe Gly Val
        195                 200                 205

Thr Trp His His Gly Lys Phe Ile Glu Pro Gln Val Thr Gly Glu Cys
    210                 215                 220

Gln Val Ala Glu Val Ala Gly Thr Ala Gly Asn Pro Val Leu Tyr Cys
225                 230                 235                 240

Ser Ala Arg Thr Pro Ser Arg Phe Arg Ala Glu Ala Phe Ser Thr Asp
```

245 250 255

Ser Gly Gly Cys Phe Gln Lys Pro Thr Leu Asn Pro Gln Leu His Glu
260 265 270

Pro Arg Thr Gly Cys Gln Gly Ser Val Val Ser Phe Arg Pro Leu Lys
275 280 285

Met Pro Asn Thr Tyr Gln Asp Ser Ile Gly Lys Gly Ala Pro Ala Thr
290 295 300

Gln Lys Cys Pro Leu Leu Asp Ser Pro Leu Glu Val Glu Lys Gly Ala
305 310 315 320

Glu Thr Pro Ser Ala Thr Trp Leu Leu Tyr Ser His Pro Thr Ser Lys
325 330 335

Arg Lys Arg Ile Asn Leu Gly Ile Tyr Tyr Asn Arg Asn Pro Leu Glu
340 345 350

Val Asn Cys Trp Ser Arg Pro Trp Ile Leu Asn Arg Gly Pro Ser Gly
355 360 365

Tyr Ser Asp Leu Ala Val Val Glu Glu Gln Asp Leu Val Ala Cys Leu
370 375 380

Phe Glu Cys Gly Glu Lys Asn Glu Tyr Glu Arg Ile Asp Phe Cys Leu
385 390 395 400

Phe Ser Asp His Glu Val Leu Ser Cys Glu Asp Cys Thr Ser Pro Ser
405 410 415

Ser Asp

<210> 41
<211> 501
<212> PRT
<213> Mus musculus

<400> 41
Met Glu Thr Ala Gly Ala Pro Phe Cys Phe His Val Asp Ser Leu Val

```
1               5                   10                  15

Pro Cys Ser Tyr Trp Lys Val Met Gly Pro Thr Arg Val Pro Arg Arg
            20                  25                  30

Thr Val Leu Phe Gln Arg Glu Arg Thr Gly Leu Thr Tyr Arg Val Pro
        35                  40                  45

Ala Leu Leu Cys Val Pro Pro Arg Pro Thr Leu Leu Ala Phe Ala Glu
    50                  55                  60

Gln Arg Leu Ser Pro Asp Asp Ser His Ala His Arg Leu Val Leu Arg
65                  70                  75                  80

Arg Gly Thr Leu Thr Arg Gly Ser Val Arg Trp Gly Thr Leu Ser Val
                85                  90                  95

Leu Glu Thr Ala Val Leu Glu Glu His Arg Ser Met Asn Pro Cys Pro
            100                 105                 110

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

Leu Gly His Thr Pro Glu Ala Val Gln Ile Ala Thr Gly Lys Asn Ala
    130                 135                 140

Ala Arg Leu Cys Cys Val Thr Ser Cys Asp Ala Gly Leu Thr Trp Gly
145                 150                 155                 160

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

Trp Ala Thr Phe Ala Val Gly Pro Gly His Gly Val Gln Leu Arg Ser
            180                 185                 190

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

Cys Phe Gly Lys Ile Cys Trp Thr Ser Pro His Ser Leu Ala Phe Tyr
    210                 215                 220
```

```
Ser Asp Asp His Gly Ile Ser Trp His Cys Gly Gly Leu Val Pro Asn
225                 230                 235                 240

Leu Arg Ser Gly Glu Cys Gln Leu Ala Ala Val Asp Gly Asp Phe Leu
                245                 250                 255

Tyr Cys Asn Ala Arg Ser Pro Leu Gly Asn Arg Val Gln Ala Leu Ser
            260                 265                 270

Ala Asp Glu Gly Thr Ser Phe Leu Pro Gly Glu Leu Val Pro Thr Leu
        275                 280                 285

Ala Glu Thr Ala Arg Gly Cys Gln Gly Ser Ile Val Gly Phe Leu Ala
    290                 295                 300

Pro Pro Ser Ile Glu Pro Gln Asp Asp Arg Trp Thr Gly Ser Pro Arg
305                 310                 315                 320

Asn Thr Pro His Ser Pro Cys Phe Asn Leu Arg Val Gln Glu Ser Ser
                325                 330                 335

Gly Glu Gly Ala Arg Gly Leu Leu Glu Arg Trp Met Pro Arg Leu Pro
            340                 345                 350

Leu Cys Tyr Pro Gln Ser Arg Ser Pro Glu Asn His Gly Leu Glu Pro
        355                 360                 365

Gly Ser Asp Gly Asp Lys Thr Ser Trp Thr Pro Glu Cys Pro Met Ser
    370                 375                 380

Ser Asp Ser Met Leu Gln Ser Pro Thr Trp Leu Leu Tyr Ser His Pro
385                 390                 395                 400

Ala Gly Arg Arg Ala Arg Leu His Met Gly Ile Tyr Leu Ser Arg Ser
                405                 410                 415

Pro Leu Asp Pro His Ser Trp Thr Glu Pro Trp Val Ile Tyr Glu Gly
            420                 425                 430

Pro Ser Gly Tyr Ser Asp Leu Ala Phe Leu Gly Pro Met Pro Gly Ala
```

435 440 445

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

Glu Asp Ile Ser Phe Cys Leu Phe Ser Leu Ala Asp Val Leu Glu Asn
465 470 475 480

Val Pro Thr Gly Leu Glu Met Leu Ser Leu Arg Asp Lys Ala Gln Gly
485 490 495

His Cys Trp Pro Ser
500

<210> 42
<211> 3850
<212> DNA
<213> Mus musculus

<400> 42
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<210> 43
<211> 1722
<212> DNA
<213> Mus musculus

<400> 43

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Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
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Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
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Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
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Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
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Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
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Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
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Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
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Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
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Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
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Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160
```

```
Pro Gly His Xaa Leu Gln Leu His Asp Arg Xaa Arg Ser Leu Val Val
                165                 170                 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
                245                 250                 255

Xaa Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Xaa
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
    370                 375                 380
```

<210> 48
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 48

```
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1               5                  10                  15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20                  25                  30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
        35                  40                  45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
    50                  55                  60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

```
Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
    370                 375                 380
```

<210> 49
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 49
Asp Ala Ser Leu Pro Tyr Leu Gln Asp Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

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

```
Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Arg Phe Ile Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
    370                 375                 380
```

<210> 50
<211> 380

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 50

```
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1               5                  10                  15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20                  25                  30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
        35                  40                  45

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190
```

```
Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
    370                 375                 380
```

<210> 51
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 51
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

```
Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
    370                 375                 380
```

<210> 52
<211> 380
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 52

```
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1               5                  10                  15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20                  25                  30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
        35                  40                  45

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205
```

```
Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
    370                 375                 380
```

<210> 53
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 53
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Thr Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

```
Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
    370                 375                 380
```

<210> 54
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 54

```
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1               5                  10                  15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20                  25                  30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
        35                  40                  45

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220
```

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 55
<211> 379
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 55
Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly Ala
1 5 10 15

```
His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln Ser
            20                  25                  30

Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His Ala
        35                  40                  45

Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His Gln
    50                  55                  60

Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp Gly
65                  70                  75                  80

His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly Thr
                85                  90                  95

Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln Gln
            100                 105                 110

Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr Ser
        115                 120                 125

Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp Ala
    130                 135                 140

Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly Pro
145                 150                 155                 160

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

Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro Ser
            180                 185                 190

Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg Gly
        195                 200                 205

His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val Glu
    210                 215                 220
```

Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu Arg
225 230 235 240

Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln Glu
245 250 255

Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys Gln
260 265 270

Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser Pro
275 280 285

Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg Ala
290 295 300

Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala Trp
305 310 315 320

Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Cys Ala Tyr Ser Asp Leu
325 330 335

Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys Leu
340 345 350

Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr Leu
355 360 365

Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375

<210> 56
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 56
Met Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

```
Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20                  25                  30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
        35                  40                  45

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240
```

```
Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Cys Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
    370                 375                 380
```

<210> 57
<211> 379
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 57

```
Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly Ala
1               5                   10                  15

His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln Ser
            20                  25                  30
```

```
Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His Ala
        35                  40                  45

Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His Gln
    50                  55                  60

Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp Gly
65                  70                  75                  80

His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly Thr
                85                  90                  95

Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln Gln
            100                 105                 110

Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr Ser
        115                 120                 125

Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp Ala
    130                 135                 140

Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly Pro
145                 150                 155                 160

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

Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro Ser
            180                 185                 190

Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg Gly
        195                 200                 205

His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val Glu
    210                 215                 220

Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu Arg
225                 230                 235                 240
```

Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln Glu
245 250 255

Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys Gln
260 265 270

Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser Pro
275 280 285

Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg Ala
290 295 300

Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala Trp
305 310 315 320

Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp Leu
325 330 335

Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys Leu
340 345 350

Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr Leu
355 360 365

Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375

<210> 58
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 58
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

```
Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
        35                  40                  45

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255
```

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 59
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 59
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

```
Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
    50                  55                  60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255
```

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Cys Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 60
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 60
Ala Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

```
Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
    50                  55                  60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270
```

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 61
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 61
Met Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

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

```
Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270
```

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 62
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 62
Ala Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

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

```
Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285
```

```
Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Cys Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
    370                 375                 380
```

<210> 63
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 63

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Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1               5                   10                  15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20                  25                  30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
        35                  40                  45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
    50                  55                  60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80
```

```
Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285
```

```
Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
    370                 375                 380
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<210> 64
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr, Val, or not present

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Ala or Lys

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Asn or Leu

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Pro or His

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Phe, Trp, Tyr or Val

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Lys or Asp

<220>
<221> MOD_RES
<222> (42)..(42)
<223> Ala or Arg

<220>
<221> MOD_RES
<222> (44)..(44)
<223> Lys, Arg, or Glu

<220>
<221> MOD_RES
<222> (45)..(45)
<223> Lys, Ala, Arg, or Glu

<220>
<221> MOD_RES
<222> (54)..(54)
<223> Leu or Met

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>
<221> MOD_RES
<222> (69)..(69)
<223> Gln or His

<220>
<221> MOD_RES
<222> (78)..(78)
<223> Arg or Lys

<220>
<221> MOD_RES
<222> (80)..(80)
<223> Asp or Pro

<220>
<221> MOD_RES
<222> (93)..(93)

<223> Ala, Glu or Lys

<220>
<221> MOD_RES
<222> (107)..(107)
<223> Gly or Asp

<220>
<221> MOD_RES
<222> (108)..(108)
<223> Gln or His

<220>
<221> MOD_RES
<222> (112)..(112)
<223> Gln, Arg, or Lys

<220>
<221> MOD_RES
<222> (125)..(125)
<223> Ala, Cys, Ile, Ser, Val, or Leu

<220>
<221> MOD_RES
<222> (126)..(126)
<223> Gln, Leu, Glu, Phe, His, Ile, Leu, or Tyr

<220>
<221> MOD_RES
<222> (150)..(150)
<223> Ala or Val

<220>
<221> MOD_RES
<222> (164)..(164)
<223> Cys or Gly

<220>
<221> MOD_RES
<222> (170)..(170)
<223> Arg or Pro

<220>
<221> MOD_RES
<222> (171)..(171)
<223> Ala or Gly

<220>
<221> MOD_RES
<222> (187)..(187)
<223> Arg, Ile, or Lys

<220>
<221> MOD_RES

<222> (188)..(188)
<223> Gln or Pro

<220>
<221> MOD_RES
<222> (189)..(189)
<223> Arg or Pro

<220>
<221> MOD_RES
<222> (196)..(196)
<223> Ala, Cys, Leu, or Val

<220>
<221> MOD_RES
<222> (213)..(213)
<223> Ala, Cys, Asn, Ser, or Thr

<220>
<221> MOD_RES
<222> (217)..(217)
<223> Leu, Ala, or Val

<220>
<221> MOD_RES
<222> (225)..(225)
<223> Glu or Pro

<220>
<221> MOD_RES
<222> (239)..(239)
<223> His or Pro

<220>
<221> MOD_RES
<222> (240)..(240)
<223> Leu, Asp, Asn, or Tyr

<220>
<221> MOD_RES
<222> (241)..(241)
<223> Arg, Ala, Asp, Leu, Gln, or Tyr

<220>
<221> MOD_RES
<222> (242)..(242)
<223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser,
Val, Trp, or Tyr

<220>
<221> MOD_RES
<222> (244)..(244)
<223> Val, Ile, or Lys

<220>
<221> MOD_RES
<222> (249)..(249)
<223> Thr or Ala

<220>
<221> MOD_RES
<222> (251)..(251)
<223> Asp or Gly

<220>
<221> MOD_RES
<222> (257)..(257)
<223> Glu, Lys, or Pro

<220>
<221> MOD_RES
<222> (258)..(258)
<223> Ser or Cys

<220>
<221> MOD_RES
<222> (260)..(260)
<223> Leu, Asp, Phe, Gln, or Thr

<220>
<221> MOD_RES
<222> (265)..(265)
<223> Val or Phe

<220>
<221> MOD_RES
<222> (270)..(270)
<223> Gln, Ala, His, Phe, Pro, Ser, or Thr

<220>
<221> MOD_RES
<222> (272)..(272)
<223> Cys or Val

<220>
<221> MOD_RES
<222> (292)..(292)
<223> Trp or Arg

<220>
<221> MOD_RES
<222> (301)..(301)
<223> Ser, Arg, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
Pro, Gln, Thr, Val, Trp, or Tyr

<220>
<221> MOD_RES
<222> (302)..(302)

<223> Trp, Lys, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, or Tyr

<220>
<221> MOD_RES
<222> (325)..(325)
<223> Lys or Val

<220>
<221> MOD_RES
<222> (332)..(332)
<223> Ala, Cys, Ser, or Val

<220>
<221> MOD_RES
<222> (352)..(352)
<223> Cys, Leu, or Val

<220>
<221> MOD_RES
<222> (363)..(363)
<223> Val or Arg

<220>
<221> MOD_RES
<222> (365)..(365)
<223> Leu, Gln, His, Ile, Lys, or Ser

<220>
<223> See specification as filed for detailed description of substitutions and preferred embodiments

<400> 64
Xaa Xaa Ser Xaa Xaa Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Xaa Ser Xaa Xaa Asp Glu His
35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Xaa
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly

```
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Xaa Xaa Pro Ile Pro
            180                 185                 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Xaa Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Xaa Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser Xaa Xaa
225                 230                 235                 240

Xaa Xaa Arg Xaa Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
                245                 250                 255

Xaa Xaa Gln Xaa Val Lys Lys Leu Xaa Glu Pro Pro Pro Xaa Gly Xaa
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
    290                 295                 300
```

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 65
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr, Val, or not present

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Phe, Trp, Tyr or Val

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Lys or Asp

<220>
<221> MOD_RES
<222> (42)..(42)
<223> Arg or Ala

<220>
<221> MOD_RES

<222> (62)..(62)
<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>
<221> MOD_RES
<222> (93)..(93)
<223> Ala, Glu, or Lys

<220>
<221> MOD_RES
<222> (126)..(126)
<223> Gln, Leu, Glu, Phe, His, Ile, Leu, or Tyr

<220>
<221> MOD_RES
<222> (187)..(187)
<223> Arg, Ile, or Lys

<220>
<221> MOD_RES
<222> (242)..(242)
<223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser, Val, Trp, or Tyr

<220>
<221> MOD_RES
<222> (270)..(270)
<223> Gln, Ala, His, Phe, Pro, Ser, or Thr

<220>
<221> MOD_RES
<222> (301)..(301)
<223> Ser, Arg, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Thr, Val, Trp, or Tyr

<220>
<221> MOD_RES
<222> (302)..(302)
<223> Trp, Lys, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, or Tyr

<220>
<221> MOD_RES
<222> (332)..(332)
<223> Ala, Cys, Ser, or Val

<220>
<221> MOD_RES
<222> (363)..(363)
<223> Val or Arg

<220>
<221> MOD_RES
<222> (365)..(365)

<223> Leu, Gln, His, Ile, Lys, or Ser

<220>
<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 65
Xaa Ala Ser Leu Pro Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Xaa Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Xaa Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
180 185 190

```
Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Xaa Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
    370                 375                 380


<210> 66
<211> 617
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr,
Val, or not present

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Ala or Lys

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Asn or Leu

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Pro or His

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Phe, Trp, Tyr or Val

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Lys or Asp

<220>
<221> MOD_RES
<222> (42)..(42)
<223> Ala or Arg

<220>
<221> MOD_RES
<222> (44)..(44)
<223> Lys, Arg, or Glu

<220>
<221> MOD_RES
<222> (45)..(45)
<223> Lys, Ala, Arg, or Glu

<220>
<221> MOD_RES
<222> (54)..(54)

<223> Leu or Met

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>
<221> MOD_RES
<222> (69)..(69)
<223> Gln or His

<220>
<221> MOD_RES
<222> (78)..(78)
<223> Arg or Lys

<220>
<221> MOD_RES
<222> (80)..(80)
<223> Asp or Pro

<220>
<221> MOD_RES
<222> (93)..(93)
<223> Ala, Glu or Lys

<220>
<221> MOD_RES
<222> (107)..(107)
<223> Gly or Asp

<220>
<221> MOD_RES
<222> (108)..(108)
<223> Gln or His

<220>
<221> MOD_RES
<222> (112)..(112)
<223> Gln, Arg, or Lys

<220>
<221> MOD_RES
<222> (125)..(125)
<223> Ala, Cys, Ile, Ser, Val, or Leu

<220>
<221> MOD_RES
<222> (126)..(126)
<223> Gln, Leu, Glu, Phe, His, Ile, Leu, or Tyr

<220>
<221> MOD_RES

<222> (150)..(150)
<223> Ala or Val

<220>
<221> MOD_RES
<222> (164)..(164)
<223> Cys or Gly

<220>
<221> MOD_RES
<222> (170)..(170)
<223> Arg or Pro

<220>
<221> MOD_RES
<222> (171)..(171)
<223> Ala or Gly

<220>
<221> MOD_RES
<222> (187)..(187)
<223> Arg, Ile, or Lys

<220>
<221> MOD_RES
<222> (188)..(188)
<223> Gln or Pro

<220>
<221> MOD_RES
<222> (189)..(189)
<223> Arg or Pro

<220>
<221> MOD_RES
<222> (196)..(196)
<223> Ala, Cys, Leu, or Val

<220>
<221> MOD_RES
<222> (213)..(213)
<223> Ala, Cys, Asn, Ser, or Thr

<220>
<221> MOD_RES
<222> (217)..(217)
<223> Leu, Ala, or Val

<220>
<221> MOD_RES
<222> (225)..(225)
<223> Glu or Pro

<220>

<221> MOD_RES
<222> (239)..(239)
<223> His or Pro

<220>
<221> MOD_RES
<222> (240)..(240)
<223> Leu, Asp, Asn, or Tyr

<220>
<221> MOD_RES
<222> (241)..(241)
<223> Arg, Ala, Asp, Leu, Gln, or Tyr

<220>
<221> MOD_RES
<222> (242)..(242)
<223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser,
Val, Trp, or Tyr

<220>
<221> MOD_RES
<222> (244)..(244)
<223> Val, Ile, or Lys

<220>
<221> MOD_RES
<222> (249)..(249)
<223> Thr or Ala

<220>
<221> MOD_RES
<222> (251)..(251)
<223> Asp or Gly

<220>
<221> MOD_RES
<222> (257)..(257)
<223> Glu, Lys, or Pro

<220>
<221> MOD_RES
<222> (258)..(258)
<223> Ser or Cys

<220>
<221> MOD_RES
<222> (260)..(260)
<223> Leu, Asp, Phe, Gln, or Thr

<220>
<221> MOD_RES
<222> (265)..(265)
<223> Val or Phe

<220>
<221> MOD_RES
<222> (270)..(270)
<223> Gln, Ala, His, Phe, Pro, Ser, or Thr

<220>
<221> MOD_RES
<222> (272)..(272)
<223> Cys or Val

<220>
<221> MOD_RES
<222> (292)..(292)
<223> Trp or Arg

<220>
<221> MOD_RES
<222> (301)..(301)
<223> Ser, Arg, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
Pro, Gln, Thr, Val, Trp, or Tyr

<220>
<221> MOD_RES
<222> (302)..(302)
<223> Trp, Lys, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
Pro, Gln, Arg, Ser, Thr, Val, or Tyr

<220>
<221> MOD_RES
<222> (325)..(325)
<223> Lys or Val

<220>
<221> MOD_RES
<222> (332)..(332)
<223> Ala, Cys, Ser, or Val

<220>
<221> MOD_RES
<222> (352)..(352)
<223> Cys, Leu, or Val

<220>
<221> MOD_RES
<222> (363)..(363)
<223> Val or Arg

<220>
<221> MOD_RES
<222> (365)..(365)
<223> Leu, Gln, His, Ile, Lys, or Ser

<220>

<221> MOD_RES
<222> (381)..(390)
<223> This region may encompass one of the following sequences:
"GGGGS" or "GGGGSGGGGS" or "EPKSS"

<220>
<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 66
Xaa Xaa Ser Xaa Xaa Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Xaa Ser Xaa Xaa Asp Glu His
35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Xaa
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

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

```
Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Xaa Xaa Pro Ile Pro
            180                 185                 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Xaa Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Xaa Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser Xaa Xaa
225                 230                 235                 240

Xaa Xaa Arg Xaa Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
                245                 250                 255

Xaa Xaa Gln Xaa Val Lys Lys Leu Xaa Glu Pro Pro Pro Xaa Gly Xaa
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Xaa Xaa Xaa
    370                 375                 380

Xaa Xaa Xaa Xaa Xaa Xaa Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385                 390                 395                 400
```

```
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                405                 410                 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            420                 425                 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        435                 440                 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    450                 455                 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465                 470                 475                 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                485                 490                 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            500                 505                 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        515                 520                 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    530                 535                 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545                 550                 555                 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                565                 570                 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            580                 585                 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        595                 600                 605
```

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 67
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 67
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
    370                 375                 380
```

```
Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385                 390                 395                 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                405                 410                 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            420                 425                 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        435                 440                 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    450                 455                 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465                 470                 475                 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                485                 490                 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            500                 505                 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        515                 520                 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    530                 535                 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545                 550                 555                 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                565                 570                 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            580                 585                 590
```

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 68
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 68
Asp Ala Ser Leu Pro Tyr Leu Gln Asp Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

```
Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Arg Phe Ile Met Phe Thr
        355                 360                 365
```

```
Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
    370                 375                 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385                 390                 395                 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                405                 410                 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            420                 425                 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        435                 440                 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    450                 455                 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465                 470                 475                 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                485                 490                 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            500                 505                 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        515                 520                 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    530                 535                 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545                 550                 555                 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                565                 570                 575
```

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 69
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 69
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

```
Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350
```

```
Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
    370                 375                 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385                 390                 395                 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                405                 410                 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            420                 425                 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        435                 440                 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    450                 455                 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465                 470                 475                 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                485                 490                 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            500                 505                 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        515                 520                 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    530                 535                 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545                 550                 555                 560
```

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 70
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 70
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

```
Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335
```

```
Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
    370                 375                 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385                 390                 395                 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                405                 410                 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            420                 425                 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        435                 440                 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    450                 455                 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465                 470                 475                 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                485                 490                 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            500                 505                 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        515                 520                 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    530                 535                 540
```

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 71
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 71
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

```
Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320
```

```
Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
    370                 375                 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385                 390                 395                 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                405                 410                 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            420                 425                 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        435                 440                 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    450                 455                 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465                 470                 475                 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                485                 490                 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            500                 505                 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        515                 520                 525
```

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 72
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 72
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Thr Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

```
Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
    290                 295                 300
```

```
Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
    370                 375                 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385                 390                 395                 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                405                 410                 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            420                 425                 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        435                 440                 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    450                 455                 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465                 470                 475                 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                485                 490                 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            500                 505                 510
```

```
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        515                 520                 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    530                 535                 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545                 550                 555                 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                565                 570                 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            580                 585                 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        595                 600                 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    610                 615
```

<210> 73
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 73

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Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1               5                   10                  15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20                  25                  30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
        35                  40                  45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Asn Thr His
    50                  55                  60
```

```
Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285
```

```
Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
    370                 375                 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385                 390                 395                 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                405                 410                 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            420                 425                 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        435                 440                 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    450                 455                 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465                 470                 475                 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                485                 490                 495
```

```
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            500                 505                 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        515                 520                 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    530                 535                 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545                 550                 555                 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                565                 570                 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            580                 585                 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        595                 600                 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    610                 615
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<210> 74
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Any amino acid

<220>
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<222> (9)..(9)
<223> Any amino acid

<220>
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<222> (62)..(62)
<223> Any amino acid

<220>
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<222> (93)..(93)
<223> Any amino acid

<220>
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<222> (187)..(187)
<223> Any amino acid

<220>
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<222> (270)..(270)
<223> Any amino acid

<220>
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<222> (301)..(302)
<223> Any amino acid

<220>
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<222> (332)..(332)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (363)..(363)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (365)..(365)
<223> Any amino acid

<400> 74
Xaa Ala Ser Leu Pro Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

```
Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
    50                  55                  60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255
```

```
Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
    370                 375                 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385                 390                 395                 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                405                 410                 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            420                 425                 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        435                 440                 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    450                 455                 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465                 470                 475                 480
```

```
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                485                 490                 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            500                 505                 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        515                 520                 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    530                 535                 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545                 550                 555                 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                565                 570                 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            580                 585                 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        595                 600                 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    610                 615
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<210> 75
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> MOD_RES
<222> (1)..(2)
<223> Any amino acid

<220>

<221> MOD_RES
<222> (4)..(6)
<223> Any amino acid

<220>
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<222> (9)..(9)
<223> Any amino acid

<220>
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<222> (44)..(45)
<223> Any amino acid

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<222> (54)..(54)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (69)..(69)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (78)..(78)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (93)..(93)
<223> Any amino acid

<220>
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<222> (107)..(108)
<223> Any amino acid

<220>
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<222> (112)..(112)
<223> Any amino acid

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<222> (125)..(126)
<223> Any amino acid

<220>
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<222> (150)..(150)
<223> Any amino acid

<220>
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<222> (164)..(164)
<223> Any amino acid

<220>
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<222> (171)..(171)
<223> Any amino acid

<220>
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<222> (187)..(187)
<223> Any amino acid

<220>
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<222> (196)..(196)
<223> Any amino acid

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<222> (217)..(217)
<223> Any amino acid

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<223> Any amino acid

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<222> (251)..(251)
<223> Any amino acid

<220>
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<222> (257)..(257)
<223> Any amino acid

<220>
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<222> (270)..(270)
<223> Any amino acid

<220>
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<222> (272)..(272)
<223> Any amino acid

<220>
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<222> (292)..(292)
<223> Any amino acid

<220>
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<222> (301)..(302)
<223> Any amino acid

<220>
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<222> (325)..(325)
<223> Any amino acid

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<222> (332)..(332)
<223> Any amino acid

<220>
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<222> (352)..(352)
<223> Any amino acid

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<222> (363)..(363)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (365)..(365)
<223> Any amino acid

<400> 75
Xaa Xaa Ser Xaa Xaa Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Xaa Xaa Asp Glu His
        35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
    50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Asp

65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
245 250 255

Xaa Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Xaa
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

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Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
    370                 375                 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385                 390                 395                 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                405                 410                 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            420                 425                 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        435                 440                 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    450                 455                 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465                 470                 475                 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                485                 490                 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
```

```
            500                 505                 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        515                 520                 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    530                 535                 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545                 550                 555                 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                565                 570                 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            580                 585                 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        595                 600                 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    610                 615
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<210> 76
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr, Val, or not present

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Phe, Trp, Tyr or Val

<220>
<221> MOD_RES

<222> (9)..(9)
<223> Lys or Asp

<220>
<221> MOD_RES
<222> (42)..(42)
<223> Arg or Ala

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>
<221> MOD_RES
<222> (93)..(93)
<223> Ala, Glu, or Lys

<220>
<221> MOD_RES
<222> (126)..(126)
<223> Gln, Leu, Glu, Phe, His, Ile, Leu, or Tyr

<220>
<221> MOD_RES
<222> (187)..(187)
<223> Arg, Ile, or Lys

<220>
<221> MOD_RES
<222> (242)..(242)
<223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser,
Val, Trp, or Tyr

<220>
<221> MOD_RES
<222> (270)..(270)
<223> Gln, Ala, His, Phe, Pro, Ser, or Thr

<220>
<221> MOD_RES
<222> (301)..(301)
<223> Ser, Arg, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
Pro, Gln, Thr, Val, Trp, or Tyr

<220>
<221> MOD_RES
<222> (302)..(302)
<223> Trp, Lys, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
Pro, Gln, Arg, Ser, Thr, Val, or Tyr

<220>
<221> MOD_RES
<222> (332)..(332)

<223> Ala, Cys, Ser, or Val

<220>
<221> MOD_RES
<222> (363)..(363)
<223> Val or Arg

<220>
<221> MOD_RES
<222> (365)..(365)
<223> Leu, Gln, His, Ile, Lys, or Ser

<220>
<221> MOD_RES
<222> (381)..(390)
<223> This region may encompass one of the following sequences: "GGGGS" or "GGGGSGGGGS" or "EPKSS"

<220>
<223> See specification as filed for detailed description of substitutions and preferred embodiments

<400> 76
Xaa Ala Ser Leu Pro Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Xaa Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Xaa Val Thr
115 120 125

```
Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Xaa Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
```

```
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Xaa Xaa Xaa
    370                 375                 380

Xaa Xaa Xaa Xaa Xaa Xaa Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385                 390                 395                 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                405                 410                 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            420                 425                 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        435                 440                 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    450                 455                 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465                 470                 475                 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                485                 490                 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            500                 505                 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        515                 520                 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    530                 535                 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545                 550                 555                 560
```

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 77
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 77
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Gly Val Ser Thr Ser
20 25 30

Gly Tyr Ser Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45

Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Ser Arg
85 90 95

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 78
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 78
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

```
Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
```

```
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
    370                 375                 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385                 390                 395                 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                405                 410                 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            420                 425                 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        435                 440                 445

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465                 470                 475                 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                485                 490                 495
```

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 79
<211> 1836
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 79
gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgtcaagt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agagccagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccacag ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960

tggagcgaac ctgttctgct ggccaagggc agcgctgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa 1140

ggcggaggcg gatccgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 1200

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 1260

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 1320

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1380

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1500

atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg 1560

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1620

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680

cccgtgctgg actccgacgg ctccttcttc ctcactagca agctcaccgt ggacaagagc 1740

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1800

tacacgcaga agagcctctc cctgtctccg ggtaaa 1836

<210> 80
<211> 1140

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 80
gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgtcaagt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agagccagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccacag ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960

tggagcgaac ctgttctgct ggccaagggc agcgctgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

gagatcgtgt tcctgatgtt caccctgaag caggcctttc agccgagta cctgcctcaa 1140

<210> 81
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 81

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Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1               5                  10                  15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20                  25                  30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
        35                  40                  45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
    50                  55                  60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205
```

```
Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
    370                 375                 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385                 390                 395                 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                405                 410                 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
```

```
            420                 425                 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        435                 440                 445

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465                 470                 475                 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                485                 490                 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500                 505                 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        515                 520                 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    530                 535                 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545                 550                 555                 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
                565                 570                 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            580                 585                 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        595                 600                 605

Ser Pro Gly Lys
    610
```

<210> 82
<211> 612
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 82
Asp Ala Ser Leu Pro Tyr Leu Gln Asp Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

```
Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Arg Phe Ile Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
    370                 375                 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385                 390                 395                 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
```

```
                405                 410                 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            420                 425                 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        435                 440                 445

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465                 470                 475                 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                485                 490                 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500                 505                 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        515                 520                 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    530                 535                 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545                 550                 555                 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
                565                 570                 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            580                 585                 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        595                 600                 605

Ser Pro Gly Lys
    610
```

<210> 83
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 83
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

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

```
Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
    370                 375                 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
```

385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
435 440 445

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 84
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 84
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
```

```
    370                 375                 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385                 390                 395                 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                405                 410                 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            420                 425                 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        435                 440                 445

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465                 470                 475                 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                485                 490                 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500                 505                 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        515                 520                 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    530                 535                 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545                 550                 555                 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
                565                 570                 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            580                 585                 590
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Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 85
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 85
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

```
Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
```

```
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
    370                 375                 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385                 390                 395                 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                405                 410                 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            420                 425                 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        435                 440                 445

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465                 470                 475                 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                485                 490                 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500                 505                 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        515                 520                 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    530                 535                 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545                 550                 555                 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
                565                 570                 575
```

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 86
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 86
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Thr Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

```
Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
```

```
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
    370                 375                 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385                 390                 395                 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                405                 410                 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            420                 425                 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        435                 440                 445

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465                 470                 475                 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                485                 490                 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500                 505                 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        515                 520                 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    530                 535                 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545                 550                 555                 560
```

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 87
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 87
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

```
Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
```

```
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
    370                 375                 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385                 390                 395                 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                405                 410                 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            420                 425                 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        435                 440                 445

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465                 470                 475                 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                485                 490                 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500                 505                 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        515                 520                 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    530                 535                 540
```

```
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545                 550                 555                 560


Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
                565                 570                 575


Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            580                 585                 590


Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        595                 600                 605


Ser Pro Gly Lys
    610


<210> 88
<211> 608
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (9)..(9)
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<220>
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<223> Any amino acid

<220>
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<223> Any amino acid

<220>
<221> MOD_RES
<222> (187)..(187)
<223> Any amino acid

<220>
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<222> (270)..(270)
<223> Any amino acid

<220>
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<222> (301)..(302)
<223> Any amino acid

<220>
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<223> Any amino acid

<220>
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<223> Any amino acid

<220>
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<222> (365)..(365)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (381)..(381)
<223> Any amino acid

<400> 88
Xaa Ala Ser Leu Pro Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

```
Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285
```

```
Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Asp Lys Thr
    370                 375                 380

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
385                 390                 395                 400

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                405                 410                 415

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            420                 425                 430

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        435                 440                 445

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    450                 455                 460

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
465                 470                 475                 480

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                485                 490                 495
```

```
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            500                 505                 510

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        515                 520                 525

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

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
545                 550                 555                 560

Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr Val Asp Lys Ser
                565                 570                 575

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            580                 585                 590

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        595                 600                 605
```

<210> 89
<211> 608
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<221> MOD_RES
<222> (1)..(2)
<223> Any amino acid

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<222> (4)..(6)
<223> Any amino acid

<220>
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<222> (9)..(9)
<223> Any amino acid

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<221> MOD_RES
<222> (44)..(45)
<223> Any amino acid

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<223> Any amino acid

<220>
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<222> (62)..(62)
<223> Any amino acid

<220>
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<222> (69)..(69)
<223> Any amino acid

<220>
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<222> (78)..(78)
<223> Any amino acid

<220>
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<222> (93)..(93)
<223> Any amino acid

<220>
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<222> (107)..(108)
<223> Any amino acid

<220>
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<222> (112)..(112)
<223> Any amino acid

<220>
<221> MOD_RES
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<223> Any amino acid

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<222> (150)..(150)
<223> Any amino acid

<220>
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<222> (164)..(164)
<223> Any amino acid

<220>
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<222> (171)..(171)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (187)..(187)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (196)..(196)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (217)..(217)
<223> Any amino acid

<220>
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<223> Any amino acid

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<223> Any amino acid

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<223> Any amino acid

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<223> Any amino acid

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<222> (332)..(332)
<223> Any amino acid

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<222> (352)..(352)
<223> Any amino acid

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<222> (363)..(363)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (365)..(365)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (381)..(381)
<223> Any amino acid

<400> 89
Xaa Xaa Ser Xaa Xaa Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Xaa Xaa Asp Glu His
        35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
    50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
                85 90 95

```
Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
                245                 250                 255

Xaa Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Xaa
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
    290                 295                 300
```

```
Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Asp Lys Thr
    370                 375                 380

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
385                 390                 395                 400

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                405                 410                 415

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            420                 425                 430

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        435                 440                 445

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    450                 455                 460

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
465                 470                 475                 480

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                485                 490                 495

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            500                 505                 510

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        515                 520                 525
```

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

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
545 550 555 560

Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr Val Asp Lys Ser
565 570 575

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
580 585 590

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
595 600 605

<210> 90
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 90
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 91
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 91
Glu Pro Lys Ser Ser
1 5

<210> 92
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 92
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 93
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 93
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

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

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125

```
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    130                 135                 140

Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225
```

<210> 94
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 94

```
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1               5                   10                  15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20                  25                  30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
        35                  40                  45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
    50                  55                  60
```

```
Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285
```

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ala Arg Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 95
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 95
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

```
Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285
```

```
Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ala Arg Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
    370                 375                 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385                 390                 395                 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                405                 410                 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            420                 425                 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        435                 440                 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    450                 455                 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465                 470                 475                 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                485                 490                 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            500                 505                 510
```

```
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        515                 520                 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    530                 535                 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545                 550                 555                 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                565                 570                 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            580                 585                 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        595                 600                 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    610                 615


<210> 96
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 96
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1               5                   10                  15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20                  25                  30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
        35                  40                  45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
    50                  55                  60
```

```
Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270
```

```
Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ala Arg Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
    370                 375                 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385                 390                 395                 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                405                 410                 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            420                 425                 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        435                 440                 445

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465                 470                 475                 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                485                 490                 495
```

```
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500                 505                 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        515                 520                 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    530                 535                 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545                 550                 555                 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
                565                 570                 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            580                 585                 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        595                 600                 605

Ser Pro Gly Lys
    610
```

<210> 97
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 97

```
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1               5                   10                  15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20                  25                  30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
        35                  40                  45
```

```
Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
    50                  55                  60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255
```

```
Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
    370                 375                 380


<210> 98
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 98
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1               5                   10                  15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20                  25                  30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
        35                  40                  45
```

```
Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
    50                  55                  60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
            260                 265                 270
```

```
Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
    370                 375                 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385                 390                 395                 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                405                 410                 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            420                 425                 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        435                 440                 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    450                 455                 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465                 470                 475                 480
```

```
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                485                 490                 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            500                 505                 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        515                 520                 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    530                 535                 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545                 550                 555                 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                565                 570                 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            580                 585                 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        595                 600                 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    610                 615
```

<210> 99
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 99

```
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1               5                   10                  15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20                  25                  30
```

```
Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
        35                  40                  45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
    50                  55                  60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255
```

```
Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
    370                 375                 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385                 390                 395                 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                405                 410                 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            420                 425                 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        435                 440                 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    450                 455                 460
```

```
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465                 470                 475                 480


Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                485                 490                 495


Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500                 505                 510


Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        515                 520                 525


Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    530                 535                 540


Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545                 550                 555                 560


Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
                565                 570                 575


Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            580                 585                 590


Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        595                 600                 605


Ser Pro Gly Lys
    610


<210> 100
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 100
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1               5                   10                  15
```

```
Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20                  25                  30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
        35                  40                  45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
    50                  55                  60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240
```

```
Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
    370                 375                 380


<210> 101
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 101
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1               5                   10                  15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20                  25                  30
```

```
Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
        35                  40                  45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
    50                  55                  60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240
```

```
Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
    370                 375                 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385                 390                 395                 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                405                 410                 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            420                 425                 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        435                 440                 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    450                 455                 460
```

```
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465                 470                 475                 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                485                 490                 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            500                 505                 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        515                 520                 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    530                 535                 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545                 550                 555                 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                565                 570                 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            580                 585                 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        595                 600                 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    610                 615


<210> 102
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 102
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1               5                   10                  15
```

```
Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20                  25                  30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
        35                  40                  45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
    50                  55                  60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220
```

```
Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
    370                 375                 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385                 390                 395                 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                405                 410                 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            420                 425                 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        435                 440                 445
```

```
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    450                 455                 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465                 470                 475                 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                485                 490                 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500                 505                 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        515                 520                 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    530                 535                 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545                 550                 555                 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
                565                 570                 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            580                 585                 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        595                 600                 605

Ser Pro Gly Lys
    610
```

<210> 103
<211> 1836
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 103
gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgtcaagt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agagccagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccacag ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960

tggagcgaac ctgttctgct ggccaagggc agcgctgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa 1140

ggcggaggcg gatccgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 1200

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 1260

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 1320

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1380

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1500

atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg 1560

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1620

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680

cccgtgctgg actccgacgg ctccttcttc ctcactagca agctcaccgt ggacaagagc 1740

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1800

tacacgcaga agagcctctc cctgtctccg ggtaaa 1836

<210> 104
<211> 654
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 104
gagatcgtgc tgacacagag ccctgccaca ctgtcactgt ctccaggcga gagagccaca 60

ctgagctgta gagcttctaa gggcgtgtcc accagcggct actcttacct gcactggtat 120

cagcagaagc ccggccaggc tcctagactg ctgatctacc tggccagcta cctggaaagc 180

ggagtgcctg ctagattcag cggctctggc tctggcaccg acttcaccct gacaatcagc 240

agcctggaac ctgaggactt cgccgtgtac tactgccagc acagcagaga tctgcccctg 300

acatttggcg gaggcaccaa ggtggaaatc aagcgtacgg tggctgcacc atctgtcttc 360

atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420

aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 480

ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540

agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600

acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgt 654

<210> 105
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 105

```
Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
            20                  25                  30

Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn Glu Lys Phe
    50                  55                  60

Lys Asn Arg Val Thr Leu Thr Thr Asp Ser Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Lys Ser Leu Gln Phe Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
```

```
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
```

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

Gly Lys
450

<210> 106
<211> 632
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 106
Thr Val Glu Lys Ser Val Val Phe Lys Ala Glu Gly Glu His Phe Thr
1 5 10 15

Asp Gln Lys Gly Asn Thr Ile Val Gly Ser Gly Ser Gly Gly Thr Thr
20 25 30

Lys Tyr Phe Arg Ile Pro Ala Met Cys Thr Thr Ser Lys Gly Thr Ile
35 40 45

Val Val Phe Ala Asp Ala Arg His Asn Thr Ala Ser Asp Gln Ser Phe
50 55 60

Ile Asp Thr Ala Ala Ala Arg Ser Thr Asp Gly Gly Lys Thr Trp Asn
65 70 75 80

Lys Lys Ile Ala Ile Tyr Asn Asp Arg Val Asn Ser Lys Leu Ser Arg
85 90 95

Val Met Asp Pro Thr Cys Ile Val Ala Asn Ile Gln Gly Arg Glu Thr
100 105 110

Ile Leu Val Met Val Gly Lys Trp Asn Asn Asn Asp Lys Thr Trp Gly
115 120 125

Ala Tyr Arg Asp Lys Ala Pro Asp Thr Asp Trp Asp Leu Val Leu Tyr
130 135 140

```
Lys Ser Thr Asp Asp Gly Val Thr Phe Ser Lys Val Glu Thr Asn Ile
145                 150                 155                 160

His Asp Ile Val Thr Lys Asn Gly Thr Ile Ser Ala Met Leu Gly Gly
                165                 170                 175

Val Gly Ser Gly Leu Gln Leu Asn Asp Gly Lys Leu Val Phe Pro Val
            180                 185                 190

Gln Met Val Arg Thr Lys Asn Ile Thr Thr Val Leu Asn Thr Ser Phe
        195                 200                 205

Ile Tyr Ser Thr Asp Gly Ile Thr Trp Ser Leu Pro Ser Gly Tyr Cys
    210                 215                 220

Glu Gly Phe Gly Ser Glu Asn Asn Ile Ile Glu Phe Asn Ala Ser Leu
225                 230                 235                 240

Val Asn Asn Ile Arg Asn Ser Gly Leu Arg Arg Ser Phe Glu Thr Lys
                245                 250                 255

Asp Phe Gly Lys Thr Trp Thr Glu Phe Pro Pro Met Asp Lys Lys Val
            260                 265                 270

Asp Asn Arg Asn His Gly Val Gln Gly Ser Thr Ile Thr Ile Pro Ser
        275                 280                 285

Gly Asn Lys Leu Val Ala Ala His Ser Ser Ala Gln Asn Lys Asn Asn
    290                 295                 300

Asp Tyr Thr Arg Ser Asp Ile Ser Leu Tyr Ala His Asn Leu Tyr Ser
305                 310                 315                 320

Gly Glu Val Lys Leu Ile Asp Asp Phe Tyr Pro Lys Val Gly Asn Ala
                325                 330                 335

Ser Gly Ala Gly Tyr Ser Cys Leu Ser Tyr Arg Lys Asn Val Asp Lys
            340                 345                 350

Glu Thr Leu Tyr Val Val Tyr Glu Ala Asn Gly Ser Ile Glu Phe Gln
        355                 360                 365
```

```
Asp Leu Ser Arg His Leu Pro Val Ile Lys Ser Tyr Asn Gly Gly Gly
    370                 375                 380

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
385                 390                 395                 400

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
                405                 410                 415

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
            420                 425                 430

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
        435                 440                 445

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
    450                 455                 460

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
465                 470                 475                 480

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
                485                 490                 495

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
            500                 505                 510

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
        515                 520                 525

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
    530                 535                 540

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
545                 550                 555                 560

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
                565                 570                 575
```

Leu Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
580 585 590

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
595 600 605

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly Gly Gly Ser
610 615 620

His His His His His His His His
625 630

<210> 107
<211> 1896
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 107
acagtggaaa agtccgtggt gttcaaggcc gagggcgagc acttcaccga ccagaaaggc 60

aataccatcg tcggctctgg cagcggcggc accaccaagt actttagaat ccccgccatg 120

tgcaccacca gcaagggcac cattgtggtg ttcgccgacg ccagacacaa caccgccagc 180

gatcagagct tcatcgatac cgctgccgcc agaagtacag acggcggcaa gacctggaac 240

aagaagatcg ccatctacaa cgaccgcgtg aacagcaagc tgagcagagt gatggaccct 300

acctgcatcg tggccaacat ccagggcaga gaaaccatcc tggtcatggt cggaaagtgg 360

aacaacaacg ataagacctg gggcgcctac agagacaagg cccctgatac cgattgggac 420

ctcgtgctgt ataagagcac cgacgacggc gtgaccttca gcaaggtgga aacaaacatc 480

cacgacatcg tgaccaagaa cggcaccatc tctgccatgc tcggcggcgt tggatctggc 540

ctgcaactga atgatggcaa gctggtgttc cccgtgcaga tggtccgaac aaagaacatc 600

accaccgtgc tgaataccag cttcatctac tccaccgacg gcatcacatg gtccctgcct 660

agcggctact gtgaaggctt tggcagcgag aacaacatca tcgagttcaa cgccagcctg 720

gtcaacaaca tccggaacag cggcctgcgg agaagcttcg agacaaagga cttcggaaag 780

acgtggaccg agtttcctcc aatggacaag aaggtggaca accggaacca cggcgtgcag 840

ggcagcacaa tcacaatccc tagcggcaac aaactggtgg ccgctcactc tagcgcccag 900

aacaagaaca acgattacac cagaagcgac atcagcctgt acgcccacaa cctgtactcc 960

ggcgaagtga agctgatcga cgacttctac cccaaagtgg gcaatgccag cggagccggc 1020

tacagctgtc tgagctaccg gaaaaatgtg gacaaagaaa ccctgtacgt ggtgtacgag 1080

gccaacggca gcatcgagtt tcaggacctg agcagacatc tgcccgtgat caagagctac 1140

aatggcggag gtggaagtgg cggaggcgga tccgacaaaa ctcacacatg cccaccgtgc 1200

ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccccaaa acccaaggac 1260

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 1320

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 1380

aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 1440

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 1500

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtctac 1560

accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 1620

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1680

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct cactagcaag 1740

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1800

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaaagcggc 1860

ggaggcggat ctcatcatca ccatcatcac catcac 1896

<210> 108
<211> 632
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 108
Thr Val Glu Lys Ser Val Val Phe Lys Ala Glu Gly Glu His Phe Thr
1 5 10 15

Asp Gln Lys Gly Asn Thr Ile Val Gly Ser Gly Ser Gly Gly Thr Thr
20 25 30

```
Lys Tyr Phe Arg Ile Pro Ala Met Cys Thr Thr Ser Lys Gly Thr Ile
        35                  40                  45

Val Val Phe Ala Asp Ala Arg His Asn Thr Ala Ser Asp Gln Ser Phe
    50                  55                  60

Ile Asp Thr Ala Ala Ala Arg Ser Thr Asp Gly Gly Lys Thr Trp Asn
65                  70                  75                  80

Lys Lys Ile Ala Ile Tyr Asn Asp Arg Val Asn Ser Lys Leu Ser Arg
                85                  90                  95

Val Met Asp Pro Thr Cys Ile Val Ala Asn Ile Gln Gly Arg Glu Thr
            100                 105                 110

Ile Leu Val Met Val Gly Lys Trp Asn Asn Asn Asp Lys Thr Trp Gly
        115                 120                 125

Ala Tyr Arg Asp Lys Ala Pro Asp Thr Asp Trp Asp Leu Val Leu Tyr
    130                 135                 140

Lys Ser Thr Asp Asp Gly Val Thr Phe Ser Lys Val Glu Thr Asn Ile
145                 150                 155                 160

His Asp Ile Val Thr Lys Asn Gly Thr Ile Ser Ala Met Leu Gly Gly
                165                 170                 175

Val Gly Ser Gly Leu Gln Leu Asn Asp Gly Lys Leu Val Phe Pro Val
            180                 185                 190

Gln Met Val Arg Thr Lys Asn Ile Thr Thr Val Leu Asn Thr Ser Phe
        195                 200                 205

Ile Tyr Ser Thr Asp Gly Ile Thr Trp Ser Leu Pro Ser Gly Tyr Cys
    210                 215                 220

Glu Gly Phe Gly Ser Glu Asn Asn Ile Ile Glu Phe Asn Ala Ser Leu
225                 230                 235                 240

Val Asn Asn Ile Arg Asn Ser Gly Leu Arg Arg Ser Phe Glu Thr Lys
```

```
                245                 250                 255

Asp Phe Gly Lys Thr Trp Thr Glu Phe Pro Pro Met Asp Lys Lys Val
            260                 265                 270

Asp Asn Arg Asn His Gly Val Gln Gly Ser Thr Ile Thr Ile Pro Ser
        275                 280                 285

Gly Asn Lys Leu Val Ala Ala His Ser Ser Ala Gln Asn Lys Asn Asn
    290                 295                 300

Asp Tyr Thr Arg Ser Asp Ile Ser Leu Tyr Ala His Asn Leu Tyr Ser
305                 310                 315                 320

Gly Glu Val Lys Leu Ile Asp Asp Phe Tyr Pro Lys Val Gly Asn Ala
                325                 330                 335

Ser Gly Ala Gly Tyr Ser Cys Leu Ser Tyr Arg Lys Asn Val Asp Lys
            340                 345                 350

Glu Thr Leu Tyr Val Val Tyr Glu Ala Asn Gly Ser Ile Glu Phe Gln
        355                 360                 365

Asp Leu Ser Arg His Leu Pro Val Ile Lys Ser Tyr Asn Gly Gly Gly
    370                 375                 380

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
385                 390                 395                 400

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
                405                 410                 415

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
            420                 425                 430

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
        435                 440                 445

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
    450                 455                 460
```

```
Glu Gln Tyr Gly Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
465                 470                 475                 480

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
                485                 490                 495

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
            500                 505                 510

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
        515                 520                 525

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
    530                 535                 540

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
545                 550                 555                 560

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
                565                 570                 575

Leu Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
            580                 585                 590

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
        595                 600                 605

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly Gly Gly Ser
    610                 615                 620

His His His His His His His His
625                 630
```

<210> 109
<211> 1896
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 109
acagtggaaa agtccgtggt gttcaaggcc gagggcgagc acttcaccga ccagaaaggc 60

aataccatcg tcggctctgg cagcggcggc accaccaagt actttagaat ccccgccatg 120

tgcaccacca gcaagggcac cattgtggtg ttcgccgacg ccagacacaa caccgccagc 180

gatcagagct tcatcgatac cgctgccgcc agaagtacag acggcggcaa gacctggaac 240

aagaagatcg ccatctacaa cgaccgcgtg aacagcaagc tgagcagagt gatggaccct 300

acctgcatcg tggccaacat ccagggcaga gaaaccatcc tggtcatggt cggaaagtgg 360

aacaacaacg ataagacctg gggcgcctac agagacaagg cccctgatac cgattgggac 420

ctcgtgctgt ataagagcac cgacgacggc gtgaccttca gcaaggtgga aacaaacatc 480

cacgacatcg tgaccaagaa cggcaccatc tctgccatgc tcggcggcgt tggatctggc 540

ctgcaactga atgatggcaa gctggtgttc cccgtgcaga tggtccgaac aaagaacatc 600

accaccgtgc tgaataccag cttcatctac tccaccgacg gcatcacatg gtccctgcct 660

agcggctact gtgaaggctt tggcagcgag aacaacatca tcgagttcaa cgccagcctg 720

gtcaacaaca tccggaacag cggcctgcgg agaagcttcg agacaaagga cttcggaaag 780

acgtggaccg agtttcctcc aatggacaag aaggtggaca accggaacca cggcgtgcag 840

ggcagcacaa tcacaatccc tagcggcaac aaactggtgg ccgctcactc tagcgcccag 900

aacaagaaca acgattacac cagaagcgac atcagcctgt acgcccacaa cctgtactcc 960

ggcgaagtga agctgatcga cgacttctac cccaaagtgg gcaatgccag cggagccggc 1020

tacagctgtc tgagctaccg gaaaaatgtg gacaaagaaa ccctgtacgt ggtgtacgag 1080

gccaacggca gcatcgagtt tcaggacctg agcagacatc tgcccgtgat caagagctac 1140

aatggcggag gtggaagtgg cggaggcgga tccgacaaaa ctcacacatg cccaccgtgc 1200

ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccccaaa acccaaggac 1260

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 1320

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 1380

aagccgcggg aggagcagta cggtagcacg taccgtgtgg tcagcgtcct caccgtcctg 1440

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 1500

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtctac 1560

accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 1620

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1680

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct cactagcaag 1740

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1800

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaaagcggc 1860

ggaggcggat ctcatcatca ccatcatcac catcac 1896

<210> 110
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 110
caggttcagc tggtgcagtc tggcgtggaa gtgaagaaac ctggggccag cgtgaaggtg 60

tcctgtaaag ccagcggcta cacctttacc aactactaca tgtactgggt ccgacaggcc 120

ccaggccaag gacttgaatg gatgggcggc atcaacccca gcaacggcgg caccaacttc 180

aacgagaagt tcaagaacag agtgaccctg accaccgaca gcagcaccac cacagcctac 240

atggaactga agtccctgca gttcgacgac accgccgtgt actactgcgc cagacgggac 300

tacagattcg acatgggctt cgactattgg ggccagggca ccaccgtgac agtctcttct 360

gctagcacca agggcccatc cgtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcc 480

tggaactcag gcgctctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacgcc 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtctacaccc tgcccccatc ccgggaggag 1080

atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctcacc agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtaaa 1350

<210> 111
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 111
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr

```
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335
```

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Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
    370                 375                 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385                 390                 395                 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                405                 410                 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            420                 425                 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        435                 440                 445

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465                 470                 475                 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                485                 490                 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500                 505                 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        515                 520                 525

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

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
```

545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 112
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 112
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln

```
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320
```

```
Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
    370                 375                 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385                 390                 395                 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                405                 410                 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            420                 425                 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        435                 440                 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    450                 455                 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465                 470                 475                 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                485                 490                 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            500                 505                 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        515                 520                 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
```

530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 113
<211> 1851
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 113
gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgtcaagt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agagccagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccacag ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960

tggagcgaac ctgttctgct ggccaagggc agcgctgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa 1140

ggcggaggtg gaagtggcgg aggcggatcc gacaaaactc acacatgccc accgtgccca 1200

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 1260

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 1320

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1380

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1440

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1500

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtctacacc 1560

ctgcccccat cccgggagga gatgaccaag aaccaggtca gcctgacctg cctggtcaaa 1620

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1680

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcac tagcaagctc 1740

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1800

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa a 1851

<210> 114
<211> 1836
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 114
gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgtcaagt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agagccagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

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aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1380

tacgccagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1500

atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg 1560

gaggagatga ccaagaacca ggtcagcctg tactgcctgg tcaaaggctt ctatcccagc 1620

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680

cccgtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc 1740

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<212> PRT
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Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly

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145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365
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Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
    370                 375                 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385                 390                 395                 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                405                 410                 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            420                 425                 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        435                 440                 445

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465                 470                 475                 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                485                 490                 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500                 505                 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        515                 520                 525

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

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545                 550                 555                 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                565                 570                 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
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580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
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<210> 116
<211> 608
<212> PRT
<213> Artificial Sequence

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Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

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Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Xaa Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Xaa Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285
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Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Asp Lys Thr
    370                 375                 380

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
385                 390                 395                 400

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                405                 410                 415

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            420                 425                 430

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        435                 440                 445

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    450                 455                 460

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
465                 470                 475                 480

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                485                 490                 495
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Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
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Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        515                 520                 525

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

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
545                 550                 555                 560

Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr Val Asp Lys Ser
                565                 570                 575

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            580                 585                 590

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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<210> 117
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Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Xaa Xaa Asp Glu His
35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Xaa
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Xaa Leu Gln Leu His Asp Xaa Xaa Arg Ser Leu Val Val

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                165                 170                 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Xaa Xaa Pro Ile Pro
            180                 185                 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Xaa Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Xaa Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser Xaa Xaa
225                 230                 235                 240

Xaa Xaa Arg Xaa Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
                245                 250                 255

Xaa Xaa Gln Xaa Val Lys Lys Leu Xaa Glu Pro Pro Pro Xaa Gly Xaa
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Asp Lys Thr
    370                 375                 380
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His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
385                 390                 395                 400

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                405                 410                 415

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            420                 425                 430

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        435                 440                 445

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    450                 455                 460

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
465                 470                 475                 480

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                485                 490                 495

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            500                 505                 510

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        515                 520                 525

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

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
545                 550                 555                 560

Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr Val Asp Lys Ser
                565                 570                 575

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
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Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

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gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

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<212> PRT
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polypeptide

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<220>
<221> MOD_RES
<222> (325)..(325)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (332)..(332)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (352)..(352)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (363)..(363)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (365)..(365)
<223> Any amino acid

<400> 119
Xaa Xaa Ser Xaa Xaa Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Xaa Xaa Asp Glu His
        35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
    50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Xaa
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
                85 90 95

```
Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Xaa Xaa Pro Ile Pro
            180                 185                 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Xaa Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Xaa Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser Xaa Xaa
225                 230                 235                 240

Xaa Xaa Arg Xaa Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
                245                 250                 255

Xaa Xaa Gln Xaa Val Lys Lys Leu Xaa Glu Pro Pro Pro Xaa Gly Xaa
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
    290                 295                 300
```

```
Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320


Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
                325                 330                 335


Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
            340                 345                 350


Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
        355                 360                 365


Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
    370                 375                 380


<210> 120
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide


<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (93)..(93)
<223> Any amino acid
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<220>
<221> MOD_RES
<222> (126)..(126)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (187)..(187)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (242)..(242)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (270)..(270)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (301)..(302)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (332)..(332)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (363)..(363)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (365)..(365)
<223> Any amino acid

<400> 120
Xaa Ala Ser Leu Pro Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
        35 40 45

```
Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
    50                  55                  60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Xaa Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Xaa Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
            260                 265                 270
```

```
Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
    370                 375                 380
```

<210> 121
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 121
```
Gly Gly Gly Gly Ser
1               5
```

<210> 122
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 122

```
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1               5                  10                  15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20                  25                  30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
        35                  40                  45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
    50                  55                  60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220
```

```
Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
    370                 375                 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385                 390                 395                 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                405                 410                 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            420                 425                 430
```

```
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        435                 440                 445

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465                 470                 475                 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                485                 490                 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500                 505                 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        515                 520                 525

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

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545                 550                 555                 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                565                 570                 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            580                 585                 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        595                 600                 605

Ser Pro Gly Lys
    610
```

<210> 123
<211> 612
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 123

```
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1               5                  10                  15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20                  25                  30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
        35                  40                  45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
    50                  55                  60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205
```

```
Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
    370                 375                 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385                 390                 395                 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                405                 410                 415
```

```
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            420                 425                 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        435                 440                 445

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465                 470                 475                 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                485                 490                 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500                 505                 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        515                 520                 525

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

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545                 550                 555                 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                565                 570                 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            580                 585                 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        595                 600                 605

Ser Pro Gly Lys
    610
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<210> 124
<211> 1836

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 124
gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgttacgt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agattcagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960

tggagcgaac ctgttctgct ggccaagggc agcgctgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa 1140

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 1200

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 1260

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 1320

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1380

tacgccagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1500

atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg 1560

gaggagatga ccaagaacca ggtcagcctg tactgcctgg tcaaaggctt ctatcccagc 1620

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680

cccgtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc 1740

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1800

tacacgcaga agagcctaag cttgtctccg ggtaaa 1836

<210> 125
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 125
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

```
Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
```

```
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
    370                 375                 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385                 390                 395                 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                405                 410                 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            420                 425                 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        435                 440                 445

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465                 470                 475                 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                485                 490                 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500                 505                 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        515                 520                 525

Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    530                 535                 540
```

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 126
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 126
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

```
Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
```

305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 127
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 127
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln

```
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320
```

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Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
    370                 375                 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385                 390                 395                 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                405                 410                 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            420                 425                 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        435                 440                 445

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465                 470                 475                 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                485                 490                 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500                 505                 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        515                 520                 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
```

530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 128
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 128
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly

```
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300
```

```
Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
    370                 375                 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385                 390                 395                 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                405                 410                 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            420                 425                 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        435                 440                 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    450                 455                 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465                 470                 475                 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                485                 490                 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            500                 505                 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
```

515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 129
<211> 1836
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 129
gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cggcggagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgttacgt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agattcagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960

tggagcgaac ctgttctgct ggccaagggc agcgctgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa 1140

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 1200

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 1260

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 1320

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1380

tacgccagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1500

atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg 1560

gaggagatga ccaagaacca ggtcagcctg tactgcctgg tcaaaggctt ctatcccagc 1620

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680

cccgtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc 1740

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1800

tacacgcaga agagcctaag cttgtctccg ggtaaa 1836

<210> 130
<211> 854
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 130
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

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Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
    370                 375                 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385                 390                 395                 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                405                 410                 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            420                 425                 430
```

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His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        435                 440                 445

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465                 470                 475                 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                485                 490                 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500                 505                 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        515                 520                 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    530                 535                 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545                 550                 555                 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                565                 570                 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            580                 585                 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        595                 600                 605

Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    610                 615                 620

Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys
625                 630                 635                 640
```

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Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
                645                 650                 655

Thr Asn Tyr Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
            660                 665                 670

Glu Trp Met Gly Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn
        675                 680                 685

Glu Lys Phe Lys Asn Arg Val Thr Leu Thr Thr Asp Ser Ser Thr Thr
    690                 695                 700

Thr Ala Tyr Met Glu Leu Lys Ser Leu Gln Phe Asp Asp Thr Ala Val
705                 710                 715                 720

Tyr Tyr Cys Ala Arg Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr
                725                 730                 735

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
            740                 745                 750

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
        755                 760                 765

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
    770                 775                 780

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
785                 790                 795                 800

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
                805                 810                 815

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
            820                 825                 830

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

Ser Cys Asp Lys Thr Ser
    850
```

<210> 131
<211> 2562
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 131
gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cggcggagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgttacgt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agattcagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960

tggagcgaac ctgttctgct ggccaagggc agcgctgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa 1140

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 1200

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 1260

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 1320

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1380

tacgccagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1500

atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg 1560

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1620

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680

cccgtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc 1740

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1800

tacacgcaga agagcctaag cttgtctccg ggtaaaggag gcggaggatc tggcggaggt 1860

ggaagtggcg gaggcggatc tcaggttcag ctggtgcagt ctggcgtgga agtgaagaaa 1920

cctggggcca gcgtgaaggt gtcctgtaaa gccagcggct acacctttac caactactac 1980

atgtactggg tccgacaggc cccaggccaa ggacttgaat ggatgggcgg catcaacccc 2040

agcaacggcg gcaccaactt caacgagaag ttcaagaaca gagtgaccct gaccaccgac 2100

agcagcacca ccacagccta catggaactg aagtccctgc agttcgacga caccgccgtg 2160

tactactgcg ccagacggga ctacagattc gacatgggct tcgactattg gggccagggc 2220

accaccgtga cagtctcttc tgctagcacc aagggcccat ccgtcttccc cctggcaccc 2280

tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctggtcaa ggactacttc 2340

cccgaaccgg tgacggtgtc ctggaactca ggcgctctga ccagcggcgt gcacaccttc 2400

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 2460

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 2520

gtggacaaga aagttgagcc caaatcttgt gacaaaacta gc 2562

<210> 132
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 132
Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn Glu Lys Phe
50 55 60

Lys Asn Arg Val Thr Leu Thr Thr Asp Ser Ser Thr Thr Thr Ala Tyr
65 70 75 80

Met Glu Leu Lys Ser Leu Gln Phe Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp

210 215 220

Lys Thr Ser
225

<210> 133
<211> 681
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 133
caggttcagc tggtgcagtc tggcgtggaa gtgaagaaac ctggggccag cgtgaaggtg 60

tcctgtaaag ccagcggcta cacctttacc aactactaca tgtactgggt ccgacaggcc 120

ccaggccaag gacttgaatg gatgggcggc atcaacccca gcaacggcgg caccaacttc 180

aacgagaagt tcaagaacag agtgaccctg accaccgaca gcagcaccac cacagcctac 240

atggaactga agtccctgca gttcgacgac accgccgtgt actactgcgc cagacgggac 300

tacagattcg acatgggctt cgactattgg ggccagggca ccaccgtgac agtctcttct 360

gctagcacca agggcccatc cgtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcc 480

tggaactcag gcgctctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactag c 681

<210> 134
<211> 845
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 134
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

```
Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20                  25                  30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
        35                  40                  45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
    50                  55                  60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65                  70                  75                  80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
                85                  90                  95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100                 105                 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
        115                 120                 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130                 135                 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145                 150                 155                 160

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

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
            180                 185                 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195                 200                 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210                 215                 220
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Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225                 230                 235                 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245                 250                 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
            260                 265                 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275                 280                 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
    290                 295                 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305                 310                 315                 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325                 330                 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340                 345                 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355                 360                 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
    370                 375                 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385                 390                 395                 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                405                 410                 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            420                 425                 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        435                 440                 445
```

```
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr
    450                 455                 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465                 470                 475                 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                485                 490                 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500                 505                 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        515                 520                 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    530                 535                 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545                 550                 555                 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                565                 570                 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            580                 585                 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        595                 600                 605

Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    610                 615                 620

Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu
625                 630                 635                 640

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Gly Val
                645                 650                 655
```

```
Ser Thr Ser Gly Tyr Ser Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly
            660                 665                 670

Gln Ala Pro Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly
        675                 680                 685

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
    690                 695                 700

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
705                 710                 715                 720

His Ser Arg Asp Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
                725                 730                 735

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
            740                 745                 750

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
        755                 760                 765

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
    770                 775                 780

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
785                 790                 795                 800

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
                805                 810                 815

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
            820                 825                 830

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
        835                 840                 845
```

<210> 135
<211> 2535
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 135
gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cggcggagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgttacgt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agattcagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960

tggagcgaac ctgttctgct ggccaagggc agcgctgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa 1140

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 1200

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 1260

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 1320

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1380

tacgccagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1500

atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg 1560

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1620

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680

cccgtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc 1740

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1800

tacacgcaga agagcctaag cttgtctccg ggtaaaggag gcggaggatc tggcggaggt 1860

ggaagtggcg gaggcggatc tgagatcgtg ctgacacaga gccctgccac actgtcactg 1920

tctccaggcg agagagccac actgagctgt agagcttcta agggcgtgtc caccagcggc 1980

tactcttacc tgcactggta tcagcagaag cccggccagg ctcctagact gctgatctac 2040

ctggccagct acctggaaag cggagtgcct gctagattca gcggctctgg ctctggcacc 2100

gacttcaccc tgacaatcag cagcctggaa cctgaggact tcgccgtgta ctactgccag 2160

cacagcagag atctgcccct gacatttggc ggaggcacca aggtggaaat caagcgtacg 2220

gtggctgcac catctgtctt catcttcccg ccatctgatg agcagttgaa atctggaact 2280

gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag 2340

gtggataacg ccctccaatc gggtaactcc caggagagtg tcacagagca ggacagcaag 2400

gacagcacct acagcctcag cagcaccctg acgctgagca aagcagacta cgagaaacac 2460

aaagtctacg cctgcgaagt cacccatcag ggcctgagct cgcccgtcac aaagagcttc 2520

aacaggggag agtgt 2535

<210> 136
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 136
Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

```
Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn Glu Lys Phe
    50                  55                  60

Lys Asn Arg Val Thr Leu Thr Thr Asp Ser Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Lys Ser Leu Gln Phe Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
    210                 215                 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
```

```
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
            260                 265                 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445

<210> 137
<211> 120
<212> PRT
```

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 137
Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn Glu Lys Phe
50 55 60

Lys Asn Arg Val Thr Leu Thr Thr Asp Ser Ser Thr Thr Thr Ala Tyr
65 70 75 80

Met Glu Leu Lys Ser Leu Gln Phe Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 138
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 138
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Gly Val Ser Thr Ser

20 25 30

Gly Tyr Ser Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45

Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Ser Arg
85 90 95

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

<210> 139
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 139
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys

```
                85                  90                  95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225                 230                 235                 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300
```

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 140
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 140
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

```
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225                 230                 235                 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
```

<210> 141
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 141
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

```
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225                 230                 235                 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285

Leu Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
```

<210> 142
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 142

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1               5                   10                  15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
```

```
        35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225                 230                 235                 240

Met Thr Lys Asn Gln Val Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255
```

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 143
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 143
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

```
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225                 230                 235                 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285

Leu Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
```

305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 144
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 144
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 145
<211> 864
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 145

```
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1               5                  10                  15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

Thr Asn Tyr Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

Glu Trp Met Gly Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn
65                  70                  75                  80

Glu Lys Phe Lys Asn Arg Val Thr Leu Thr Thr Asp Ser Ser Thr Thr
                85                  90                  95

Thr Ala Tyr Met Glu Leu Lys Ser Leu Gln Phe Asp Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Arg Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr
        115                 120                 125

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
    130                 135                 140

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
145                 150                 155                 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
                165                 170                 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
            180                 185                 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
        195                 200                 205
```

```
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
    210                 215                 220

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
225                 230                 235                 240

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
                245                 250                 255

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

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

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
    290                 295                 300

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser
305                 310                 315                 320

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
                325                 330                 335

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
            340                 345                 350

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
        355                 360                 365

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
    370                 375                 380

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385                 390                 395                 400

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
                405                 410                 415

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
```

```
            420                 425                 430

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
        435                 440                 445

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
    450                 455                 460

Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
465                 470                 475                 480

Gly Gly Gly Ser Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val
                485                 490                 495

Phe Gln Ser Gly Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu
            500                 505                 510

Pro Gly Gln Gln Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys
        515                 520                 525

Lys Asp Glu His Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp
    530                 535                 540

Ala Gly Thr His Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln
545                 550                 555                 560

Ala Arg Leu Asp Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp
                565                 570                 575

Glu Gln Thr Gly Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln
            580                 585                 590

Val Thr Glu Gln Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu
        595                 600                 605

Cys Tyr Val Thr Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg
    610                 615                 620

Asp Leu Thr Asp Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr
625                 630                 635                 640
```

```
Phe Ala Val Gly Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg
                645                 650                 655

Ser Leu Val Val Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln
            660                 665                 670

Arg Pro Ile Pro Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg
        675                 680                 685

Thr Trp Ala Arg Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln
    690                 695                 700

Val Ala Glu Val Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala
705                 710                 715                 720

Arg Ser His Leu Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly
                725                 730                 735

Leu Asp Phe Gln Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro
            740                 745                 750

Pro Thr Gly Cys Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser
        755                 760                 765

Gly Pro Gly Ser Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His
    770                 775                 780

Ser Trp Gln Arg Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro
785                 790                 795                 800

Ala Pro Glu Ala Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala
                805                 810                 815

Ala Tyr Ser Asp Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro
            820                 825                 830

Leu Phe Gly Cys Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe
        835                 840                 845

Leu Met Phe Thr Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
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850 855 860

<210> 146
<211> 2598
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 146
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gttcagctgg tgcagtctgg cgtggaagtg aagaaacctg gggccagcgt gaaggtgtcc 120

tgtaaagcca gcggctacac ctttaccaac tactacatgt actgggtccg acaggcccca 180

ggccaaggac ttgaatggat gggcggcatc aaccccagca acggcggcac caacttcaac 240

gagaagttca agaacagagt gaccctgacc accgacagca gcaccaccac agcctacatg 300

gaactgaagt ccctgcagtt cgacgacacc gccgtgtact actgcgccag acgggactac 360

agattcgaca tgggcttcga ctattggggc cagggcacca ccgtgacagt ctcttctgct 420

agcaccaagg gcccatccgt cttccccctg gcaccctcct ccaagagcac ctctgggggc 480

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcctgg 540

aactcaggcg ctctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 600

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 660

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 720

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 780

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 840

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 900

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacgccagc 960

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 1020

tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1080

gccaaagggc agccccgaga accacaggtc tacaccctgc ccccatcccg ggaggagatg 1140

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1200

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1260

gactccgacg gctccttctt cctctatagc aagctcaccg tggacaagag caggtggcag 1320

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1380

aagagcctaa gcttgtctcc gggtaaagga ggcggaggat ctggcggagg tggaagtggc 1440

ggaggcggat ctgatgcatc tctgccttac ctgcagaaag aaagcgtgtt ccagtctggc 1500

gcccacgcct acagaattcc cgctctgctg tatctgccag gccagcagtc tctgctggct 1560

ttcgctgaac agcgggccag caagaaggat gagcacgccg aactgatcgt gctgcggaga 1620

ggcgattacg acgccggcac acatcaggtg cagtggcagg ctcaagaggt ggtggctcag 1680

gctagactgg acggccacag atctatgaac ccctgtcctc tgtacgatga acagaccggc 1740

acactgtttc tgttctttat cgctatcccc ggccaagtga ccgagcagca gcagctgcag 1800

acaagagcca acgtgaccag actgtgttac gtgacctcca ccgaccacgg cagaacctgg 1860

tctagcccta gagatctgac cgacgccgcc atcggacctg cctatagaga gtggtccacc 1920

ttcgccgttg gacctggaca ctgtctccag ctgcacgaca gggctagatc tctggtggtg 1980

cctgcctacg cctatagaaa gctgcacccc aaacagcggc ctattcctag cgccttctgc 2040

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ctggaatgcc aggtggccga agtggaaacc ggcgagcaga gagtcgtgac cctgaacgcc 2160

agatctcacc tgagattcag agtgcaggcc cagagcacaa acgacggcct ggatttccaa 2220

gagagccagc tggtcaagaa actggtggaa cctcctccaa ccggctgtca gggaagcgtg 2280

atcagctttc catctcctag aagcggccct ggctctcctg ctcagtggct gctgtataca 2340

caccccacac acagctggca gagagccgat ctgggcgcct acctgaatcc tagacctcct 2400

gctcctgagg cttggagcga acctgttctg ctggccaagg gcagcgctgc ctacagcgat 2460

ctgcagtcta tgggcacagg ccctgatggc agccctctgt ttggctgtct gtacgaggcc 2520

aacgactacg aagagatcgt gttcctgatg ttcaccctga agcaggcctt tccagccgag 2580

tacctgcctc aatagtga 2598

<210> 147
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
10xHis tag

<400> 147
His His His His His His His His His His
1 5 10

<210> 148
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> SITE
<222> (1)..(15)
<223> This sequence may encompass 1-5 "Gly Gly Pro"
repeating units

<400> 148
Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly Gly Pro
1 5 10 15

<210> 149
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> SITE
<222> (1)..(25)
<223> This sequence may encompass 1-5 "Gly Gly Gly Gly Ser"
repeating units

<400> 149
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 150
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
6xHis tag

<400> 150
His His His His His His
1 5