SEQUENCE LISTING

<110> PALLEON PHARMACEUTICALS INC.

<120> ANTI-PD-L1 ANTIBODIES AND FUSION PROTEINS THEREOF

<130> PAL-024WO

<140> PCT/US2022/011504
<141> 2022-01-06

<150> 63/134,412
<151> 2021-01-06

<160> 259

<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

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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

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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


<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
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<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
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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

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tggagcgaac ctgttctgct ggccaagggc agctgtgcct acagcgatct gcagtctatg 1020

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gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa 1140

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

<400> 25
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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

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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

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atgagacctg cggacctgcc cccgcgcccc atggaagaat ccccggcgtc cagctctgcc       60

ccgacagaga cggaggagcc ggggtccagt gcagaggtca tggaagaagt gacaacatgc      120

tccttcaaca gccctctgtt ccggcaggaa gatgacagag ggattaccta ccggatccca      180

gccctgctct acatacccca 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
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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

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aagatctgcc ggaccagccc tcactccttc gccttctaca gcgatgacca cggccgcacc 660

tggcgctgtg gaggcctcgt gcccaacctg cgctcaggcg agtgccagct ggcagcggtg 720

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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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<210> 37
<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

ggcgttttaa ccaatgcaga tggaatgccc gcttggttgg tgcaaggtat tggagggaga 300

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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ggcgacgtca tcttcagagg cccagaccgt ataccgtcca ttgtagcaag tagcgtaaca 780

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agtaatacca atgacataat cactcgtacc tcacgagatg gcggtataac ttgggatacc 900

gagctcaacc tcactgagca aatcaatgtc agtgatgagt ttgatttctc cgatcctcgg 960

cctatctatg atccttcctc caatacggtt cttgtctctt atgctcgatg gccgaccgat 1020

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<210> 38
<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

```
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

```
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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gtgaccagtt cctggacagg gatcgccggg agctatggtg ggggcagacc cgaccagacc 180

ccggggaccg ctgagctatt gggcgggccg tcggggtcag gggctcgcag cgatcttcct 240

gctcctggtg tccgcggcgg aatccgaggc cagggcagag gatgacttca gcctggtgca 300

gccgctggtg accatggagc agctgctgtg ggtgagcggg aagcagatcg gctctgtaga 360

cactttccgc atcccgctca tcacagccac ccctcggggc acgctcctgg ccttcgctga 420

ggccaggaaa aaatctgcat ccgatgaggg ggccaagttc atcgccatga ggaggtccac 480

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tcaagacagg gttgtttctc tgtatagccc tggctgtctt ggaattcact ctgtagacca 3780

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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
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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 Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
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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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Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
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Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
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Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
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Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
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Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
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Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
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Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Xaa Xaa Asp Glu His
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Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu 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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Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
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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
    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
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<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> 450
<212> PRT
<213> Artificial Sequence

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

<400> 63
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala Asp Thr Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu 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 Asn 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 Tyr 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> 64
<211> 216
<212> PRT
<213> Artificial Sequence

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

<400> 64
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln

```
1               5                   10                  15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
            20                  25                  30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
    50                  55                  60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Ser
                85                  90                  95

Ser Thr Arg Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Gln
            100                 105                 110

Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
        115                 120                 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
    130                 135                 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys
145                 150                 155                 160

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

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
            180                 185                 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
        195                 200                 205

Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
```

<210> 65
<211> 216
<212> PRT
<213> Artificial Sequence

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

<400> 65
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Ser
85 90 95

Ser Thr Arg Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Gln
100 105 110

Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
115 120 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys
145 150 155 160

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

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 66
<211> 450
<212> PRT
<213> Artificial Sequence

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

<400> 66
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala Asp Thr Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu 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 Asn 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

Tyr 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 Tyr 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> 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
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

<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>
<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

<220>
<221> MOD_RES
<222> (187)..(187)
<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> 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
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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> 75
<211> 617
<212> PRT
<213> Artificial Sequence

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

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<223> Any amino acid

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<222> (4)..(6)
<223> Any amino acid

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<223> Any amino acid

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<222> (44)..(45)
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<223> Any amino acid

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<222> (62)..(62)
<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> (112)..(112)
<223> Any amino acid

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<223> Any amino acid

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<222> (150)..(150)
<223> Any amino acid

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<223> Any amino acid

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<222> (257)..(257)
<223> Any amino acid

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<223> Any amino acid

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<221> MOD_RES
<222> (272)..(272)
<223> Any amino acid

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<222> (292)..(292)
<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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<221> MOD_RES
<222> (363)..(363)
<223> Any amino acid

<220>
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<222> (365)..(365)
<223> Any amino acid

<400> 75

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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 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
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Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 76
<211> 648
<212> DNA
<213> Artificial Sequence

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

<400> 76
caatctgctc ttacacagcc tgccagcgtg tccggatctc ctggccagag catcaccatc 60

agctgtaccg gcaccagctc tgatgtcggc ggctacaatt acgtgtcctg gtatcagcag 120

caccccggca aggcccctaa gctgatgatc tacgacgtgt ccaacagacc cagcggcgtg 180

tccaatagat tctccggcag caagagcggc aacaccgcca gcctgacaat tagcggactg 240

caggccgagg acgaggccga ttactactgt agcagctaca ccagctccag caccagagtg 300

tttggcaccg gcacaaaagt gaccgtgctg ggccagccta aggccaatcc taccgtgaca 360

ctgttccctc caagcagcga ggaactgcag gctaacaagg ccacactcgt gtgcctgatc 420

agcgactttt atcctggcgc cgtgaccgtg gcctggaagg ctgatggatc tccagtgaaa 480

gccggcgtgg aaaccaccaa gcctagcaag cagagcaaca acaaatacgc cgccagcagc 540

tacctgagcc tgacacctga gcagtggaag tcccacagat cctacagctg ccaagtgacc 600

cacgagggca gcaccgtgga aaaaacagtg gcccctaccg agtgctct 648

<210> 77
<211> 1350
<212> DNA
<213> Artificial Sequence

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

<400> 77
gaggtgcagc tgctggaatc tggcggagga cttgttcagc ctggcggctc tctgagactg 60

tcttgtgccg ccagcggctt caccttcagc agctatatca tgatgtgggt ccgacaggcc 120

cctggcaaag gccttgaatg ggtgtccagc atctatccca gcggcggcat caccttttac 180

gccgacacag tgaagggcag attcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgag agccgaggac accgccgtgt actactgcgc cagaatcaag 300

ctgggcaccg tgaccaccgt ggattattgg ggacagggca ccctggtcac cgtgtcatct 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 ccggaccccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtctacaccc tgccccatc ccgggaggag 1080

atgaccaaga accaggtcag cctgtactgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtaaa 1350

<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

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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 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
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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
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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
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<210> 79
<211> 1836
<212> DNA
<213> Artificial Sequence

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

<400> 79

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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
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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
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
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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

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
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<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

<220>
<221> MOD_RES
<222> (187)..(187)
<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

<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
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```
    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


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<223> Any amino acid
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<222> (9)..(9)
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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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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
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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

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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
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```
            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
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```
                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
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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 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
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<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
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<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> 450
<212> PRT
<213> Artificial Sequence

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

<400> 104
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala Asp Thr Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

```
Ala Arg Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu 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 Gly 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

Tyr 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 Tyr 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> 105
<211> 1350
<212> DNA
<213> Artificial Sequence

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

<400> 105
gaggtgcagc tgctggaatc tggcggagga cttgttcagc ctggcggctc tctgagactg 60

tcttgtgccg ccagcggctt caccttcagc agctatatca tgatgtgggt ccgacaggcc 120

cctggcaaag gccttgaatg ggtgtccagc atctatccca gcggcggcat cacctttac 180

gccgacacag tgaagggcag attcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgag agccgaggac accgccgtgt actactgcgc cagaatcaag 300

ctgggcaccg tgaccaccgt ggattattgg ggacagggca ccctggtcac cgtgtcatct 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 ccggaccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacggt 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtctacaccc tgccccatc ccgggaggag 1080

atgaccaaga accaggtcag cctgtactgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtaaa 1350

<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 tcccccaaa 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> 715
<212> PRT
<213> Artificial Sequence

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

polypeptide

<400> 110

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala Asp Thr Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu 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 Asn 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

Tyr 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 Tyr 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

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

Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly
                485                 490                 495

Tyr Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys
            500                 505                 510

Leu Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg
        515                 520                 525

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

Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser
545                 550                 555                 560

Ser Ser Thr Arg Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly
                565                 570                 575

Gln Pro Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
            580                 585                 590

Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
        595                 600                 605

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
    610                 615                 620

Ser Ser Tyr Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
625                 630                 635                 640
```

Glu Trp Val Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala
645 650 655

Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
660 665 670

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
675 680 685

Tyr Tyr Cys Ala Arg Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr
690 695 700

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
705 710 715

<210> 111
<211> 2145
<212> DNA
<213> Artificial Sequence

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

<400> 111
gaggtgcagc tgctggaatc tggcggagga cttgttcagc ctggcggctc tctgagactg 60

tcttgtgccg ccagcggctt caccttcagc agctatatca tgatgtgggt ccgacaggcc 120

cctggcaaag gccttgaatg ggtgtccagc atctatccca gcggcggcat caccttttac 180

gccgacacag tgaagggcag attcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgag agccgaggac accgccgtgt actactgcgc cagaatcaag 300

ctgggcaccg tgaccaccgt ggattattgg ggacagggca ccctggtcac cgtgtcatct 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 gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtctacaccc tgcccccatc ccgggaggag 1080

atgaccaaga accaggtcag cctgtactgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc taagcttgtc tccgggtaaa ggaggcggag gatctggcgg aggtggaagt 1380

ggcggaggcg gatctcaatc tgctcttaca cagcctgcca gcgtgtccgg atctcctggc 1440

cagagcatca ccatcagctg taccggcacc agctctgatg tcggcggcta caattacgtg 1500

tcctggtatc agcagcaccc cggcaaggcc cctaagctga tgatctacga cgtgtccaac 1560

agacccagcg gcgtgtccaa tagattctcc ggcagcaaga gcggcaacac cgccagcctg 1620

acaattagcg gactgcaggc cgaggacgag gccgattact actgtagcag ctacaccagc 1680

tccagcacca gagtgtttgg caccggcaca aaagtgaccg tgctgggcca gcctaaggcc 1740

ggtggaggtg ggtctggagg gggtggatct ggaggtggcg gatcggaggt gcagctgctg 1800

gaatctggcg gaggacttgt tcagcctggc ggctctctga gactgtcttg tgccgccagc 1860

ggcttcacct tcagcagcta tatcatgatg tgggtccgac aggcccctgg caaaggcctt 1920

gaatgggtgt ccagcatcta tcccagcggc ggcatcacct tttacgccga cacagtgaag 1980

ggcagattca ccatcagccg ggacaacagc aagaacaccc tgtacctgca gatgaacagc 2040

ctgagagccg aggacaccgc cgtgtactac tgcgccagaa tcaagctggg caccgtgacc 2100

accgtggatt attggggaca gggcaccctg gtcaccgtgt catct 2145

<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

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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
```

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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> 113
<211> 1851
<212> DNA
<213> Artificial Sequence

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

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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

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> 877
<212> PRT
<213> Artificial Sequence

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

<400> 114
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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

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            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
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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
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    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 Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser
625                 630                 635                 640

Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val
                645                 650                 655

Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala
            660                 665                 670

Pro Lys Leu Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser
        675                 680                 685

Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile
    690                 695                 700

Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr
705                 710                 715                 720

Thr Ser Ser Ser Thr Arg Val Phe Gly Thr Gly Thr Lys Val Thr Val
                725                 730                 735

Leu Gly Gln Pro Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            740                 745                 750
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Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
        755                 760                 765

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
    770                 775                 780

Thr Phe Ser Ser Tyr Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys
785                 790                 795                 800

Gly Leu Glu Trp Val Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe
                805                 810                 815

Tyr Ala Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
            820                 825                 830

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
        835                 840                 845

Ala Val Tyr Tyr Cys Ala Arg Ile Lys Leu Gly Thr Val Thr Thr Val
    850                 855                 860

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
865                 870                 875
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<210> 115
<211> 2631
<212> DNA
<213> Artificial Sequence

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

<400> 115

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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
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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

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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

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1500

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ggaagtggcg gaggcggatc tcaatctgct cttacacagc ctgccagcgt gtccggatct 1920

cctggccaga gcatcaccat cagctgtacc ggcaccagct ctgatgtcgg cggctacaat 1980

tacgtgtcct ggtatcagca gcaccccggc aaggccccta agctgatgat ctacgacgtg 2040

tccaacagac ccagcggcgt gtccaataga ttctccggca gcaagagcgg caacaccgcc 2100

agcctgacaa ttagcggact gcaggccgag gacgaggccg attactactg tagcagctac 2160

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aaggccggtg gaggtgggtc tggaggggt ggatctggag gtggcggatc ggaggtgcag 2280

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ggccttgaat gggtgtccag catctatccc agcggcggca tcacctttta cgccgacaca 2460

gtgaagggca gattcaccat cagccgggac aacagcaaga acaccctgta cctgcagatg 2520

aacagcctga gagccgagga caccgccgtg tactactgcg ccagaatcaa gctgggcacc 2580

gtgaccaccg tggattattg gggacagggc accctggtca ccgtgtcatc t 2631

<210> 116
<211> 608
<212> PRT
<213> Artificial Sequence

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

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<222> (1)..(1)
<223> Any amino acid

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<223> Any amino acid

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<400> 116
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1   5   10   15

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            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
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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 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
```

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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
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<210> 117
<211> 608
<212> PRT
<213> Artificial Sequence

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

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<222> (1)..(2)

<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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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

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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
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```
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
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<210> 118
<211> 1140
<212> DNA
<213> Artificial Sequence

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

<400> 118

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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
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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

<210> 119
<211> 380
<212> PRT
<213> Artificial Sequence

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

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<222> (6)..(6)
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<222> (9)..(9)
<223> Any amino acid

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<222> (126)..(126)
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<222> (270)..(270)
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<222> (301)..(302)
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Xaa Ala Ser Leu Pro Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
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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 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

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                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
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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> 120
<211> 380
<212> PRT
<213> Artificial Sequence

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


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<220>
<221> MOD_RES
<222> (365)..(365)
<223> Any amino acid

<400> 120
Xaa Xaa Ser Xaa Xaa Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
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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 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

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    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> 121
<211> 5
<212> PRT
<213> Artificial Sequence

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

<400> 121
Gly Gly Gly Gly Ser
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1 5

<210> 122
<211> 612
<212> PRT
<213> Artificial Sequence

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

<400> 122
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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
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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
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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 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> 124
<211> 450
<212> PRT
<213> Artificial Sequence

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

<400> 124
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala Asp Thr Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu 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 Asn 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> 125
<211> 250
<212> PRT
<213> Artificial Sequence

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

<400> 125

```
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1               5                   10                  15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
            20                  25                  30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
    50                  55                  60
```

```
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Ser
                85                  90                  95

Ser Thr Arg Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Gln
            100                 105                 110

Pro Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

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

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
145                 150                 155                 160

Ser Tyr Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Val Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala Asp
            180                 185                 190

Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
        195                 200                 205

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
    210                 215                 220

Tyr Cys Ala Arg Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr Trp
225                 230                 235                 240

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
                245                 250


<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

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> 8
<212> PRT
<213> Artificial Sequence

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

<400> 129
Gly His Ala Phe Thr Ser Asp Ser
1 5

<210> 130
<211> 8
<212> PRT
<213> Artificial Sequence

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

<400> 130
Ile Tyr Pro Arg Ser Gly Asn Pro
1 5

<210> 131
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 131
Asp Tyr Tyr Gly Arg Tyr Phe Asp Val
1 5

<210> 132
<211> 118
<212> PRT
<213> Artificial Sequence

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

<400> 132
Glu Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala

1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly His Ala Phe Thr Ser Asp
20 25 30

Ser Ile Asn Trp Val Lys Gln Arg Ile Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Tyr Pro Arg Ser Gly Asn Pro Tyr Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Thr Asp Tyr Tyr Gly Arg Tyr Phe Asp Val Trp Gly Thr Gly Thr
100 105 110

Thr Val Thr Val Ser Ser
115

<210> 133
<211> 6
<212> PRT
<213> Artificial Sequence

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

<400> 133
Glu Asp Ile Tyr Asn Arg
1 5

<210> 134
<211> 3
<212> PRT
<213> Artificial Sequence

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

<400> 134
Gly Ala Thr
1

<210> 135
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 135
Gln Gln Tyr Trp Ser Thr Pro Trp Thr
1 5

<210> 136
<211> 107
<212> PRT
<213> Artificial Sequence

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

<400> 136
Asp Ile Gln Met Thr Gln Ser Ser Phe Ser Phe Ser Val Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ile Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg
20 25 30

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

Ser Gly Ala Thr Ser Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Lys Asp Tyr Thr Leu Ser Ile Thr Ser Leu Gln Thr
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ser Thr Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 137
<211> 8
<212> PRT
<213> Artificial Sequence

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

<400> 137
Gly Tyr Ser Phe Thr Asp Tyr Tyr
1 5

<210> 138
<211> 8
<212> PRT
<213> Artificial Sequence

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

<400> 138
Ile Tyr Pro Gly Ser Gly Asn Thr
1 5

<210> 139
<211> 12
<212> PRT
<213> Artificial Sequence

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

<400> 139
Ser Tyr Tyr Tyr Gly Ser Ser Tyr Leu Phe Asp Tyr
1 5 10

<210> 140
<211> 121
<212> PRT
<213> Artificial Sequence

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

<400> 140
Glu Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Ala Arg Ile Tyr Pro Gly Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Glu Lys Ser Ser Ile Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Ser Tyr Tyr Tyr Gly Ser Ser Tyr Leu Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 141
<211> 6
<212> PRT
<213> Artificial Sequence

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

<400> 141
Gln Ser Ile Gly Thr Ser
1 5

<210> 142
<211> 3
<212> PRT
<213> Artificial Sequence

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

peptide

<400> 142
Tyr Ala Ser
1

<210> 143
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 143
Gln Gln Ser Asn Asn Trp Pro Phe Thr
1 5

<210> 144
<211> 107
<212> PRT
<213> Artificial Sequence

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

<400> 144
Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Ser
20 25 30

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser
65 70 75 80

Glu Asp Ile Gly Asp Tyr Tyr Cys Gln Gln Ser Asn Asn Trp Pro Phe
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 145
<211> 8
<212> PRT
<213> Artificial Sequence

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

<400> 145
Gly Tyr Thr Phe Thr Asp Tyr Tyr
1 5

<210> 146
<211> 8
<212> PRT
<213> Artificial Sequence

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

<400> 146
Ile Asn Pro Asn Asn Gly Tyr Thr
1 5

<210> 147
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 147
Ser Ala Ala Tyr Tyr Val Leu Asp Asp
1 5

<210> 148
<211> 118
<212> PRT
<213> Artificial Sequence

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

polypeptide

<400> 148
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Leu Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Lys Ser His Gly Arg Ser Leu Glu Trp Ile
35 40 45

Gly Asp Ile Asn Pro Asn Asn Gly Tyr Thr Asn Tyr Asn Gln Asn Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Ala Ala Tyr Tyr Val Leu Asp Asp Trp Gly Gln Gly Thr
100 105 110

Ser Val Thr Val Ser Ser
115

<210> 149
<211> 11
<212> PRT
<213> Artificial Sequence

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

<400> 149
Lys Lys Val Thr Ile Phe Gly Ser Ile Ser Val
1 5 10

<210> 150
<211> 3
<212> PRT
<213> Artificial Sequence

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

<400> 150
Asn Gly Ala
1

<210> 151
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 151
Leu Gln Asn Lys Glu Val Pro Tyr Thr
1 5

<210> 152
<211> 119
<212> PRT
<213> Artificial Sequence

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

<400> 152
Asp Ile Val Met Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Lys Ala Thr Ile Ser Cys Lys Ala Ser Lys Lys Val Thr Ile Phe
20 25 30

Gly Ser Ile Ser Val Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro
35 40 45

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

Arg Phe Ser Asp Ser Gly Ser Gln Asn Arg Ser Pro Phe Gly Asn Gln
65 70 75 80

Leu Asn Phe Thr Leu Thr Ile Asp Pro Val Glu Ala Asp Asp Ala Ala

85 90 95

Thr Tyr Tyr Cys Leu Gln Asn Lys Glu Val Pro Tyr Thr Phe Gly Gly
100 105 110

Gly Thr Glu Leu Glu Ile Lys
115

<210> 153
<211> 8
<212> PRT
<213> Artificial Sequence

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

<400> 153
Gly Asp Ser Ile Thr Ser Gly Tyr
1 5

<210> 154
<211> 7
<212> PRT
<213> Artificial Sequence

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

<400> 154
Ile Ser Tyr Thr Gly Ser Thr
1 5

<210> 155
<211> 10
<212> PRT
<213> Artificial Sequence

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

<400> 155
Gln Gly Gly Trp Leu Gln Ala Met Asp Tyr
1 5 10

<210> 156

<211> 118
<212> PRT
<213> Artificial Sequence

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

<400> 156
Glu Val Gln Leu Gln Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly
20 25 30

Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr Met
35 40 45

Gly Tyr Ile Ser Tyr Thr Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys
50 55 60

Arg Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Tyr Leu
65 70 75 80

Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

Ser Gln Gly Gly Trp Leu Gln Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Ser Val Thr Val Ser Ser
115

<210> 157
<211> 12
<212> PRT
<213> Artificial Sequence

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

<400> 157
Gln Ser Leu Leu Tyr Ser Ser Asn Gln Lys Asn Ser
1 5 10

<210> 158
<211> 3
<212> PRT
<213> Artificial Sequence

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

<400> 158
Trp Ala Ser
1

<210> 159
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 159
Gln Gln Tyr Tyr Gly Tyr Pro Trp Thr
1 5

<210> 160
<211> 113
<212> PRT
<213> Artificial Sequence

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

<400> 160
Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

Ser Asn Gln Lys Asn Ser Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

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

Ile Ser Ser Val Lys Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Gly Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 161
<211> 8
<212> PRT
<213> Mus musculus

<400> 161
Gly Phe Asn Ile Lys Asp Thr Tyr
1 5

<210> 162
<211> 8
<212> PRT
<213> Mus musculus

<400> 162
Ile Asp Pro Ala Asn Asp Asn Thr
1 5

<210> 163
<211> 11
<212> PRT
<213> Mus musculus

<400> 163
Glu Gly Tyr Gly Gly Ser Tyr Gly Glu Gly Tyr
1 5 10

<210> 164
<211> 120
<212> PRT
<213> Mus musculus

<400> 164
Glu Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Val Lys Pro Gly Ala

1 5 10 15

Ser Val Thr Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Ala Asn Asp Asn Thr Lys Tyr Asp Pro Lys Phe
50 55 60

Gln Asp Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asp Thr Ala Tyr
65 70 75 80

Leu Arg Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Tyr Gly Gly Ser Tyr Gly Glu Gly Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 165
<211> 6
<212> PRT
<213> Artificial Sequence

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

<400> 165
Gln Ser Val Ser Asn Asp
1 5

<210> 166
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 166
Gln Gln Asp Tyr Asn Ser Pro Trp Thr
1 5

<210> 167
<211> 107
<212> PRT
<213> Mus musculus

<400> 167
Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Ser Asn Asp
20 25 30

Val Ile Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Tyr Ala Ser Ile Arg Phe Thr Gly Val Pro Asp Arg Phe Ala Gly
50 55 60

Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Asn Thr Val Gln Ala
65 70 75 80

Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Asn Ser Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 168
<211> 8
<212> PRT
<213> Artificial Sequence

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

<400> 168
Ile Asp Pro Ala Asn Gly Asn Thr
1 5

<210> 169

<211> 14
<212> PRT
<213> Artificial Sequence

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

<400> 169
Pro Phe Asn Tyr Arg Phe Tyr Asp Val Tyr Tyr Phe Asp Tyr
1 5 10

<210> 170
<211> 123
<212> PRT
<213> Artificial Sequence

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

<400> 170
Glu Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Tyr Asp Pro Lys Phe
50 55 60

Pro Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Ala Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Phe Asn Tyr Arg Phe Tyr Asp Val Tyr Tyr Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Thr
115 120

<210> 171
<211> 5
<212> PRT
<213> Artificial Sequence

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

<400> 171
Ser Ser Val Ser Tyr
1 5

<210> 172
<211> 3
<212> PRT
<213> Artificial Sequence

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

<400> 172
Asp Thr Ser
1

<210> 173
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 173
Gln Gln Trp Ser Thr Tyr Pro Leu Thr
1 5

<210> 174
<211> 106
<212> PRT
<213> Artificial Sequence

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

<400> 174
Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly

1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Arg Leu Leu Ile Tyr
35 40 45

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

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

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Thr Tyr Pro Leu Thr
85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 175
<211> 8
<212> PRT
<213> Artificial Sequence

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

<400> 175
Gly Tyr Thr Phe Thr Ser Tyr Val
1 5

<210> 176
<211> 8
<212> PRT
<213> Artificial Sequence

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

<400> 176
Ile Asn Pro Tyr Asn Asp Gly Ser
1 5

<210> 177
<211> 5
<212> PRT
<213> Artificial Sequence

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

<400> 177
Gln Thr Leu Asp Phe
1 5

<210> 178
<211> 114
<212> PRT
<213> Artificial Sequence

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

<400> 178
Glu Val Gln Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Thr
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Val Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

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

Lys Gly Lys Ala Thr Leu Thr Ser Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Gln Thr Leu Asp Phe Trp Gly Gln Gly Thr Ser Val Thr Val
100 105 110

Ser Thr

<210> 179
<211> 10
<212> PRT
<213> Artificial Sequence

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

<400> 179
Glu Ser Val Glu Phe Tyr Gly Thr Thr Leu
1 5 10

<210> 180
<211> 3
<212> PRT
<213> Artificial Sequence

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

<400> 180
Ala Ala Ser
1

<210> 181
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 181
Gln Gln Ser Arg Lys Val Pro Tyr Thr
1 5

<210> 182
<211> 111
<212> PRT
<213> Artificial Sequence

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

<400> 182
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Glu Phe Tyr
20 25 30

Gly Thr Thr Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
65 70 75 80

Pro Val Glu Glu Gly Asp Ile Gly Met Tyr Phe Cys Gln Gln Ser Arg
85 90 95

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

<210> 183
<211> 10
<212> PRT
<213> Artificial Sequence

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

<400> 183
Gly Phe Ser Leu Ser Thr Tyr Gly Leu Gly
1 5 10

<210> 184
<211> 7
<212> PRT
<213> Artificial Sequence

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

<400> 184
Ile Trp Trp Asn Asp Asp Lys

1 5

<210> 185
<211> 13
<212> PRT
<213> Artificial Sequence

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

<400> 185
Thr Leu His Tyr Tyr Asp Gly Ile Ala Trp Phe Ala Tyr
1 5 10

<210> 186
<211> 123
<212> PRT
<213> Artificial Sequence

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

<400> 186
Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Tyr
20 25 30

Gly Leu Gly Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Gly Leu Glu
35 40 45

Trp Leu Ala Asn Ile Trp Trp Asn Asp Asp Lys Phe Tyr Asp Ser Val
50 55 60

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

Phe Leu Lys Ile Ser Ser Val Asp Thr Ser Glu Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Gln Thr Leu His Tyr Tyr Asp Gly Ile Ala Trp Phe Ala Tyr
100 105 110

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

<210> 187
<211> 6
<212> PRT
<213> Artificial Sequence

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

<400> 187
His Tyr Val Gly Thr Phe
1 5

<210> 188
<211> 3
<212> PRT
<213> Artificial Sequence

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

<400> 188
Ser Thr Ser
1

<210> 189
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 189
Gln Gln Tyr Tyr Asn Ser Pro Leu Thr
1 5

<210> 190
<211> 107
<212> PRT
<213> Artificial Sequence

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

polypeptide

<400> 190
Asp Ile Val Met Thr Gln Ser Gln Asn Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Val Thr Cys Lys Ala Ser His Tyr Val Gly Thr Phe
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
35 40 45

Phe Ser Thr Ser Tyr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Tyr Asn Ser Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 191
<211> 8
<212> PRT
<213> Artificial Sequence

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

<400> 191
Gly Tyr Thr Phe Thr Ser Asn Trp
1 5

<210> 192
<211> 8
<212> PRT
<213> Artificial Sequence

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

<400> 192
Ile His Pro Ser Asp Ser Glu Thr
1 5

<210> 193
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 193
Ser Ser Gly Asp Tyr Gly Arg Asp Tyr
1 5

<210> 194
<211> 118
<212> PRT
<213> Artificial Sequence

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

<400> 194
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Asn
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile His Pro Ser Asp Ser Glu Thr His Tyr His Gln Lys Phe
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala His Ser Ser Gly Asp Tyr Gly Arg Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Thr Leu Thr Val Ser Ser
115

<210> 195
<211> 10
<212> PRT
<213> Artificial Sequence

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

<400> 195
Glu Ser Val Asp Ser Tyr Gly Asn Ser Phe
1 5 10

<210> 196
<211> 3
<212> PRT
<213> Artificial Sequence

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

<400> 196
Leu Ala Ser
1

<210> 197
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 197
Gln Gln Asn Asn Glu Asp Pro Trp Thr
1 5

<210> 198
<211> 111
<212> PRT
<213> Artificial Sequence

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

<400> 198
Asn Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr
20 25 30

Gly Asn Ser Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Gln Ser Gly Val Pro Ala
50 55 60

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

Pro Val Glu Ala Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Asn
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 199
<211> 120
<212> PRT
<213> Artificial Sequence

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

<400> 199
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Met His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

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

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

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Gly Tyr Gly Gly Ser Tyr Gly Glu Gly Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 200
<211> 107
<212> PRT
<213> Artificial Sequence

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

<400> 200

```
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Asp
            20                  25                  30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45

Tyr Tyr Ala Ser Ile Arg Phe Thr Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asp Tyr Asn Ser Pro Trp
                85                  90                  95
```

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 201
<211> 107
<212> PRT
<213> Artificial Sequence

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

<400> 201
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Asp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Tyr Ala Ser Ile Arg Phe Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asp Tyr Asn Ser Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 202
<211> 107
<212> PRT
<213> Artificial Sequence

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

<400> 202
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly

1 5 10 15

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Asp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Tyr Ala Ser Ile Arg Phe Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Asp Tyr Asn Ser Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 203
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 203
Gln Gln Asp Tyr Thr Ser Pro Trp Thr
1 5

<210> 204
<211> 107
<212> PRT
<213> Artificial Sequence

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

<400> 204
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Asp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Tyr Ala Ser Ile Arg Phe Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asp Tyr Thr Ser Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 205
<211> 214
<212> PRT
<213> Artificial Sequence

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

<400> 205
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Asp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Tyr Ala Ser Ile Arg Phe Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

```
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asp Tyr Thr Ser Pro Trp
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

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

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

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

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

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

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 206
<211> 450
<212> PRT
<213> Artificial Sequence

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

<400> 206

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

Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Asn Ile Lys Asp Thr
            20                  25                  30
```

```
Tyr Met His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
        35                  40                  45

Gly Leu Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Ala Glu Lys Phe
    50                  55                  60

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

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Gly Tyr Gly Gly Ser Tyr Gly Glu Gly Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu 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

Tyr 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 Tyr 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> 207
<211> 612
<212> PRT
<213> Artificial Sequence

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

<400> 207
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 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 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> 208
<211> 642
<212> DNA
<213> Artificial Sequence

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

<400> 208
gaaattgtga tgacacagag ccctccaacg ctgagcctgt ctcctggcga aagagtgacc 60

ctgagctgta gagccagcca gagcgtgtcc aacgacctga gctggtatca gcagaagcct 120

ggacaggccc ctcggctgct gatctactac gccagcatca gattcacagg catccccgcc 180

agattttccg gcagcggctc tggcacagat ttcaccctga ccataagcag cctgcagcct 240

gaggacttcg ccgtgtacta ctgtcagcag gactacacta gcccctggac ctttggccag 300

ggcaccaagg tggaaatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 209
<211> 1350
<212> DNA
<213> Artificial Sequence

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

<400> 209
gaggtgcagc tggttcagtc tggcgccgaa gtgaaaaagc ctggcgccac cgtgaagatc 60

agctgcaagg tgtccggctt caacatcaag gacacctaca tgcactgggt gcagcaggcc 120

cctggcaaag gacttgaatg gatgggcctg atcgaccccg ccaacgacaa taccatctac 180

gccgagaagt tccagggcag agtgaccatc accgccgaca cctctaccga caccgcctac 240

atggaactga gcagcctgag aagcgaggac accgccgtgt actactgtgc cagagaaggc 300

tacggcggca gctacggcga aggatattgg ggacagggca ccctggtcac cgttagctct 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 ccggaccccct 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 cctgtactgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc taagcttgtc tccgggtaaa 1350

<210> 210
<211> 1836
<212> DNA
<213> Artificial Sequence

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

<400> 210
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

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 ctcaccagca agctcaccgt ggacaagagc 1740

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1800

tacacgcaga agagcctctc cctgtctccg ggtaaa 1836

<210> 211
<211> 612
<212> PRT
<213> Artificial Sequence

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

<400> 211
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
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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 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> 212
<211> 1836
<212> DNA
<213> Artificial Sequence

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

<400> 212
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 acctgcctgg tcaaaggctt ctatcccagc 1620

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680

cccgtgctgg actccgacgg ctccttcttc ctcaccagca agctcaccgt ggacaagagc 1740

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1800

tacacgcaga agagcctctc cctgtctccg ggtaaa 1836

<210> 213
<211> 450
<212> PRT
<213> Artificial Sequence

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

<400> 213
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Met His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Leu Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Ala Glu Lys Phe
50 55 60

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

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Gly Tyr Gly Gly Ser Tyr Gly Glu Gly Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu 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
```

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        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> 214
<211> 612
<212> PRT
<213> Artificial Sequence

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

polypeptide

<400> 214

```
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 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> 215
<211> 1350
<212> DNA

<213> Artificial Sequence

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

<400> 215
gaggtgcagc tggttcagtc tggcgccgaa gtgaaaaagc ctggcgccac cgtgaagatc 60

agctgcaagg tgtccggctt caacatcaag gacacctaca tgcactgggt gcagcaggcc 120

cctggcaaag gacttgaatg gatgggcctg atcgaccccg ccaacgacaa taccatctac 180

gccgagaagt tccagggcag agtgaccatc accgccgaca cctctaccga caccgcctac 240

atggaactga gcagcctgag aagcgaggac accgccgtgt actactgtgc cagagaaggc 300

tacggcggca gctacggcga aggatattgg ggacagggca ccctggtcac cgttagctct 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 tgccccatc 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> 216
<211> 1836
<212> DNA
<213> Artificial Sequence

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

<400> 216
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> 217
<211> 612
<212> PRT
<213> Artificial Sequence

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

<400> 217
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 Ala Asn 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 Arg 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> 218
<211> 1836
<212> DNA
<213> Artificial Sequence

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

<400> 218
gatgcatctc tgccttacct gcaggatgaa 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 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 ggcgaatcag 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

gagatccgtt tccgtatgtt 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> 219
<211> 612
<212> PRT
<213> Artificial Sequence

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

<400> 219
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> 220
<211> 1836
<212> DNA
<213> Artificial Sequence

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

<400> 220
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> 221
<211> 330
<212> PRT
<213> Homo sapiens

<400> 221
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> 222
<211> 330
<212> PRT
<213> Homo sapiens

<400> 222
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> 223
<211> 330
<212> PRT
<213> Homo sapiens

<400> 223
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> 224
<211> 330
<212> PRT
<213> Homo sapiens

<400> 224
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> 225
<211> 330
<212> PRT
<213> Homo sapiens

<400> 225
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> 226
<211> 330
<212> PRT
<213> Homo sapiens

<400> 226

```
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> 227
<211> 330
<212> PRT
<213> Homo sapiens

<400> 227
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 Asp Glu
225 230 235 240

Leu 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> 228
<211> 326
<212> PRT
<213> Homo sapiens

<400> 228
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg

```
1               5                   10                  15

Ser Thr Ser Glu Ser 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 Asn Phe Gly Thr Gln Thr
65                  70                  75                  80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        115                 120                 125

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    130                 135                 140

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145                 150                 155                 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
                165                 170                 175

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
            180                 185                 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
        195                 200                 205

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
    210                 215                 220
```

```
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225                 230                 235                 240


Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                245                 250                 255


Ser Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            260                 265                 270


Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
        275                 280                 285


Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    290                 295                 300


Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305                 310                 315                 320


Ser Leu Ser Pro Gly Lys
                325


<210> 229
<211> 377
<212> PRT
<213> Homo sapiens

<400> 229
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
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 Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
            100                 105                 110

Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
        115                 120                 125

Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
    130                 135                 140

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
145                 150                 155                 160

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                165                 170                 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            180                 185                 190

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
        195                 200                 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    210                 215                 220

Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
225                 230                 235                 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                245                 250                 255

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        275                 280                 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
```

```
    290                 295                 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
305                 310                 315                 320

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
                325                 330                 335

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

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
        355                 360                 365

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    370                 375


<210> 230
<211> 327
<212> PRT
<213> Homo sapiens

<400> 230
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1               5                   10                  15

Ser Thr Ser Glu Ser 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 Lys Thr
65                  70                  75                  80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
```

```
            100                 105                 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115                 120                 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    130                 135                 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145                 150                 155                 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165                 170                 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195                 200                 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225                 230                 235                 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275                 280                 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
    290                 295                 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305                 310                 315                 320
```

Leu Ser Leu Ser Leu Gly Lys
325

<210> 231
<211> 106
<212> PRT
<213> Homo sapiens

<400> 231
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
20 25 30

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 232
<211> 107
<212> PRT
<213> Homo sapiens

<400> 232
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln

```
        35                  40                  45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
    50                  55                  60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65                  70                  75                  80

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            100                 105


<210> 233
<211> 105
<212> PRT
<213> Homo sapiens

<400> 233
Gly Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser
1               5                   10                  15

Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
            20                  25                  30

Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro
        35                  40                  45

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

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
65                  70                  75                  80

Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
                85                  90                  95

Glu Lys Thr Val Ala Pro Thr Glu Cys
            100                 105


<210> 234
```

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

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

<400> 234
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


<210> 235
<211> 450
<212> PRT
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<213> Artificial Sequence

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

<400> 235
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Val Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Met His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Leu Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Ala Glu Lys Phe
50 55 60

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

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Tyr Gly Gly Ser Tyr Gly Glu Gly Tyr Trp Gly Gln
100 105 110

Gly Thr Leu 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 Asn 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 Tyr 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> 236
<211> 120
<212> PRT
<213> Artificial Sequence

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

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Gln or Val

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Glu or Gln

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Leu or Val

<220>
<221> MOD_RES
<222> (12)..(12)
<223> Val or Lys

<220>
<221> MOD_RES
<222> (17)..(17)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (19)..(19)
<223> Thr or Lys

<220>
<221> MOD_RES
<222> (20)..(20)
<223> Leu or Ile

<220>
<221> MOD_RES
<222> (23)..(23)
<223> Thr or Lys

<220>
<221> MOD_RES
<222> (24)..(24)
<223> Ala or Val

<220>
<221> MOD_RES
<222> (38)..(38)
<223> Lys or Gln

<220>
<221> MOD_RES
<222> (40)..(40)
<223> Arg or Ala

<220>
<221> MOD_RES
<222> (42)..(42)
<223> Glu or Gly

<220>
<221> MOD_RES
<222> (43)..(43)
<223> Gln or Lys

<220>
<221> MOD_RES
<222> (48)..(48)
<223> Ile or Met

<220>
<221> MOD_RES
<222> (50)..(50)
<223> Arg or Leu

<220>
<221> MOD_RES
<222> (59)..(59)
<223> Lys or Ile

<220>
<221> MOD_RES
<222> (61)..(61)

<223> Asp or Ala

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Pro or Glu

<220>
<221> MOD_RES
<222> (66)..(66)
<223> Asp or Gly

<220>
<221> MOD_RES
<222> (67)..(67)
<223> Lys or Arg

<220>
<221> MOD_RES
<222> (68)..(68)
<223> Ala or Val

<220>
<221> MOD_RES
<222> (76)..(76)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (81)..(81)
<223> Leu or Met

<220>
<221> MOD_RES
<222> (82)..(82)
<223> Arg or Glu

<220>
<221> MOD_RES
<222> (87)..(87)
<223> Thr or Arg

<220>
<221> MOD_RES
<222> (115)..(115)
<223> Thr or Leu

<220>
<221> MOD_RES
<222> (116)..(116)
<223> Leu or Val

<400> 236
Glu Val Gln Leu Xaa Xaa Ser Gly Ala Glu Xaa Xaa Lys Pro Gly Ala

1 5 10 15

Xaa Val Xaa Xaa Ser Cys Xaa Xaa Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Met His Trp Val Xaa Gln Xaa Pro Xaa Xaa Gly Leu Glu Trp Xaa
35 40 45

Gly Xaa Ile Asp Pro Ala Asn Asp Asn Thr Xaa Tyr Xaa Xaa Lys Phe
50 55 60

Gln Xaa Xaa Xaa Thr Ile Thr Ala Asp Thr Ser Xaa Asp Thr Ala Tyr
65 70 75 80

Xaa Xaa Leu Ser Ser Leu Xaa Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Tyr Gly Gly Ser Tyr Gly Glu Gly Tyr Trp Gly Gln
100 105 110

Gly Thr Xaa Xaa Thr Val Ser Ser
115 120

<210> 237
<211> 107
<212> PRT
<213> Artificial Sequence

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

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Ser or Glu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Thr or Ser

<220>
<221> MOD_RES
<222> (9)..(9)

<223> Lys or Pro

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Phe or Thr

<220>
<221> MOD_RES
<222> (12)..(12)
<223> Leu or Ser

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Val or Leu

<220>
<221> MOD_RES
<222> (15)..(15)
<223> Ala or Pro

<220>
<221> MOD_RES
<222> (17)..(17)
<223> Asp or Glu

<220>
<221> MOD_RES
<222> (21)..(21)
<223> Ile or Leu

<220>
<221> MOD_RES
<222> (22)..(22)
<223> Thr or Ser

<220>
<221> MOD_RES
<222> (24)..(24)
<223> Lys or Arg

<220>
<221> MOD_RES
<222> (33)..(33)
<223> Val or Leu

<220>
<221> MOD_RES
<222> (34)..(34)
<223> Ile or Ser

<220>
<221> MOD_RES

<222> (43)..(43)
<223> Ser or Ala

<220>
<221> MOD_RES
<222> (45)..(45)
<223> Lys or Arg

<220>
<221> MOD_RES
<222> (58)..(58)
<223> Val or Ile

<220>
<221> MOD_RES
<222> (60)..(60)
<223> Asp or Ala

<220>
<221> MOD_RES
<222> (63)..(63)
<223> Ala or Ser

<220>
<221> MOD_RES
<222> (67)..(67)
<223> Tyr or Ser

<220>
<221> MOD_RES
<222> (73)..(73)
<223> Phe or Leu

<220>
<221> MOD_RES
<222> (76)..(76)
<223> Asn or Ser

<220>
<221> MOD_RES
<222> (77)..(77)
<223> Thr or Ser

<220>
<221> MOD_RES
<222> (78)..(78)
<223> Val or Leu

<220>
<221> MOD_RES
<222> (80)..(80)
<223> Ala or Pro

<220>

<221> MOD_RES
<222> (83)..(83)
<223> Leu or Phe

<220>
<221> MOD_RES
<222> (87)..(87)
<223> Phe or Tyr

<220>
<221> MOD_RES
<222> (93)..(93)
<223> Tyr or Thr

<220>
<221> MOD_RES
<222> (100)..(100)
<223> Gly or Gln

<220>
<221> MOD_RES
<222> (104)..(104)
<223> Leu or Val

<400> 237
Xaa Ile Val Met Thr Gln Xaa Pro Xaa Xaa Leu Xaa Xaa Ser Xaa Gly
1 5 10 15

Xaa Arg Val Thr Xaa Xaa Cys Xaa Ala Ser Gln Ser Val Ser Asn Asp
20 25 30

Xaa Xaa Trp Tyr Gln Gln Lys Pro Gly Gln Xaa Pro Xaa Leu Leu Ile
35 40 45

Tyr Tyr Ala Ser Ile Arg Phe Thr Gly Xaa Pro Xaa Arg Phe Xaa Gly
50 55 60

Ser Gly Xaa Gly Thr Asp Phe Thr Xaa Thr Ile Xaa Xaa Xaa Gln Xaa
65 70 75 80

Glu Asp Xaa Ala Val Tyr Xaa Cys Gln Gln Asp Tyr Xaa Ser Pro Trp
85 90 95

Thr Phe Gly Xaa Gly Thr Lys Xaa Glu Ile Lys
100 105

<210> 238

<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> 238
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> 239
<211> 380
<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> (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> 239
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

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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
    370                 375                 380
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<210> 240
<211> 617
<212> PRT
<213> Artificial Sequence

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

<220>
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<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> 240
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
```

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        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
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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> 241
<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> 241
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
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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 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> 242
<211> 107
<212> PRT
<213> Artificial Sequence

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

<400> 242
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Asp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Tyr Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asp Tyr Asn Ser Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 243
<211> 107
<212> PRT
<213> Artificial Sequence

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

<400> 243
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Asp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Tyr Ala Ser Ile Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asp Tyr Asn Ser Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 244
<211> 107
<212> PRT
<213> Artificial Sequence

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

<400> 244
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Asp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Tyr Ala Ser Thr Arg Phe Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asp Tyr Asn Ser Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 245
<211> 107
<212> PRT
<213> Artificial Sequence

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

<400> 245
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Asp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Tyr Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asp Tyr Asn Ser Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 246
<211> 107
<212> PRT
<213> Artificial Sequence

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

<400> 246
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Asp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Tyr Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Asp Tyr Asn Ser Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 247
<211> 107
<212> PRT
<213> Artificial Sequence

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

polypeptide

<400> 247
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Asp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Tyr Ala Ser Ile Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asp Tyr Asn Ser Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 248
<211> 107
<212> PRT
<213> Artificial Sequence

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

<400> 248
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Asp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Tyr Ala Ser Ile Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly

```
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Asp Tyr Asn Ser Pro Trp
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105

<210> 249
<211> 107
<212> PRT
<213> Artificial Sequence

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

<400> 249
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Asp
            20                  25                  30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45

Tyr Tyr Ala Ser Ile Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60

Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Asp Tyr Asn Ser Pro Trp
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105

<210> 250
```

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

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

<400> 250
Asp Thr Tyr Met His
1 5

<210> 251
<211> 17
<212> PRT
<213> Artificial Sequence

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

<400> 251
Arg Ile Asp Pro Ala Asn Asp Asn Thr Lys Tyr Asp Pro Lys Phe Gln
1 5 10 15

Asp

<210> 252
<211> 17
<212> PRT
<213> Artificial Sequence

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

<400> 252
Leu Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Ala Glu Lys Phe Gln
1 5 10 15

Gly

<210> 253
<211> 11
<212> PRT
<213> Artificial Sequence

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

<400> 253
Lys Ala Ser Gln Ser Val Ser Asn Asp Val Ile
1 5 10

<210> 254
<211> 7
<212> PRT
<213> Artificial Sequence

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

<400> 254
Tyr Ala Ser Ile Arg Phe Thr
1 5

<210> 255
<211> 11
<212> PRT
<213> Artificial Sequence

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

<400> 255
Arg Ala Ser Gln Ser Val Ser Asn Asp Leu Ser
1 5 10

<210> 256
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic 10xHis tag

<400> 256
His His His His His His His His His His
1 5 10

<210> 257
<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> 257
Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly Gly Pro
1 5 10 15

<210> 258
<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> 258
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> 259
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
6xHis tag

<400> 259
His His His His His His

1 5