SEQUENCE LISTING

<110> UCB BIOPHARMA sprl

<120> Tau-binding antibodies

<130> PF0032-WO

<160> 57

<170> PatentIn version 3.5

<210> 1
<211> 16
<212> PRT
<213> Rattus norvegicus

<400> 1

Arg Ser Ser Gln Ser Leu Glu Tyr Ser Asp Gly Tyr Thr Tyr Leu Glu
1 5 10 15

<210> 2
<211> 7
<212> PRT
<213> Rattus norvegicus

<400> 2

Glu Val Ser Asn Arg Phe Ser
1 5

<210> 3
<211> 9
<212> PRT
<213> Rattus norvegicus

<400> 3

Phe Gln Ala Thr His Asn Pro Tyr Thr
1 5

<210> 4
<211> 10
<212> PRT
<213> Rattus norvegicus

<400> 4

Gly Phe Ser Leu Thr Ser Asn Asp Ile Ala
1 5 10

<210> 5
<211> 16
<212> PRT
<213> Rattus norvegicus

<220>
<221> misc_feature
<222> (12)..(12)
<223> Xaa can be Ser, Ala, Thr

<400> 5

```
Thr Ile Trp Thr Asp Gly Ser Thr Asn Tyr Asn Xaa Ala Val Gln Ser
1               5                   10                  15


<210>  6
<211>  10
<212>  PRT
<213>  Rattus norvegicus

<400>  6

His Arg Leu Tyr Tyr Gly Ala Phe Asp Tyr
1               5                   10


<210>  7
<211>  112
<212>  PRT
<213>  Rattus norvegicus

<400>  7

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


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


Asp Gly Tyr Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45


Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60


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


Ser Arg Val Glu Pro Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Ala
                85                  90                  95


Thr His Asn Pro Tyr Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210>  8
<211>  117
<212>  PRT
<213>  Rattus norvegicus

<400>  8

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


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asn
            20                  25                  30


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

```
Gly Thr Ile Trp Thr Asp Gly Ser Thr Asn Tyr Asn Ser Ala Val Gln
    50                  55                  60

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

Lys Met Asn Ser Leu Gln Pro Glu Asp Thr Gly Thr Tyr Tyr Cys Ala
                85                  90                  95

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

Met Val Thr Val Ser
        115


<210>  9
<211>  112
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  humanized

<400>  9

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Glu Tyr Ser
            20                  25                  30

Asp Gly Tyr Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Ala
                85                  90                  95

Thr His Asn Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210>  10
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  humanized
```

<220>
<221> MISC_FEATURE
<222> (48)..(48)
<223> Xaa can be Ile and Met

<220>
<221> MISC_FEATURE
<222> (61)..(61)
<223> Xaa can be Ser, Ala, Thr

<400> 10

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


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asn
            20                  25                  30


Asp Ile Ala Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Xaa
        35                  40                  45


Gly Thr Ile Trp Thr Asp Gly Ser Thr Asn Tyr Asn Xaa Ala Val Gln
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


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


Met Val Thr Val Ser Ser
        115
```

<210> 11
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized

<400> 11

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


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asn
            20                  25                  30


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


Gly Thr Ile Trp Thr Asp Gly Ser Thr Asn Tyr Asn Ser Ala Val Gln
```

50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

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

Met Val Thr Val Ser Ser
115

<210> 12
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized

<400> 12

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asn
20 25 30

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

Gly Thr Ile Trp Thr Asp Gly Ser Thr Asn Tyr Asn Ala Ala Val Gln
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

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

Met Val Thr Val Ser Ser
115

<210> 13
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized

<400> 13

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asn
20 25 30

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

Gly Thr Ile Trp Thr Asp Gly Ser Thr Asn Tyr Asn Thr Ala Val Gln
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

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

Met Val Thr Val Ser Ser
115

<210> 14
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized

<400> 14

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Glu Tyr Ser
20 25 30

Asp Gly Tyr Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Ala
85 90 95

```
Thr His Asn Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215


<210>  15
<211>  445
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  humanized


<220>
<221>  misc_feature
<222>  (48)..(48)
<223>  Xaa can be Ile or Met

<220>
<221>  misc_feature
<222>  (61)..(61)
<223>  Xaa can be Ser Ala or Thr

<400>  15

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asn
            20                  25                  30

Asp Ile Ala Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Xaa
        35                  40                  45

Gly Thr Ile Trp Thr Asp Gly Ser Thr Asn Tyr Asn Xaa Ala Val Gln
    50                  55                  60
```

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

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

Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

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

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

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335
```

```
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445


<210>  16
<211>  445
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  humanized

<400>  16

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asn
            20                  25                  30

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

Gly Thr Ile Trp Thr Asp Gly Ser Thr Asn Tyr Asn Ser Ala Val Gln
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg His Arg Leu Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110
```

```
Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

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

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

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

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

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380
```

```
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445


<210>  17
<211>  445
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  humanized

<400>  17

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asn
            20                  25                  30

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

Gly Thr Ile Trp Thr Asp Gly Ser Thr Asn Tyr Asn Ala Ala Val Gln
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

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

Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

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

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175
```

```
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

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

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445
```

<210> 18
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized

<400> 18

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asn
            20                  25                  30

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

Gly Thr Ile Trp Thr Asp Gly Ser Thr Asn Tyr Asn Thr Ala Val Gln
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

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

Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

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

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

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
    210                 215                 220
```

```
Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

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

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445


<210>  19
<211>  336
<212>  DNA
<213>  Rattus norvegicus

<400>  19
gatattgtga tgacccagac tccagtttcc ctgtctgtca cacttggaga tcaagcttct       60

atatcttgca ggtctagtca gagcctggaa tatagtgatg gctacactta tttggaatgg      120

tacctacaga agccaggcca gtctcctcag ctcctcatct atgaagtttc caaccgattt      180
```

tctggggtcc cagacaggtt cattggcagt gggtcaggga cagatttcac cctcaagatc 240

agcagagtag agcctgagga cttgggagtt tattactgct tccaagctac acataatccg 300

tacacgtttg gagctgggac caagctggaa ataaaa 336

<210> 20
<211> 354
<212> DNA
<213> Rattus norvegicus

<400> 20
gaggtgaagc tggaggagtc tggacctggc ttgatgcagc cctcagagac cctgtccctc 60

acctgcactg tctctggctt ctcactaacc agcaatgata tagcctgggt tcgacaacct 120

ctaggaaagg gtttggtgtg gatgggaaca atatggactg atggaagtac aaattataat 180

tcagctgtcc aatcccgact gagcatcagc agggacacct ccaagagcca atttttctta 240

aaaatgaaca gtctgcaacc tgaagacaca ggcacttact actgtgccag acatcgccta 300

tactacgggg cctttgatta ctggggccaa ggaaccatgg tcaccgtctc gagt 354

<210> 21
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized

<400> 21
gatatcgtga tgactcagac cccactctca ctgtccgtca ccccgggaca gcccgcgtca 60

atctcgtgta ggagctccca atccctcgaa tactcggacg gctatactta cctggagtgg 120

tacttgcaga agcccggaca gagcccgcag cttctgatct acgaagtgtc caacagattc 180

tccggcgtgc ctgaccgctt ttcggggtcg ggctccggta ctgatttcac cctgaaaatc 240

tcccgggtgg aagccgagga cgtgggagtc tactactgct tccaagccac ccacaaccct 300

tacaccttcg gacaggggac caagctggag atcaag 336

<210> 22
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized

<400> 22
gaggtgcagc tgcaggaatc cggtcccggc ctcgtgaagc cttcagaaac cctgtcgctc 60

acatgcactg tgtccgggtt ctccctgacc tctaacgaca tcgcctggat tcggcagccg 120

ccaggaaagg gactggagtg gatgggcacc atttggaccg acgggtcaac caactacaat 180

gccgcggtgc aatccagagt gaccatcagc gtggacacgt ccaagaacca gttctcgctg 240

aaattgagct ccgtgactgc cgctgatact gccgtgtatt actgtgcccg gcaccgcctt 300

tactacggcg catttgacta ctggggacag ggaaccatgg tcactgtctc gagt 354

<210> 23
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized

<400> 23
gaggtgcaac tgcaggaatc cggtcccggc ctcgtgaagc cttcagaaac cctgtcgctc 60

acatgcactg tgtccgggtt ctccctgacc tctaacgaca tcgcctggat tcggcagccg 120

ccaggaaagg gactggagtg gatgggcacc atttggaccg acgggtcaac caactacaat 180

accgcggtgc aatccagagt gaccatcagc gtggacacgt ccaagaacca gttctcgctg 240

aaattgagct ccgtgactgc cgctgatact gccgtgtatt actgtgcccg gcaccgcctt 300

tactacggcg catttgacta ctggggacag ggaaccatgg tcactgtctc gagt 354

<210> 24
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized

<400> 24
gatatcgtga tgactcagac cccactctca ctgtccgtca ccccgggaca gcccgcgtca 60

atctcgtgta ggagctccca atccctcgaa tactcggacg gctatactta cctggagtgg 120

tacttgcaga agcccggaca gagcccgcag cttctgatct acgaagtgtc caacagattc 180

tccggcgtgc ctgaccgctt ttcggggtcg ggctccggta ctgatttcac cctgaaaatc 240

tcccgggtgg aagccgagga cgtgggagtc tactactgct tccaagccac ccacaaccct 300

tacaccttcg gacaggggac caagctggag atcaagcgga ccgtggccgc tccctccgtg 360

ttcatcttcc caccctccga cgagcagctt aagtccggca ccgcctccgt cgtgtgcctg 420

ctgaacaact tctacccccg cgaggccaag gtgcagtgga aggtggacaa cgccctgcag 480

tccggcaact cccaggaatc cgtcaccgag caggactcca aggacagcac ctactccctg 540

tcctccaccc tgaccctgtc caaggccgac tacgagaagc acaaggtgta cgcctgcgaa 600

gtgacccacc agggcctgtc agccccgtg accaagtcct tcaaccgggg cgagtgc 657

<210> 25
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized

<400> 25
gaggtgcagc tgcaggaatc cggtcccggc ctcgtgaagc cttcagaaac cctgtcgctc 60

acatgcactg tgtccgggtt ctccctgacc tctaacgaca tcgcctggat tcggcagccg 120

ccaggaaagg gactggagtg gatgggcacc atttggaccg acgggtcaac caactacaat 180

gccgcggtgc aatccagagt gaccatcagc gtggacacgt ccaagaacca gttctcgctg 240

aaattgagct ccgtgactgc cgctgatact gccgtgtatt actgtgcccg gcaccgcctt 300

tactacggcg catttgacta ctggggacag ggaaccatgg tcactgtctc gagtgcctcc 360

accaagggcc cctccgtgtt ccctctggcc ccttgctccc ggtccacctc cgagtctacc 420

gccgctctgg gctgcctggt caaggactac ttccccgagc ccgtgacagt gtcctggaac 480

tctggcgccc tgacctccgg cgtgcacacc ttccctgccg tgctgcagtc ctccggcctg 540

tactccctgt cctccgtcgt gaccgtgccc tcctccagcc tgggcaccaa gacctacacc 600

tgtaacgtgg accacaagcc ctccaacacc aaggtggaca agcgggtgga atctaagtac 660

ggccctccct gccccccctg ccctgccct gaatttctgg gcggaccttc cgtgttcctg 720

ttcccccaa agcccaagga caccctgatg atctcccgga cccccgaagt gacctgcgtg 780

gtggtggacg tgtcccagga agatcccgag gtccagttca attggtacgt ggacggcgtg 840

gaagtgcaca atgccaagac caagcccaga gaggaacagt tcaactccac ctaccgggtg 900

gtgtccgtgc tgaccgtgct gcaccaggac tggctgaacg gcaaagagta caagtgcaag 960

gtgtccaaca agggcctgcc ctccagcatc gaaaagacca tctccaaggc caagggccag 1020

ccccgcgagc cccaggtgta caccctgccc cctagccagg aagagatgac caagaaccag 1080

gtgtccctga cctgtctggt caagggcttc taccctccg acattgccgt ggaatgggag 1140

tccaacggcc agcccgagaa caactacaag accacccccc ctgtgctgga cagcgacggc 1200

tccttcttcc tgtactctcg gctgaccgtg gacaagtccc ggtggcagga aggcaacgtc 1260

ttctcctgct ccgtgatgca cgaggccctg cacaaccact acacccagaa gtccctgtcc 1320

ctgagcctgg gcaag 1335

<210> 26
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized

<400> 26
gaggtgcaac tgcaggaatc cggtcccggc ctcgtgaagc cttcagaaac cctgtcgctc 60

acatgcactg tgtccgggtt ctccctgacc tctaacgaca tcgcctggat tcggcagccg 120

ccaggaaagg gactggagtg gatgggcacc atttggaccg acgggtcaac caactacaat 180

accgcggtgc aatccagagt gaccatcagc gtggacacgt ccaagaacca gttctcgctg 240

aaattgagct ccgtgactgc cgctgatact gccgtgtatt actgtgcccg gcaccgcctt 300

tactacggcg catttgacta ctggggacag ggaaccatgg tcactgtctc gagtgcctcc 360

accaagggcc cctccgtgtt ccctctggcc ccttgctccc ggtccacctc cgagtctacc 420

gccgctctgg gctgcctggt caaggactac ttccccgagc ccgtgacagt gtcctggaac 480

tctggcgccc tgacctccgg cgtgcacacc ttccctgccg tgctgcagtc ctccggcctg 540

tactccctgt cctccgtcgt gaccgtgccc tcctccagcc tgggcaccaa gacctacacc 600

tgtaacgtgg accacaagcc ctccaacacc aaggtggaca agcgggtgga atctaagtac 660

ggccctccct gccccccctg ccctgccccc gaatttctgg gcggaccttc cgtgttcctg 720

ttcccccaa agcccaagga caccctgatg atctcccgga cccccgaagt gacctgcgtg 780

gtggtggacg tgtcccagga agatcccgag gtccagttca attggtacgt ggacggcgtg 840

gaagtgcaca atgccaagac caagcccaga gaggaacagt tcaactccac ctaccgggtg 900

gtgtccgtgc tgaccgtgct gcaccaggac tggctgaacg gcaaagagta caagtgcaag 960

gtgtccaaca agggcctgcc ctccagcatc gaaaagacca tctccaaggc caagggccag 1020

ccccgcgagc cccaggtgta caccctgccc cctagccagg aagagatgac caagaaccag 1080

gtgtccctga cctgtctggt caagggcttc taccctccg acattgccgt ggaatgggag 1140

tccaacggcc agcccgagaa caactacaag accacccccc ctgtgctgga cagcgacggc 1200

tccttcttcc tgtactctcg gctgaccgtg gacaagtccc ggtggcagga aggcaacgtc 1260

ttctcctgct ccgtgatgca cgaggccctg cacaaccact acacccagaa gtccctgtcc 1320

ctgagcctgg gcaag 1335

<210> 27
<211> 134
<212> PRT
<213> Rattus norvegicus

<220>
<221> MISC_FEATURE
<222> (1)..(22)
<223> leader sequence

<400> 27

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

Phe Pro Gly Thr Arg Cys Asp Ile Val Met Thr Gln Thr Pro Val Ser
20 25 30

Leu Ser Val Thr Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser
35 40 45

Gln Ser Leu Glu Tyr Ser Asp Gly Tyr Thr Tyr Leu Glu Trp Tyr Leu
50 55 60

Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn
65 70 75 80

Arg Phe Ser Gly Val Pro Asp Arg Phe Ile Gly Ser Gly Ser Gly Thr
85 90 95

```
Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Pro Glu Asp Leu Gly Val
            100                 105                 110


Tyr Tyr Cys Phe Gln Ala Thr His Asn Pro Tyr Thr Phe Gly Ala Gly
        115                 120                 125


Thr Lys Leu Glu Ile Lys
    130


<210>  28
<211>  136
<212>  PRT
<213>  Rattus norvegicus

<400>  28

Met Glu Trp Ser Trp Val Phe Leu Phe Phe Leu Ser Val Thr Thr Gly
1               5                   10                  15


Val His Ser Glu Val Lys Leu Glu Glu Ser Gly Pro Gly Leu Met Gln
            20                  25                  30


Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu
        35                  40                  45


Thr Ser Asn Asp Ile Ala Trp Val Arg Gln Pro Leu Gly Lys Gly Leu
    50                  55                  60


Val Trp Met Gly Thr Ile Trp Thr Asp Gly Ser Thr Asn Tyr Asn Ser
65                  70                  75                  80


Ala Val Gln Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln
                85                  90                  95


Phe Phe Leu Lys Met Asn Ser Leu Gln Pro Glu Asp Thr Gly Thr Tyr
            100                 105                 110


Tyr Cys Ala Arg His Arg Leu Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
        115                 120                 125


Gln Gly Thr Met Val Thr Val Ser
    130                 135


<210>  29
<211>  402
<212>  DNA
<213>  Rattus norvegicus


<220>
<221>  misc_feature
<222>  (1)..(66)
<223>  leader sequence

<400>  29
```

atggacatga gggttcctgc tcaggttttt ggcttcttgt tgctctggtt tccaggcacc 60

aggtgtgata ttgtgatgac ccagactcca gtttccctgt ctgtcacact tggagatcaa 120

gcttctatat cttgcaggtc tagtcagagc ctggaatata gtgatggcta cacttatttg 180

gaatggtacc tacagaagcc aggccagtct cctcagctcc tcatctatga agtttccaac 240

cgattttctg gggtcccaga caggttcatt ggcagtgggt cagggacaga tttcaccctc 300

aagatcagca gagtagagcc tgaggacttg ggagtttatt actgcttcca agctacacat 360

aatccgtaca cgtttggagc tgggaccaag ctggaaataa aa 402

<210> 30
<211> 411
<212> DNA
<213> Rattus norvegicus

<220>
<221> misc_feature
<222> (1)..(57)
<223> leader sequence

<400> 30
atggaatgga gctgggtctt tctcttcttc ctgtcagtaa ctaccggtgt ccattctgag 60

gtgaagctgg aggagtctgg acctggcttg atgcagccct cagagaccct gtccctcacc 120

tgcactgtct ctggcttctc actaaccagc aatgatatag cctgggttcg acaacctcta 180

ggaaagggtt tggtgtggat gggaacaata tggactgatg gaagtacaaa ttataattca 240

gctgtccaat cccgactgag catcagcagg gacacctcca agagccaatt tttcttaaaa 300

atgaacagtc tgcaacctga agacacaggc acttactact gtgccagaca tcgcctatac 360

tacggggcct ttgattactg gggccaagga accatggtca ccgtctcgag t 411

<210> 31
<211> 112
<212> PRT
<213> Homo sapiens

<400> 31

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Ser Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
85 90 95

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

<210> 32
<211> 113
<212> PRT
<213> Homo sapiens

<400> 32

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

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

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

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

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Ala Phe Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser
100 105 110

Ser

<210> 33
<211> 336
<212> DNA
<213> Homo sapiens

<400> 33
gatattgtga tgacccagac tccactctct ctgtccgtca cccctggaca gccggcctcc 60

atctcctgca agtctagtca gagcctcctg catagtgatg gaaagaccta tttgtattgg 120

tacctgcaga agccaggcca gtctccacag ctcctaatct atgaagtttc cagccggttc 180

tctggagtgc cagataggtt cagtggcagc gggtcaggga cagatttcac actgaaaatc 240

agccgggtgg aggctgagga tgttggggtt tattactgca tgcaaggtat acaccttcct 300

tacacttttg gccaggggac caagctggag atcaaa 336

<210> 34

<211> 339
<212> DNA
<213> Homo sapiens

<400> 34
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60

acctgcactg tctctggtgg ctccatcagt agttactact ggagctggat ccggcagccc 120

ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180

ccctccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 240

aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agatgctttt 300

gatgtctggg gccaagggac aatggtcacc gtctcttca 339

<210> 35
<211> 441
<212> PRT
<213> Homo sapiens

<400> 35

Met Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly
1 5 10 15

Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His
20 25 30

Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu
35 40 45

Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser
50 55 60

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

Asp Glu Gly Ala Pro Gly Lys Gln Ala Ala Ala Gln Pro His Thr Glu
85 90 95

Ile Pro Glu Gly Thr Thr Ala Glu Glu Ala Gly Ile Gly Asp Thr Pro
100 105 110

Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Ala Arg Met Val
115 120 125

Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Lys Ala Lys Gly
130 135 140

Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala Ala Pro Pro
145 150 155 160

Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala Lys Thr Pro
165 170 175

```
Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro Lys Ser Gly
            180                 185                 190

Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro Gly Ser
        195                 200                 205

Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg Glu Pro Lys
    210                 215                 220

Lys Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser Ser Ala Lys
225                 230                 235                 240

Ser Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn Val
                245                 250                 255

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

Gly Lys Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser Asn Val Gln
        275                 280                 285

Ser Lys Cys Gly Ser Lys Asp Asn Ile Lys His Val Pro Gly Gly Gly
    290                 295                 300

Ser Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr Ser
305                 310                 315                 320

Lys Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gly Gln
                325                 330                 335

Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln Ser
            340                 345                 350

Lys Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Gly Asn
        355                 360                 365

Lys Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn Ala Lys Ala
    370                 375                 380

Lys Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro Val Val Ser
385                 390                 395                 400

Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser Thr Gly Ser
                405                 410                 415

Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu Val
            420                 425                 430

Ser Ala Ser Leu Ala Lys Gln Gly Leu
        435                 440
```

<210> 36
<211> 16
<212> PRT
<213> Rattus norvegicus

<400> 36

Thr Ile Trp Thr Asp Gly Ser Thr Asn Tyr Asn Ser Ala Val Gln Ser
1 5 10 15

<210> 37
<211> 16
<212> PRT
<213> Rattus norvegicus

<400> 37

Thr Ile Trp Thr Asp Gly Ser Thr Asn Tyr Asn Ala Ala Val Gln Ser
1 5 10 15

<210> 38
<211> 16
<212> PRT
<213> Rattus norvegicus

<400> 38

Thr Ile Trp Thr Asp Gly Ser Thr Asn Tyr Asn Thr Ala Val Gln Ser
1 5 10 15

<210> 39
<211> 6757
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 39
tggcgaatgg gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg 60

cagcgtgacc gctacacttg ccagcgccct agcgcccgct cctttcgctt tcttcccttc 120

ctttctcgcc acgttcgccg gctttccccg tcaagctcta aatcgggggc tccctttagg 180

gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc 240

acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt 300

ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc 360

ttttgattta taagggattt tgccgatttc ggcctattgg ttaaaaaatg agctgattta 420

acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt 480

tcggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt caaatatgta 540

tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat 600

gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt gccttcctgt 660

ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg 720

agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt ttcgccccga 780

agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg tattatcccg 840

tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttggt 900

tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg 960

cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga caacgatcgg 1020

aggaccgaag gagctaaccg ctttttttgca caacatgggg gatcatgtaa ctcgccttga 1080

tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca ccacgatgcc 1140

tgcagcaatg gcaacaacgt tgcgcaaact attaactggc gaactactta ctctagcttc 1200

ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac ttctgcgctc 1260

ggcccttccg gctggctggt ttattgctga taaatctgga gccggtgagc gtgggtctcg 1320

cggtatcatt gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac 1380

gacggggagt caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc 1440

actgattaag cattggtaac tgtcagacca agtttactca tatatacttt agattgattt 1500

aaaacttcat ttttaattta aaaggatcta ggtgaagatc ctttttgata atctcatgac 1560

caaaatccct taacgtgagt tttcgttcca ctgagcgtca gaccccgtag aaaagatcaa 1620

aggatcttct tgagatcctt tttttctgcg cgtaatctgc tgcttgcaaa caaaaaaacc 1680

accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt ttccgaaggt 1740

aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc cgtagttagg 1800

ccaccacttc aagaactctg tagcaccgcc tacatacctc gctctgctaa tcctgttacc 1860

agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa gacgatagtt 1920

accggataag gcgcagcggt cgggctgaac ggggggttcg tgcacacagc ccagcttgga 1980

gcgaacgacc tacaccgaac tgagatacct acagcgtgag ctatgagaaa gcgccacgct 2040

tcccgaaggg agaaaggcgg acaggtatcc ggtaagcggc agggtcggaa caggagagcg 2100

cacgagggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg ggtttcgcca 2160

cctctgactt gagcgtcgat ttttgtgatg ctcgtcaggg gggcggagcc tatggaaaaa 2220

cgccagcaac gcggcctttt tacggttcct ggccttttgc tggccttttg ctcacatgtt 2280

ctttcctgcg ttatcccctg attctgtgga taaccgtatt accgcctttg agtgagctga 2340

taccgctcgc cgcagccgaa cgaccgagcg cagcgagtca gtgagcgagg aagcggaaga 2400

gcgcctgatg cggtattttc tccttacgca tctgtgcggt atttcacacc gcatatatgg 2460

tgcactctca gtacaatctg ctctgatgcc gcatagttaa gccagtatac actccgctat 2520

cgctacgtga ctgggtcatg gctgcgcccc gacacccgcc aacacccgct gacgcgccct 2580

gacgggcttg tctgctcccg gcatccgctt acagacaagc tgtgaccgtc tccgggagct 2640

gcatgtgtca gaggttttca ccgtcatcac cgaaacgcgc gaggcagctg cggtaaagct 2700

catcagcgtg gtcgtgaagc gattcacaga tgtctgcctg ttcatccgcg tccagctcgt 2760

tgagtttctc cagaagcgtt aatgtctggc ttctgataaa gcgggccatg ttaagggcgg 2820

```
tttttcctg tttggtcact gatgcctccg tgtaaggggg atttctgttc atgggggtaa     2880
tgataccgat gaaacgagag aggatgctca cgatacgggt tactgatgat gaacatgccc     2940
ggttactgga acgttgtgag ggtaaacaac tggcggtatg gatgcggcgg gaccagagaa     3000
aaatcactca gggtcaatgc cagcgcttcg ttaatacaga tgtaggtgtt ccacagggta     3060
gccagcagca tcctgcgatg cagatccgga acataatggt gcagggcgct gacttccgcg     3120
tttccagact ttacgaaaca cggaaaccga agaccattca tgttgttgct caggtcgcag     3180
acgttttgca gcagcagtcg cttcacgttc gctcgcgtat cggtgattca ttctgctaac     3240
cagtaaggca accccgccag cctagccggg tcctcaacga caggagcacg atcatgcgca     3300
cccgtggggc cgccatgccg gcgataatgg cctgcttctc gccgaaacgt ttggtggcgg     3360
gaccagtgac gaaggcttga gcgagggcgt gcaagattcc gaataccgca agcgacaggc     3420
cgatcatcgt cgcgctccag cgaaagcggt cctcgccgaa aatgacccag agcgctgccg     3480
gcacctgtcc tacgagttgc atgataaaga agacagtcat aagtgcggcg acgatagtca     3540
tgccccgcgc ccaccggaag gagctgactg ggttgaaggc tctcaagggc atcggtcgag     3600
atcccggtgc ctaatgagtg agctaactta cattaattgc gttgcgctca ctgcccgctt     3660
tccagtcggg aaacctgtcg tgccagctgc attaatgaat cggccaacgc gcggggagag     3720
gcggtttgcg tattgggcgc cagggtggtt tttcttttca ccagtgagac gggcaacagc     3780
tgattgccct tcaccgcctg gccctgagag agttgcagca agcggtccac gctggtttgc     3840
cccagcaggc gaaaatcctg tttgatggtg gttaacggcg ggatataaca tgagctgtct     3900
tcggtatcgt cgtatcccac taccgagatg tccgcaccaa cgcgcagccc ggactcggta     3960
atggcgcgca ttgcgcccag cgccatctga tcgttggcaa ccagcatcgc agtgggaacg     4020
atgccctcat tcagcatttg catggtttgt tgaaaaccgg acatggcact ccagtcgcct     4080
tcccgttccg ctatcggctg aatttgattg cgagtgagat atttatgcca gccagccaga     4140
cgcagacgcg ccgagacaga acttaatggg cccgctaaca gcgcgatttg ctggtgaccc     4200
aatgcgacca gatgctccac gcccagtcgc gtaccgtctt catgggagaa aataatactg     4260
ttgatgggtg tctggtcaga gacatcaaga aataacgccg gaacattagt gcaggcagct     4320
tccacagcaa tggcatcctg gtcatccagc ggatagttaa tgatcagccc actgacgcgt     4380
tgcgcgagaa gattgtgcac cgccgcttta caggcttcga cgccgcttcg ttctaccatc     4440
gacaccacca cgctggcacc cagttgatcg gcgcgagatt taatcgccgc gacaatttgc     4500
gacggcgcgt gcagggccag actggaggtg gcaacgccaa tcagcaacga ctgtttgccc     4560
gccagttgtt gtgccacgcg gttgggaatg taattcagct ccgccatcgc cgcttccact     4620
ttttcccgcg ttttcgcaga aacgtggctg gcctggttca ccacgcggga aacggtctga     4680
taagagacac cggcatactc tgcgacatcg tataacgtta ctggtttcac attcaccacc     4740
ctgaattgac tctcttccgg gcgctatcat gccataccgc gaaaggtttt gcgccattcg     4800
atggtgtccg ggatctcgac gctctccctt atgcgactcc tgcattagga agcagcccag     4860
```

tagtaggttg aggccgttga gcaccgccgc cgcaaggaat ggtgcatgca aggagatggc 4920

gcccaacagt cccccggcca cggggcctgc caccataccc acgccgaaac aagcgctcat 4980

gagcccgaag tggcgagccc gatcttcccc atcggtgatg tcggcgatat aggcgccagc 5040

aaccgcacct gtggcgccgg tgatgccggc cacgatgcgt ccggcgtaga ggatcgagat 5100

cgatctcgat cccgcgaaat taatacgact cactataggg gaattgtgag cggataacaa 5160

ttcccctcta gaaataattt tgtttaactt taagaaggag atatacatat gggctcaagc 5220

caccaccacc accaccacag cagcggcgag aacttgtact ttcaaggatc cgcagaacca 5280

cgtcaagaat ttgaggttat ggaagatcac gcgggcactt acggtttggg tgatcgtaaa 5340

gaccagggcg gctataccat gcatcaagat caagagggcg acaccgatgc tggcttgaaa 5400

gagtcgccgc tgcagactcc gaccgaggat ggcagcgaag agccgggcag cgagactagc 5460

gatgcgaagt cgaccccgac cgccgaggac gttaccgcac cgctggtcga cgagggtgct 5520

ccgggtaaac aggcggctgc acagccgcac acggagattc cggaaggcac caccgcagaa 5580

gaggcgggta tcggcgacac tccgtccctg gaagatgagg cagccggtca tgtcacgcag 5640

gcgcgtatgg tgagcaagag caaagatggt acgggtagcg acgacaagaa ggcgaagggc 5700

gcagatggca agaccaaaat tgcgacgccg cgtggtgcgg caccgccagg ccagaaaggt 5760

caggcgaatg ccacgcgcat cccggcaaag acgccaccgg ctccgaaaac cccgccttcc 5820

agcggtgaac cgccgaaatc cggtgaccgc agcggttata gctctccggg tagcccgggt 5880

accccaggca gccgtagccg caccccgagc ctgccgaccc caccgacccg cgagccgaag 5940

aaagtggcgg tggttcgtac gccgccaaaa agcccgagct ctgccaagag ccgtctgcaa 6000

accgctcctg tgccgatgcc ggacctgaag aacgttaagt ctaaaatcgg tagcaccgaa 6060

aatctgaagc accaacctgg tggcggtaag gttcaaatca tcaacaaaaa gctggacttg 6120

agcaatgtac aaagcaagtg tggtagcaag gacaatatca aacacgtccc gggtggtggt 6180

tccgtccaga ttgtgtacaa accggtggac ctgagcaagg ttaccagcaa atgcggttcc 6240

ctgggtaaca tccatcataa accgggtggc ggccaagttg aggtcaagag cgagaaactg 6300

gacttcaaag accgcgttca gtccaaaatc ggttctctgg acaacattac gcacgtgcct 6360

ggtggtggca acaagaagat tgaaacccat aaactgacgt ttcgtgaaaa tgcgaaggcg 6420

aaaaccgacc acggcgcaga gattgtctac aaaagcccgg tggtgagcgg tgataccagc 6480

ccgcgtcacc tgtccaacgt cagcagcacg ggcagcattg atatggtgga tagcccgcag 6540

ttggctacgc tggccgatga ggttagcgcg agcctggcga agcagggtct gtgactcgag 6600

caccaccacc accaccactg agatccggct gctaacaaag cccgaaagga agctgagttg 6660

gctgctgcca ccgctgagca ataactagca taacccctttg gggcctctaa acgggtcttg 6720

aggggttttt tgctgaaagg aggaactata tccggat 6757

<210> 40
<211> 461

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 40

```
Met Gly Ser Ser His His His His His His Ser Ser Gly Glu Asn Leu
1               5                  10                  15

Tyr Phe Gln Gly Ser Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu
            20                  25                  30

Asp His Ala Gly Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly
        35                  40                  45

Tyr Thr Met His Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys
    50                  55                  60

Glu Ser Pro Leu Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly
65                  70                  75                  80

Ser Glu Thr Ser Asp Ala Lys Ser Thr Pro Thr Ala Glu Asp Val Thr
                85                  90                  95

Ala Pro Leu Val Asp Glu Gly Ala Pro Gly Lys Gln Ala Ala Ala Gln
            100                 105                 110

Pro His Thr Glu Ile Pro Glu Gly Thr Thr Ala Glu Glu Ala Gly Ile
        115                 120                 125

Gly Asp Thr Pro Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln
    130                 135                 140

Ala Arg Met Val Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys
145                 150                 155                 160

Lys Ala Lys Gly Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly
                165                 170                 175

Ala Ala Pro Pro Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro
            180                 185                 190

Ala Lys Thr Pro Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro
        195                 200                 205

Pro Lys Ser Gly Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly
    210                 215                 220

Thr Pro Gly Ser Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr
225                 230                 235                 240
```

Arg Glu Pro Lys Lys Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro
245 250 255

Ser Ser Ala Lys Ser Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp
260 265 270

Leu Lys Asn Val Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His
275 280 285

Gln Pro Gly Gly Gly Lys Val Gln Ile Ile Asn Lys Lys Leu Asp Leu
290 295 300

Ser Asn Val Gln Ser Lys Cys Gly Ser Lys Asp Asn Ile Lys His Val
305 310 315 320

Pro Gly Gly Gly Ser Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser
325 330 335

Lys Val Thr Ser Lys Cys Gly Ser Leu Gly Asn Ile His His Lys Pro
340 345 350

Gly Gly Gly Gln Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp
355 360 365

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

Gly Gly Gly Asn Lys Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu
385 390 395 400

Asn Ala Lys Ala Lys Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser
405 410 415

Pro Val Val Ser Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser
420 425 430

Ser Thr Gly Ser Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu
435 440 445

Ala Asp Glu Val Ser Ala Ser Leu Ala Lys Gln Gly Leu
450 455 460

<210> 41
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 41

Gly Ser Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala
1 5 10 15

```
Gly Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met
            20                  25                  30

His Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro
        35                  40                  45

Leu Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr
    50                  55                  60

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

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

Glu Ile Pro Glu Gly Thr Thr Ala Glu Glu Ala Gly Ile Gly Asp Thr
            100                 105                 110

Pro Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Ala Arg Met
        115                 120                 125

Val Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Lys Ala Lys
    130                 135                 140

Gly Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala Ala Pro
145                 150                 155                 160

Pro Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala Lys Thr
                165                 170                 175

Pro Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro Lys Ser
            180                 185                 190

Gly Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro Gly
        195                 200                 205

Ser Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg Glu Pro
    210                 215                 220

Lys Lys Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser Ser Ala
225                 230                 235                 240

Lys Ser Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn
                245                 250                 255

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

Gly Gly Lys Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser Asn Val
        275                 280                 285
```

```
Gln Ser Lys Cys Gly Ser Lys Asp Asn Ile Lys His Val Pro Gly Gly
    290                 295                 300

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

Ser Lys Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gly
                325                 330                 335

Gln Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln
            340                 345                 350

Ser Lys Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Gly
        355                 360                 365

Asn Lys Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn Ala Lys
    370                 375                 380

Ala Lys Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro Val Val
385                 390                 395                 400

Ser Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser Thr Gly
                405                 410                 415

Ser Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu
            420                 425                 430

Val Ser Ala Ser Leu Ala Lys Gln Gly Leu
        435                 440


<210>  42
<211>  6583
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  synthetic

<400>  42
tggcgaatgg gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg       60

cagcgtgacc gctacacttg ccagcgccct agcgcccgct cctttcgctt tcttcccttc      120

ctttctcgcc acgttcgccg gctttccccg tcaagctcta aatcgggggc tccctttagg      180

gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc      240

acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt      300

ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc      360

ttttgattta taagggattt tgccgatttc ggcctattgg ttaaaaaatg agctgattta      420

acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt      480

tcggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt caaatatgta      540
```

```
tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat      600
gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt gccttcctgt      660
ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg      720
agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt ttcgccccga      780
agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg tattatcccg      840
tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttggt      900
tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg      960
cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga caacgatcgg     1020
aggaccgaag gagctaaccg ctttttgca caacatgggg gatcatgtaa ctcgccttga     1080
tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca ccacgatgcc     1140
tgcagcaatg gcaacaacgt tgcgcaaact attaactggc gaactactta ctctagcttc     1200
ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac ttctgcgctc     1260
ggcccttccg gctggctggt ttattgctga taaatctgga gccggtgagc gtgggtctcg     1320
cggtatcatt gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac     1380
gacggggagt caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc     1440
actgattaag cattggtaac tgtcagacca agtttactca tatatacttt agattgattt     1500
aaaacttcat ttttaattta aaaggatcta ggtgaagatc ctttttgata atctcatgac     1560
caaaatccct taacgtgagt tttcgttcca ctgagcgtca gaccccgtag aaaagatcaa     1620
aggatcttct tgagatcctt tttttctgcg cgtaatctgc tgcttgcaaa caaaaaaacc     1680
accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt ttccgaaggt     1740
aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc cgtagttagg     1800
ccaccacttc aagaactctg tagcaccgcc tacatacctc gctctgctaa tcctgttacc     1860
agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa gacgatagtt     1920
accggataag gcgcagcggt cgggctgaac gggggggttcg tgcacacagc ccagcttgga     1980
gcgaacgacc tacaccgaac tgagatacct acagcgtgag ctatgagaaa gcgccacgct     2040
tcccgaaggg agaaaggcgg acaggtatcc ggtaagcggc agggtcggaa caggagagcg     2100
cacgagggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg ggtttcgcca     2160
cctctgactt gagcgtcgat ttttgtgatg ctcgtcaggg gggcggagcc tatggaaaaa     2220
cgccagcaac gcggcctttt tacggttcct ggccttttgc tggccttttg ctcacatgtt     2280
ctttcctgcg ttatcccctg attctgtgga taaccgtatt accgcctttg agtgagctga     2340
taccgctcgc cgcagccgaa cgaccgagcg cagcgagtca gtgagcgagg aagcggaaga     2400
gcgcctgatg cggtattttc tccttacgca tctgtgcggt atttcacacc gcatatatgg     2460
tgcactctca gtacaatctg ctctgatgcc gcatagttaa gccagtatac actccgctat     2520
cgctacgtga ctgggtcatg gctgcgcccc gacacccgcc aacacccgct gacgcgccct     2580
```

gacgggcttg tctgctcccg gcatccgctt acagacaagc tgtgaccgtc tccgggagct 2640

gcatgtgtca gaggttttca ccgtcatcac cgaaacgcgc gaggcagctg cggtaaagct 2700

catcagcgtg gtcgtgaagc gattcacaga tgtctgcctg ttcatccgcg tccagctcgt 2760

tgagtttctc cagaagcgtt aatgtctggc ttctgataaa gcgggccatg ttaagggcgg 2820

ttttttcctg tttggtcact gatgcctccg tgtaaggggg atttctgttc atgggggtaa 2880

tgataccgat gaaacgagag aggatgctca cgatacgggt tactgatgat gaacatgccc 2940

ggttactgga acgttgtgag ggtaaacaac tggcggtatg gatgcggcgg gaccagagaa 3000

aaatcactca gggtcaatgc cagcgcttcg ttaatacaga tgtaggtgtt ccacagggta 3060

gccagcagca tcctgcgatg cagatccgga acataatggt gcagggcgct gacttccgcg 3120

tttccagact ttacgaaaca cggaaaccga agaccattca tgttgttgct caggtcgcag 3180

acgttttgca gcagcagtcg cttcacgttc gctcgcgtat cggtgattca ttctgctaac 3240

cagtaaggca accccgccag cctagccggg tcctcaacga caggagcacg atcatgcgca 3300

cccgtggggc cgccatgccg gcgataatgg cctgcttctc gccgaaacgt ttggtggcgg 3360

gaccagtgac gaaggcttga gcgagggcgt gcaagattcc gaataccgca agcgacaggc 3420

cgatcatcgt cgcgctccag cgaaagcggt cctcgccgaa aatgacccag agcgctgccg 3480

gcacctgtcc tacgagttgc atgataaaga agacagtcat aagtgcggcg acgatagtca 3540

tgccccgcgc ccaccggaag gagctgactg ggttgaaggc tctcaagggc atcggtcgag 3600

atcccggtgc ctaatgagtg agctaactta cattaattgc gttgcgctca ctgcccgctt 3660

tccagtcggg aaacctgtcg tgccagctgc attaatgaat cggccaacgc gcggggagag 3720

gcggtttgcg tattgggcgc cagggtggtt tttcttttca ccagtgagac gggcaacagc 3780

tgattgccct tcaccgcctg gccctgagag agttgcagca agcggtccac gctggtttgc 3840

cccagcaggc gaaaatcctg tttgatggtg gttaacggcg ggatataaca tgagctgtct 3900

tcggtatcgt cgtatcccac taccgagatg tccgcaccaa cgcgcagccc ggactcggta 3960

atggcgcgca ttgcgcccag cgccatctga tcgttggcaa ccagcatcgc agtgggaacg 4020

atgccctcat tcagcatttg catggtttgt tgaaaaccgg acatggcact ccagtcgcct 4080

tcccgttccg ctatcggctg aatttgattg cgagtgagat atttatgcca gccagccaga 4140

cgcagacgcg ccgagacaga acttaatggg cccgctaaca gcgcgatttg ctggtgaccc 4200

aatgcgacca gatgctccac gcccagtcgc gtaccgtctt catgggagaa aataatactg 4260

ttgatgggtg tctggtcaga gacatcaaga aataacgccg gaacattagt gcaggcagct 4320

tccacagcaa tggcatcctg gtcatccagc ggatagttaa tgatcagccc actgacgcgt 4380

tgcgcgagaa gattgtgcac cgccgcttta caggcttcga cgccgcttcg ttctaccatc 4440

gacaccacca cgctggcacc cagttgatcg gcgcgagatt taatcgccgc gacaatttgc 4500

gacggcgcgt gcagggccag actggaggtg gcaacgccaa tcagcaacga ctgtttgccc 4560

gccagttgtt gtgccacgcg gttgggaatg taattcagct ccgccatcgc cgcttccact 4620

ttttcccgcg ttttcgcaga aacgtggctg gcctggttca ccacgcggga aacggtctga 4680
taagagacac cggcatactc tgcgacatcg tataacgtta ctggtttcac attcaccacc 4740
ctgaattgac tctcttccgg gcgctatcat gccataccgc gaaaggtttt gcgccattcg 4800
atggtgtccg ggatctcgac gctctccctt atgcgactcc tgcattagga agcagcccag 4860
tagtaggttg aggccgttga gcaccgccgc cgcaaggaat ggtgcatgca aggagatggc 4920
gcccaacagt cccccggcca cggggcctgc caccataccc acgccgaaac aagcgctcat 4980
gagcccgaag tggcgagccc gatcttcccc atcggtgatg tcggcgatat aggcgccagc 5040
aaccgcacct gtggcgccgg tgatgccggc cacgatgcgt ccggcgtaga ggatcgagat 5100
cgatctcgat cccgcgaaat taatacgact cactataggg gaattgtgag cggataacaa 5160
ttcccctcta gaaataattt tgtttaactt taagaaggag atatacatat gggctcaagc 5220
caccaccacc accaccacag cagcggcgag aacttgtact ttcaaggatc cgcagaacca 5280
cgtcaagaat ttgaggttat ggaagatcac gcgggcactt acggtttggg tgatcgtaaa 5340
gaccagggcg gctataccat gcatcaagat caagagggcg acaccgatgc tggcttgaaa 5400
gcagaagagg cgggtatcgg cgacactccg tccctggaag atgaggcagc cggtcatgtc 5460
acgcaggcgc gtatggtgag caagagcaaa gatggtacgg gtagcgacga caagaaggcg 5520
aagggcgcag atggcaagac caaaattgcg acgccgcgtg gtgcggcacc gccaggccag 5580
aaaggtcagg cgaatgccac gcgcatcccg gcaaagacgc caccggctcc gaaaaccccg 5640
ccttccagcg gtgaaccgcc gaaatccggt gaccgcagcg gttatagctc tccgggtagc 5700
ccgggtaccc caggcagccg tagccgcacc ccgagcctgc cgaccccacc gacccgcgag 5760
ccgaagaaag tggcggtggt tcgtacgccg ccaaaaagcc cgagctctgc caagagccgt 5820
ctgcaaaccg ctcctgtgcc gatgccggac ctgaagaacg ttaagtctaa aatcggtagc 5880
accgaaaatc tgaagcacca acctggtggc ggtaaggttc aaatcatcaa caaaaagctg 5940
gacttgagca atgtacaaag caagtgtggt agcaaggaca atatcaaaca cgtcccgggt 6000
ggtggttccg tccagattgt gtacaaaccg gtggacctga gcaaggttac cagcaaatgc 6060
ggttccctgg gtaacatcca tcataaaccg ggtggcggcc aagttgaggt caagagcgag 6120
aaactggact tcaaagaccg cgttcagtcc aaaatcggtt ctctggacaa cattacgcac 6180
gtgcctggtg gtggcaacaa gaagattgaa acccataaac tgacgtttcg tgaaaatgcg 6240
aaggcgaaaa ccgaccacgg cgcagagatt gtctacaaaa gcccggtggt gagcggtgat 6300
accagcccgc gtcacctgtc caacgtcagc agcacgggca gcattgatat ggtggatagc 6360
ccgcagttgg ctacgctggc cgatgaggtt agcgcgagcc tggcgaagca gggtctgtga 6420
ctcgagcacc accaccacca ccactgagat ccggctgcta acaaagcccg aaaggaagct 6480
gagttggctg ctgccaccgc tgagcaataa ctagcataac cccttggggc ctctaaacgg 6540
gtcttgaggg gttttttgct gaaaggagga actatatccg gat 6583

<210> 43
<211> 403
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 43

```
Met Gly Ser Ser His His His His His His Ser Ser Gly Glu Asn Leu
1               5                  10                  15

Tyr Phe Gln Gly Ser Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu
            20                  25                  30

Asp His Ala Gly Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly
        35                  40                  45

Tyr Thr Met His Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys
    50                  55                  60

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

Ala Gly His Val Thr Gln Ala Arg Met Val Ser Lys Ser Lys Asp Gly
                85                  90                  95

Thr Gly Ser Asp Asp Lys Lys Ala Lys Gly Ala Asp Gly Lys Thr Lys
            100                 105                 110

Ile Ala Thr Pro Arg Gly Ala Ala Pro Pro Gly Gln Lys Gly Gln Ala
        115                 120                 125

Asn Ala Thr Arg Ile Pro Ala Lys Thr Pro Pro Ala Pro Lys Thr Pro
    130                 135                 140

Pro Ser Ser Gly Glu Pro Pro Lys Ser Gly Asp Arg Ser Gly Tyr Ser
145                 150                 155                 160

Ser Pro Gly Ser Pro Gly Thr Pro Gly Ser Arg Ser Arg Thr Pro Ser
                165                 170                 175

Leu Pro Thr Pro Pro Thr Arg Glu Pro Lys Lys Val Ala Val Val Arg
            180                 185                 190

Thr Pro Pro Lys Ser Pro Ser Ser Ala Lys Ser Arg Leu Gln Thr Ala
        195                 200                 205

Pro Val Pro Met Pro Asp Leu Lys Asn Val Lys Ser Lys Ile Gly Ser
    210                 215                 220

Thr Glu Asn Leu Lys His Gln Pro Gly Gly Gly Lys Val Gln Ile Ile
225                 230                 235                 240
```

```
Asn Lys Lys Leu Asp Leu Ser Asn Val Gln Ser Lys Cys Gly Ser Lys
                245                 250                 255

Asp Asn Ile Lys His Val Pro Gly Gly Gly Ser Val Gln Ile Val Tyr
            260                 265                 270

Lys Pro Val Asp Leu Ser Lys Val Thr Ser Lys Cys Gly Ser Leu Gly
        275                 280                 285

Asn Ile His His Lys Pro Gly Gly Gly Gln Val Glu Val Lys Ser Glu
    290                 295                 300

Lys Leu Asp Phe Lys Asp Arg Val Gln Ser Lys Ile Gly Ser Leu Asp
305                 310                 315                 320

Asn Ile Thr His Val Pro Gly Gly Gly Asn Lys Lys Ile Glu Thr His
                325                 330                 335

Lys Leu Thr Phe Arg Glu Asn Ala Lys Ala Lys Thr Asp His Gly Ala
            340                 345                 350

Glu Ile Val Tyr Lys Ser Pro Val Val Ser Gly Asp Thr Ser Pro Arg
        355                 360                 365

His Leu Ser Asn Val Ser Ser Thr Gly Ser Ile Asp Met Val Asp Ser
    370                 375                 380

Pro Gln Leu Ala Thr Leu Ala Asp Glu Val Ser Ala Ser Leu Ala Lys
385                 390                 395                 400

Gln Gly Leu
```

<210> 44
<211> 384
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 44

```
Gly Ser Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala
1               5                   10                  15

Gly Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met
            20                  25                  30

His Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Ala Glu Glu
        35                  40                  45
```

```
Ala Gly Ile Gly Asp Thr Pro Ser Leu Glu Asp Glu Ala Ala Gly His
    50                  55                  60

Val Thr Gln Ala Arg Met Val Ser Lys Ser Lys Asp Gly Thr Gly Ser
65                  70                  75                  80

Asp Asp Lys Lys Ala Lys Gly Ala Asp Gly Lys Thr Lys Ile Ala Thr
                85                  90                  95

Pro Arg Gly Ala Ala Pro Pro Gly Gln Lys Gly Gln Ala Asn Ala Thr
            100                 105                 110

Arg Ile Pro Ala Lys Thr Pro Pro Ala Pro Lys Thr Pro Pro Ser Ser
        115                 120                 125

Gly Glu Pro Pro Lys Ser Gly Asp Arg Ser Gly Tyr Ser Ser Pro Gly
    130                 135                 140

Ser Pro Gly Thr Pro Gly Ser Arg Ser Arg Thr Pro Ser Leu Pro Thr
145                 150                 155                 160

Pro Pro Thr Arg Glu Pro Lys Lys Val Ala Val Val Arg Thr Pro Pro
                165                 170                 175

Lys Ser Pro Ser Ser Ala Lys Ser Arg Leu Gln Thr Ala Pro Val Pro
            180                 185                 190

Met Pro Asp Leu Lys Asn Val Lys Ser Lys Ile Gly Ser Thr Glu Asn
        195                 200                 205

Leu Lys His Gln Pro Gly Gly Gly Lys Val Gln Ile Ile Asn Lys Lys
    210                 215                 220

Leu Asp Leu Ser Asn Val Gln Ser Lys Cys Gly Ser Lys Asp Asn Ile
225                 230                 235                 240

Lys His Val Pro Gly Gly Gly Ser Val Gln Ile Val Tyr Lys Pro Val
                245                 250                 255

Asp Leu Ser Lys Val Thr Ser Lys Cys Gly Ser Leu Gly Asn Ile His
            260                 265                 270

His Lys Pro Gly Gly Gly Gln Val Glu Val Lys Ser Glu Lys Leu Asp
        275                 280                 285

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

His Val Pro Gly Gly Gly Asn Lys Lys Ile Glu Thr His Lys Leu Thr
305                 310                 315                 320
```

Phe Arg Glu Asn Ala Lys Ala Lys Thr Asp His Gly Ala Glu Ile Val
325 330 335

Tyr Lys Ser Pro Val Val Ser Gly Asp Thr Ser Pro Arg His Leu Ser
340 345 350

Asn Val Ser Ser Thr Gly Ser Ile Asp Met Val Asp Ser Pro Gln Leu
355 360 365

Ala Thr Leu Ala Asp Glu Val Ser Ala Ser Leu Ala Lys Gln Gly Leu
370 375 380

<210> 45
<211> 6490
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 45
tggcgaatgg gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg 60

cagcgtgacc gctacacttg ccagcgccct agcgcccgct cctttcgctt tcttcccttc 120

ctttctcgcc acgttcgccg gctttccccg tcaagctcta aatcgggggc tccctttagg 180

gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc 240

acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt 300

ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc 360

ttttgattta taagggattt tgccgatttc ggcctattgg ttaaaaaatg agctgattta 420

acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt 480

tcggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt caaatatgta 540

tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat 600

gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt gccttcctgt 660

ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg 720

agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt ttcgccccga 780

agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg tattatcccg 840

tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttggt 900

tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg 960

cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga caacgatcgg 1020

aggaccgaag gagctaaccg ctttttttgca caacatgggg gatcatgtaa ctcgccttga 1080

tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca ccacgatgcc 1140

tgcagcaatg gcaacaacgt tgcgcaaact attaactggc gaactactta ctctagcttc 1200

ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac ttctgcgctc 1260

ggcccttccg gctggctggt ttattgctga taaatctgga gccggtgagc gtgggtctcg 1320

```
cggtatcatt gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac     1380
gacggggagt caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc     1440
actgattaag cattggtaac tgtcagacca agtttactca tatatacttt agattgattt     1500
aaaacttcat ttttaattta aaaggatcta ggtgaagatc ctttttgata atctcatgac     1560
caaaatccct taacgtgagt tttcgttcca ctgagcgtca gaccccgtag aaaagatcaa     1620
aggatcttct tgagatcctt tttttctgcg cgtaatctgc tgcttgcaaa caaaaaaacc     1680
accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt ttccgaaggt     1740
aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc cgtagttagg     1800
ccaccacttc aagaactctg tagcaccgcc tacatacctc gctctgctaa tcctgttacc     1860
agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa gacgatagtt     1920
accggataag gcgcagcggt cgggctgaac ggggggttcg tgcacacagc ccagcttgga     1980
gcgaacgacc tacaccgaac tgagatacct acagcgtgag ctatgagaaa gcgccacgct     2040
tcccgaaggg agaaaggcgg acaggtatcc ggtaagcggc agggtcggaa caggagagcg     2100
cacgagggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg ggtttcgcca     2160
cctctgactt gagcgtcgat ttttgtgatg ctcgtcaggg gggcggagcc tatggaaaaa     2220
cgccagcaac gcggcctttt tacggttcct ggccttttgc tggccttttg ctcacatgtt     2280
ctttcctgcg ttatcccctg attctgtgga taaccgtatt accgcctttg agtgagctga     2340
taccgctcgc cgcagccgaa cgaccgagcg cagcgagtca gtgagcgagg aagcggaaga     2400
gcgcctgatg cggtattttc tccttacgca tctgtgcggt atttcacacc gcatatatgg     2460
tgcactctca gtacaatctg ctctgatgcc gcatagttaa gccagtatac actccgctat     2520
cgctacgtga ctgggtcatg gctgcgcccc gacacccgcc aacacccgct gacgcgccct     2580
gacgggcttg tctgctcccg gcatccgctt acagacaagc tgtgaccgtc tccgggagct     2640
gcatgtgtca gaggttttca ccgtcatcac cgaaacgcgc gaggcagctg cggtaaagct     2700
catcagcgtg gtcgtgaagc gattcacaga tgtctgcctg ttcatccgcg tccagctcgt     2760
tgagtttctc cagaagcgtt aatgtctggc ttctgataaa gcgggccatg ttaagggcgg     2820
ttttttcctg tttggtcact gatgcctccg tgtaaggggg atttctgttc atgggggtaa     2880
tgataccgat gaaacgagag aggatgctca cgatacgggt tactgatgat gaacatgccc     2940
ggttactgga acgttgtgag ggtaaacaac tggcggtatg gatgcggcgg gaccagagaa     3000
aaatcactca gggtcaatgc cagcgcttcg ttaatacaga tgtaggtgtt ccacagggta     3060
gccagcagca tcctgcgatg cagatccgga acataatggt gcagggcgct gacttccgcg     3120
tttccagact ttacgaaaca cggaaaccga agaccattca tgttgttgct caggtcgcag     3180
acgttttgca gcagcagtcg cttcacgttc gctcgcgtat cggtgattca ttctgctaac     3240
cagtaaggca accccgccag cctagccggg tcctcaacga caggagcacg atcatgcgca     3300
cccgtggggc cgccatgccg gcgataatgg cctgcttctc gccgaaacgt ttggtggcgg     3360
```

gaccagtgac gaaggcttga gcgagggcgt gcaagattcc gaataccgca agcgacaggc 3420
cgatcatcgt cgcgctccag cgaaagcggt cctcgccgaa aatgacccag agcgctgccg 3480
gcacctgtcc tacgagttgc atgataaaga agacagtcat aagtgcggcg acgatagtca 3540
tgccccgcgc ccaccggaag gagctgactg ggttgaaggc tctcaagggc atcggtcgag 3600
atcccggtgc ctaatgagtg agctaactta cattaattgc gttgcgctca ctgcccgctt 3660
tccagtcggg aaacctgtcg tgccagctgc attaatgaat cggccaacgc gcggggagag 3720
gcggtttgcg tattgggcgc cagggtggtt tttcttttca ccagtgagac gggcaacagc 3780
tgattgccct tcaccgcctg gccctgagag agttgcagca agcggtccac gctggtttgc 3840
cccagcaggc gaaaatcctg tttgatggtg gttaacggcg ggatataaca tgagctgtct 3900
tcggtatcgt cgtatcccac taccgagatg tccgcaccaa cgcgcagccc ggactcggta 3960
atggcgcgca ttgcgcccag cgccatctga tcgttggcaa ccagcatcgc agtgggaacg 4020
atgccctcat tcagcatttg catggtttgt tgaaaaccgg acatggcact ccagtcgcct 4080
tcccgttccg ctatcggctg aatttgattg cgagtgagat atttatgcca gccagccaga 4140
cgcagacgcg ccgagacaga acttaatggg cccgctaaca gcgcgatttg ctggtgaccc 4200
aatgcgacca gatgctccac gcccagtcgc gtaccgtctt catgggagaa aataatactg 4260
ttgatgggtg tctggtcaga gacatcaaga aataacgccg gaacattagt gcaggcagct 4320
tccacagcaa tggcatcctg gtcatccagc ggatagttaa tgatcagccc actgacgcgt 4380
tgcgcgagaa gattgtgcac cgccgcttta caggcttcga cgccgcttcg ttctaccatc 4440
gacaccacca cgctggcacc cagttgatcg gcgcgagatt taatcgccgc gacaatttgc 4500
gacggcgcgt gcagggccag actggaggtg gcaacgccaa tcagcaacga ctgtttgccc 4560
gccagttgtt gtgccacgcg gttgggaatg taattcagct ccgccatcgc cgcttccact 4620
ttttcccgcg ttttcgcaga aacgtggctg gcctggttca ccacgcggga aacggtctga 4680
taagagacac cggcatactc tgcgacatcg tataacgtta ctggtttcac attcaccacc 4740
ctgaattgac tctcttccgg gcgctatcat gccataccgc gaaaggtttt gcgccattcg 4800
atggtgtccg ggatctcgac gctctccctt atgcgactcc tgcattagga agcagcccag 4860
tagtaggttg aggccgttga gcaccgccgc cgcaaggaat ggtgcatgca aggagatggc 4920
gcccaacagt cccccggcca cggggcctgc caccataccc acgccgaaac aagcgctcat 4980
gagcccgaag tggcgagccc gatcttcccc atcggtgatg tcggcgatat aggcgccagc 5040
aaccgcacct gtggcgccgg tgatgccggc cacgatgcgt ccggcgtaga ggatcgagat 5100
cgatctcgat cccgcgaaat taatacgact cactataggg gaattgtgag cggataacaa 5160
ttcccctcta gaaataattt tgtttaactt taagaaggag atatacatat gggctcaagc 5220
caccaccacc accaccacag cagcggcgag aacttgtact ttcaaggatc cgcagaacca 5280
cgtcaagaat ttgaggttat ggaagatcac gcgggcactt acggtttggg tgatcgtaaa 5340
gaccagggcg gctataccat gcatcaagat caagagggcg acaccgatgc tggcttgaaa 5400

gcagaagagg cgggtatcgg cgacactccg tccctggaag atgaggcagc cggtcatgtc 5460

acgcaggcgc gtatggtgag caagagcaaa gatggtacgg gtagcgacga caagaaggcg 5520

aagggcgcag atggcaagac caaaattgcg acgccgcgtg gtgcggcacc gccaggccag 5580

aaaggtcagg cgaatgccac gcgcatcccg gcaaagacgc caccggctcc gaaaaccccg 5640

ccttccagcg gtgaaccgcc gaaatccggt gaccgcagcg gttatagctc tccgggtagc 5700

ccgggtaccc caggcagccg tagccgcacc ccgagcctgc cgaccccacc gacccgcgag 5760

ccgaagaaag tggcggtggt tcgtacgccg ccaaaaagcc cgagctctgc caagagccgt 5820

ctgcaaaccg ctcctgtgcc gatgccggac ctgaagaacg ttaagtctaa aatcggtagc 5880

accgaaaatc tgaagcacca acctggtggc ggtaaggtcc agattgtgta caaaccggtg 5940

gacctgagca aggttaccag caaatgcggt tccctgggta acatccatca taaaccgggt 6000

ggcggccaag ttgaggtcaa gagcgagaaa ctggacttca aagaccgcgt tcagtccaaa 6060

atcggttctc tggacaacat tacgcacgtg cctggtggtg gcaacaagaa gattgaaacc 6120

cataaactga cgtttcgtga aaatgcgaag gcgaaaaccg accacggcgc agagattgtc 6180

tacaaaagcc cggtggtgag cggtgatacc agcccgcgtc acctgtccaa cgtcagcagc 6240

acgggcagca ttgatatggt ggatagcccg cagttggcta cgctggccga tgaggttagc 6300

gcgagcctgg cgaagcaggg tctgtgactc gagcaccacc accaccacca ctgagatccg 6360

gctgctaaca aagcccgaaa ggaagctgag ttggctgctg ccaccgctga gcaataacta 6420

gcataacccc ttggggcctc taaacgggtc ttgaggggtt ttttgctgaa aggaggaact 6480

atatccggat 6490

<210> 46
<211> 372
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 46

Met Gly Ser Ser His His His His His His Ser Ser Gly Glu Asn Leu
1 5 10 15

Tyr Phe Gln Gly Ser Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu
20 25 30

Asp His Ala Gly Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly
35 40 45

Tyr Thr Met His Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys
50 55 60

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

```
Ala Gly His Val Thr Gln Ala Arg Met Val Ser Lys Ser Lys Asp Gly
                85                  90                  95

Thr Gly Ser Asp Asp Lys Lys Ala Lys Gly Ala Asp Gly Lys Thr Lys
            100                 105                 110

Ile Ala Thr Pro Arg Gly Ala Ala Pro Pro Gly Gln Lys Gly Gln Ala
        115                 120                 125

Asn Ala Thr Arg Ile Pro Ala Lys Thr Pro Pro Ala Pro Lys Thr Pro
    130                 135                 140

Pro Ser Ser Gly Glu Pro Pro Lys Ser Gly Asp Arg Ser Gly Tyr Ser
145                 150                 155                 160

Ser Pro Gly Ser Pro Gly Thr Pro Gly Ser Arg Ser Arg Thr Pro Ser
                165                 170                 175

Leu Pro Thr Pro Pro Thr Arg Glu Pro Lys Lys Val Ala Val Val Arg
            180                 185                 190

Thr Pro Pro Lys Ser Pro Ser Ser Ala Lys Ser Arg Leu Gln Thr Ala
        195                 200                 205

Pro Val Pro Met Pro Asp Leu Lys Asn Val Lys Ser Lys Ile Gly Ser
    210                 215                 220

Thr Glu Asn Leu Lys His Gln Pro Gly Gly Gly Lys Val Gln Ile Val
225                 230                 235                 240

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

Gly Asn Ile His His Lys Pro Gly Gly Gly Gln Val Glu Val Lys Ser
            260                 265                 270

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

Asp Asn Ile Thr His Val Pro Gly Gly Gly Asn Lys Lys Ile Glu Thr
    290                 295                 300

His Lys Leu Thr Phe Arg Glu Asn Ala Lys Ala Lys Thr Asp His Gly
305                 310                 315                 320

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

Arg His Leu Ser Asn Val Ser Ser Thr Gly Ser Ile Asp Met Val Asp
            340                 345                 350
```

Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu Val Ser Ala Ser Leu Ala
355 360 365

Lys Gln Gly Leu
370

<210> 47
<211> 353
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 47

Gly Ser Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala
1 5 10 15

Gly Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met
20 25 30

His Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Ala Glu Glu
35 40 45

Ala Gly Ile Gly Asp Thr Pro Ser Leu Glu Asp Glu Ala Ala Gly His
50 55 60

Val Thr Gln Ala Arg Met Val Ser Lys Ser Lys Asp Gly Thr Gly Ser
65 70 75 80

Asp Asp Lys Lys Ala Lys Gly Ala Asp Gly Lys Thr Lys Ile Ala Thr
85 90 95

Pro Arg Gly Ala Ala Pro Pro Gly Gln Lys Gly Gln Ala Asn Ala Thr
100 105 110

Arg Ile Pro Ala Lys Thr Pro Pro Ala Pro Lys Thr Pro Pro Ser Ser
115 120 125

Gly Glu Pro Pro Lys Ser Gly Asp Arg Ser Gly Tyr Ser Ser Pro Gly
130 135 140

Ser Pro Gly Thr Pro Gly Ser Arg Ser Arg Thr Pro Ser Leu Pro Thr
145 150 155 160

Pro Pro Thr Arg Glu Pro Lys Lys Val Ala Val Val Arg Thr Pro Pro
165 170 175

Lys Ser Pro Ser Ser Ala Lys Ser Arg Leu Gln Thr Ala Pro Val Pro
180 185 190

```
Met Pro Asp Leu Lys Asn Val Lys Ser Lys Ile Gly Ser Thr Glu Asn
        195                 200                 205

Leu Lys His Gln Pro Gly Gly Gly Lys Val Gln Ile Val Tyr Lys Pro
    210                 215                 220

Val Asp Leu Ser Lys Val Thr Ser Lys Cys Gly Ser Leu Gly Asn Ile
225                 230                 235                 240

His His Lys Pro Gly Gly Gly Gln Val Glu Val Lys Ser Glu Lys Leu
                245                 250                 255

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

Thr His Val Pro Gly Gly Gly Asn Lys Lys Ile Glu Thr His Lys Leu
        275                 280                 285

Thr Phe Arg Glu Asn Ala Lys Ala Lys Thr Asp His Gly Ala Glu Ile
    290                 295                 300

Val Tyr Lys Ser Pro Val Val Ser Gly Asp Thr Ser Pro Arg His Leu
305                 310                 315                 320

Ser Asn Val Ser Ser Thr Gly Ser Ile Asp Met Val Asp Ser Pro Gln
                325                 330                 335

Leu Ala Thr Leu Ala Asp Glu Val Ser Ala Ser Leu Ala Lys Gln Gly
            340                 345                 350

Leu
```

<210> 48
<211> 6670
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 48

```
tggcgaatgg gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg       60

cagcgtgacc gctacacttg ccagcgccct agcgcccgct cctttcgctt tcttcccttc      120

ctttctcgcc acgttcgccg gctttccccg tcaagctcta aatcgggggc tccctttagg      180

gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc      240

acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt      300

ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc      360

ttttgattta taagggattt tgccgatttc ggcctattgg ttaaaaaatg agctgattta      420

acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt      480
```

tcggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt caaatatgta 540
tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat 600
gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt gccttcctgt 660
ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg 720
agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt ttcgccccga 780
agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg tattatcccg 840
tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttggt 900
tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg 960
cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga caacgatcgg 1020
aggaccgaag gagctaaccg ctttttttgca caacatgggg gatcatgtaa ctcgccttga 1080
tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca ccacgatgcc 1140
tgcagcaatg gcaacaacgt tgcgcaaact attaactggc gaactactta ctctagcttc 1200
ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac ttctgcgctc 1260
ggcccttccg gctggctggt ttattgctga taaatctgga gccggtgagc gtgggtctcg 1320
cggtatcatt gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac 1380
gacggggagt caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc 1440
actgattaag cattggtaac tgtcagacca agtttactca tatatacttt agattgattt 1500
aaaacttcat ttttaattta aaaggatcta ggtgaagatc ctttttgata atctcatgac 1560
caaaatccct taacgtgagt tttcgttcca ctgagcgtca gaccccgtag aaaagatcaa 1620
aggatcttct tgagatcctt tttttctgcg cgtaatctgc tgcttgcaaa caaaaaaacc 1680
accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt ttccgaaggt 1740
aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc cgtagttagg 1800
ccaccacttc aagaactctg tagcaccgcc tacatacctc gctctgctaa tcctgttacc 1860
agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa gacgatagtt 1920
accggataag gcgcagcggt cgggctgaac gggggggttcg tgcacacagc ccagcttgga 1980
gcgaacgacc tacaccgaac tgagatacct acagcgtgag ctatgagaaa gcgccacgct 2040
tcccgaaggg agaaaggcgg acaggtatcc ggtaagcggc agggtcggaa caggagagcg 2100
cacgagggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg ggtttcgcca 2160
cctctgactt gagcgtcgat ttttgtgatg ctcgtcaggg gggcggagcc tatggaaaaa 2220
cgccagcaac gcggcctttt tacggttcct ggccttttgc tggccttttg ctcacatgtt 2280
ctttcctgcg ttatcccctg attctgtgga taaccgtatt accgcctttg agtgagctga 2340
taccgctcgc cgcagccgaa cgaccgagcg cagcgagtca gtgagcgagg aagcggaaga 2400
gcgcctgatg cggtattttc tccttacgca tctgtgcggt atttcacacc gcatatatgg 2460
tgcactctca gtacaatctg ctctgatgcc gcatagttaa gccagtatac actccgctat 2520

cgctacgtga ctgggtcatg gctgcgcccc gacacccgcc aacacccgct gacgcgccct 2580

gacgggcttg tctgctcccg gcatccgctt acagacaagc tgtgaccgtc tccgggagct 2640

gcatgtgtca gaggttttca ccgtcatcac cgaaacgcgc gaggcagctg cggtaaagct 2700

catcagcgtg gtcgtgaagc gattcacaga tgtctgcctg ttcatccgcg tccagctcgt 2760

tgagtttctc cagaagcgtt aatgtctggc ttctgataaa gcgggccatg ttaagggcgg 2820

ttttttcctg tttggtcact gatgcctccg tgtaaggggg atttctgttc atgggggtaa 2880

tgataccgat gaaacgagag aggatgctca cgatacgggt tactgatgat gaacatgccc 2940

ggttactgga acgttgtgag ggtaaacaac tggcggtatg gatgcggcgg gaccagagaa 3000

aaatcactca gggtcaatgc cagcgcttcg ttaatacaga tgtaggtgtt ccacagggta 3060

gccagcagca tcctgcgatg cagatccgga acataatggt gcagggcgct gacttccgcg 3120

tttccagact ttacgaaaca cggaaaccga agaccattca tgttgttgct caggtcgcag 3180

acgttttgca gcagcagtcg cttcacgttc gctcgcgtat cggtgattca ttctgctaac 3240

cagtaaggca accccgccag cctagccggg tcctcaacga caggagcacg atcatgcgca 3300

cccgtggggc cgccatgccg gcgataatgg cctgcttctc gccgaaacgt ttggtggcgg 3360

gaccagtgac gaaggcttga gcgagggcgt gcaagattcc gaataccgca agcgacaggc 3420

cgatcatcgt cgcgctccag cgaaagcggt cctcgccgaa aatgacccag agcgctgccg 3480

gcacctgtcc tacgagttgc atgataaaga agacagtcat aagtgcggcg acgatagtca 3540

tgccccgcgc ccaccggaag gagctgactg ggttgaaggc tctcaagggc atcggtcgag 3600

atcccggtgc ctaatgagtg agctaactta cattaattgc gttgcgctca ctgcccgctt 3660

tccagtcggg aaacctgtcg tgccagctgc attaatgaat cggccaacgc gcggggagag 3720

gcggtttgcg tattgggcgc cagggtggtt tttcttttca ccagtgagac gggcaacagc 3780

tgattgccct tcaccgcctg gccctgagag agttgcagca agcggtccac gctggtttgc 3840

cccagcaggc gaaaatcctg tttgatggtg gttaacggcg ggatataaca tgagctgtct 3900

tcggtatcgt cgtatcccac taccgagatg tccgcaccaa cgcgcagccc ggactcggta 3960

atggcgcgca ttgcgcccag cgccatctga tcgttggcaa ccagcatcgc agtgggaacg 4020

atgccctcat tcagcatttg catggtttgt tgaaaaccgg acatggcact ccagtcgcct 4080

tcccgttccg ctatcggctg aatttgattg cgagtgagat atttatgcca gccagccaga 4140

cgcagacgcg ccgagacaga acttaatggg cccgctaaca gcgcgatttg ctggtgaccc 4200

aatgcgacca gatgctccac gcccagtcgc gtaccgtctt catgggagaa aataatactg 4260

ttgatgggtg tctggtcaga gacatcaaga aataacgccg gaacattagt gcaggcagct 4320

tccacagcaa tggcatcctg gtcatccagc ggatagttaa tgatcagccc actgacgcgt 4380

tgcgcgagaa gattgtgcac cgccgcttta caggcttcga cgccgcttcg ttctaccatc 4440

gacaccacca cgctggcacc cagttgatcg gcgcgagatt taatcgccgc gacaatttgc 4500

gacggcgcgt gcagggccag actggaggtg gcaacgccaa tcagcaacga ctgtttgccc 4560

gccagttgtt gtgccacgcg gttgggaatg taattcagct ccgccatcgc cgcttccact 4620

ttttcccgcg ttttcgcaga aacgtggctg gcctggttca ccacgcggga aacggtctga 4680

taagagacac cggcatactc tgcgacatcg tataacgtta ctggtttcac attcaccacc 4740

ctgaattgac tctcttccgg gcgctatcat gccataccgc gaaaggtttt gcgccattcg 4800

atggtgtccg ggatctcgac gctctccctt atgcgactcc tgcattagga agcagcccag 4860

tagtaggttg aggccgttga gcaccgccgc cgcaaggaat ggtgcatgca aggagatggc 4920

gcccaacagt cccccggcca cggggcctgc caccataccc acgccgaaac aagcgctcat 4980

gagcccgaag tggcgagccc gatcttcccc atcggtgatg tcggcgatat aggcgccagc 5040

aaccgcacct gtggcgccgg tgatgccggc cacgatgcgt ccggcgtaga ggatcgagat 5100

cgatctcgat cccgcgaaat taatacgact cactataggg gaattgtgag cggataacaa 5160

ttcccctcta gaaataattt tgtttaactt taagaaggag atatacatat gggctcaagc 5220

caccaccacc accaccacag cagcggcgag aacttgtact ttcaaggatc cgcagaacca 5280

cgtcaagaat ttgaggttat ggaagatcac gcgggcactt acggtttggg tgatcgtaaa 5340

gaccagggcg gctataccat gcatcaagat caagagggcg acaccgatgc tggcttgaaa 5400

gagtcgccgc tgcagactcc gaccgaggat ggcagcgaag agccgggcag cgagactagc 5460

gatgcgaagt cgaccccgac cgccgaggca gaagaggcgg gtatcggcga cactccgtcc 5520

ctggaagatg aggcagccgg tcatgtcacg caggcgcgta tggtgagcaa gagcaaagat 5580

ggtacgggta gcgacgacaa gaaggcgaag ggcgcagatg gcaagaccaa aattgcgacg 5640

ccgcgtggtg cggcaccgcc aggccagaaa ggtcaggcga atgccacgcg catcccggca 5700

aagacgccac cggctccgaa aaccccgcct tccagcggtg aaccgccgaa atccggtgac 5760

cgcagcggtt atagctctcc gggtagcccg ggtaccccag gcagccgtag ccgcaccccg 5820

agcctgccga ccccaccgac ccgcgagccg aagaaagtgg cggtggttcg tacgccgcca 5880

aaaagcccga gctctgccaa gagccgtctg caaaccgctc ctgtgccgat gccggacctg 5940

aagaacgtta agtctaaaat cggtagcacc gaaaatctga agcaccaacc tggtggcggt 6000

aaggttcaaa tcatcaacaa aaagctggac ttgagcaatg tacaaagcaa gtgtggtagc 6060

aaggacaata tcaaacacgt cccgggtggt ggttccgtcc agattgtgta caaaccggtg 6120

gacctgagca aggttaccag caaatgcggt tccctgggta acatccatca taaaccgggt 6180

ggcggccaag ttgaggtcaa gagcgagaaa ctggacttca aagaccgcgt tcagtccaaa 6240

atcggttctc tggacaacat tacgcacgtg cctggtggtg gcaacaagaa gattgaaacc 6300

cataaactga cgtttcgtga aaatgcgaag gcgaaaaccg accacggcgc agagattgtc 6360

tacaaaagcc cggtggtgag cggtgatacc agcccgcgtc acctgtccaa cgtcagcagc 6420

acgggcagca ttgatatggt ggatagcccg cagttggcta cgctggccga tgaggttagc 6480

gcgagcctgg cgaagcaggg tctgtgactc gagcaccacc accaccacca ctgagatccg 6540

gctgctaaca aagcccgaaa ggaagctgag ttggctgctg ccaccgctga gcaataacta 6600

gcataacccc ttggggcctc taaacgggtc ttgaggggtt ttttgctgaa aggaggaact 6660

atatccggat 6670

<210> 49
<211> 432
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 49

Met Gly Ser Ser His His His His His His Ser Ser Gly Glu Asn Leu
1 5 10 15

Tyr Phe Gln Gly Ser Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu
20 25 30

Asp His Ala Gly Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly
35 40 45

Tyr Thr Met His Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys
50 55 60

Glu Ser Pro Leu Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly
65 70 75 80

Ser Glu Thr Ser Asp Ala Lys Ser Thr Pro Thr Ala Glu Ala Glu Glu
85 90 95

Ala Gly Ile Gly Asp Thr Pro Ser Leu Glu Asp Glu Ala Ala Gly His
100 105 110

Val Thr Gln Ala Arg Met Val Ser Lys Ser Lys Asp Gly Thr Gly Ser
115 120 125

Asp Asp Lys Lys Ala Lys Gly Ala Asp Gly Lys Thr Lys Ile Ala Thr
130 135 140

Pro Arg Gly Ala Ala Pro Pro Gly Gln Lys Gly Gln Ala Asn Ala Thr
145 150 155 160

Arg Ile Pro Ala Lys Thr Pro Pro Ala Pro Lys Thr Pro Pro Ser Ser
165 170 175

Gly Glu Pro Pro Lys Ser Gly Asp Arg Ser Gly Tyr Ser Ser Pro Gly
180 185 190

Ser Pro Gly Thr Pro Gly Ser Arg Ser Arg Thr Pro Ser Leu Pro Thr
195 200 205

Pro Pro Thr Arg Glu Pro Lys Lys Val Ala Val Val Arg Thr Pro Pro
210 215 220

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

Met Pro Asp Leu Lys Asn Val Lys Ser Lys Ile Gly Ser Thr Glu Asn
245 250 255

Leu Lys His Gln Pro Gly Gly Gly Lys Val Gln Ile Ile Asn Lys Lys
260 265 270

Leu Asp Leu Ser Asn Val Gln Ser Lys Cys Gly Ser Lys Asp Asn Ile
275 280 285

Lys His Val Pro Gly Gly Gly Ser Val Gln Ile Val Tyr Lys Pro Val
290 295 300

Asp Leu Ser Lys Val Thr Ser Lys Cys Gly Ser Leu Gly Asn Ile His
305 310 315 320

His Lys Pro Gly Gly Gly Gln Val Glu Val Lys Ser Glu Lys Leu Asp
325 330 335

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

His Val Pro Gly Gly Gly Asn Lys Lys Ile Glu Thr His Lys Leu Thr
355 360 365

Phe Arg Glu Asn Ala Lys Ala Lys Thr Asp His Gly Ala Glu Ile Val
370 375 380

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

Asn Val Ser Ser Thr Gly Ser Ile Asp Met Val Asp Ser Pro Gln Leu
405 410 415

Ala Thr Leu Ala Asp Glu Val Ser Ala Ser Leu Ala Lys Gln Gly Leu
420 425 430

<210> 50
<211> 413
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 50

Gly Ser Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala
1 5 10 15

```
Gly Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met
            20                  25                  30

His Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro
        35                  40                  45

Leu Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr
    50                  55                  60

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

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

Ala Arg Met Val Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys
            100                 105                 110

Lys Ala Lys Gly Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly
        115                 120                 125

Ala Ala Pro Pro Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro
    130                 135                 140

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

Pro Lys Ser Gly Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly
                165                 170                 175

Thr Pro Gly Ser Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr
            180                 185                 190

Arg Glu Pro Lys Lys Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro
        195                 200                 205

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

Leu Lys Asn Val Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His
225                 230                 235                 240

Gln Pro Gly Gly Gly Lys Val Gln Ile Ile Asn Lys Lys Leu Asp Leu
                245                 250                 255

Ser Asn Val Gln Ser Lys Cys Gly Ser Lys Asp Asn Ile Lys His Val
            260                 265                 270

Pro Gly Gly Gly Ser Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser
        275                 280                 285
```

```
Lys Val Thr Ser Lys Cys Gly Ser Leu Gly Asn Ile His His Lys Pro
    290                 295                 300

Gly Gly Gly Gln Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp
305                 310                 315                 320

Arg Val Gln Ser Lys Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro
                325                 330                 335

Gly Gly Gly Asn Lys Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu
            340                 345                 350

Asn Ala Lys Ala Lys Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser
        355                 360                 365

Pro Val Val Ser Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser
    370                 375                 380

Ser Thr Gly Ser Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu
385                 390                 395                 400

Ala Asp Glu Val Ser Ala Ser Leu Ala Lys Gln Gly Leu
                405                 410
```

<210> 51
<211> 6016
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 51

```
gctgcttcgc gatgtacggg ccagatatac gcgttttgag atttctgtcg ccgactaaat       60

tcatgtcgcg cgatagtggt gtttatcgcc gatagagatg gcgatattgg aaaaatcggc      120

ggccgccgat atttgaaaat atggcatatt gaaaatgtcg ccgatgtgag tttctgtgta      180

actgacatcg ccatttttcc aaaagtgatt tttgggcata cgcggtatct ggcgatagcg      240

cttatatcgt ttacggggga tggcgataga cgactttggt gacttgggcg attctgtgtg      300

tcgcaaatat cgcagtttcg atataggtga cagacgatat gaggctatat cgccgataga      360

ggcgacatca agctggcaca tggccaatgc atatcgatct atacattgaa tcaatattgg      420

ccattagcca tattattcat tggttatata gcataaatca atattggcta ttggccattg      480

catacgttgt atccatatca taatatgtac atttatattg gctcatgtcc aacattaccg      540

ccatgttgac attgattatt gactagttat taatagtaat caattacggg gtcattagtt      600

catagcccat atatggagtt ccgcgttaca taacttacgg taaatggccc gcctggctga      660

ccgcccaacg acccccgccc attgacgtca ataatgacgt atgttcccat agtaacgcca      720

atagggactt tccattgacg tcaatgggtg gagtatttac ggtaaactgc ccacttggca      780
```

gtacatcaag tgtatcatat gccaagtacg ccccctattg acgtcaatga cggtaaatgg 840

cccgcctggc attatgccca gtacatgacc ttatgggact ttcctacttg gcagtacatc 900

tacgtattag tcatcgctat tacaatggtg atgcggtttt ggcagtacat caatgggcgt 960

ggatagcggt ttgactcacg gggatttcca agtctccacc ccattgacgt caatgggagt 1020

ttgttttggc accaaaatca acgggacttt ccaaaatgtc gtaacaactc cgccccattg 1080

acgcaaatgg gcggtaggcg tgtacggtgg gaggtctata taagcagaac tcgtttagtg 1140

aaccgtcaga tcgcctggag acgccatcca cgctgttttg acctccatag aagacaccgg 1200

gaccgatcca gcctccgcgg ccgggaacgg tgcattggaa cgcggattcc ccgtgccaag 1260

agtgacgtaa gtaccgccta tagagtctat aggcccaccc cattggcttc ttatgcatgc 1320

tatactgttt ttggcttggg gtctatacac ccccgcttcc tcatgttata ggtgatggta 1380

tagcttagcc tataggtgtg ggttattgac cattattgac cactccccta ttggtgacga 1440

tactttccat tactaatcca taacatggct ctttgccaca actctcttta ttggctatat 1500

gccaatacac tgtccttcag agactgacac ggactctgta tttttacagg atggggtctc 1560

atttattatt tacaaattca catatacaac accaccgtcc ccagtgcccg cagtttttat 1620

taaacataac gtgggatctc cacgcgaatc tagggtacgt gttacggaca tgggctattc 1680

tcaggtagcg gcggagcttc tacatccgag ccctgctccc atgcctccag cgaatcatgg 1740

tcgctcggca gctccttgct cctaacagtg gaggccagac ttaggcacag cacgatgccc 1800

accaccacca gtgtgccgca caaggccgtg gcggtagggt atgtgtctga aaatgaacta 1860

ggggagcggg cttgcaccgc tgacgcattt ggaagactta aggcagcggc agaagaagat 1920

gcaggcaact gagttgttgt gttctgataa gagtcagagg taactcccgt tgcggtgctg 1980

ttaacggtgg agggcagtgt agtctgagca gtactcgttg ctgccgcacg cgccaccaga 2040

cataatagct gacagactaa cagactgttc ctttcaatgg gtcttttatg cagtcaccgt 2100

ccttgacacg aagcttgcca ccatgggctc aagccaccat caccaccacc atcatcacca 2160

ccacagcagc ggcgagaact tgtactttca aggatccgct gagccccgcc aggagttcga 2220

agtgatggaa gatcacgctg ggacgtacgg gttgggggac aggaaagatc agggggggcta 2280

caccatgcac caagaccaag agggtgacac ggacgctggc ctgaaagaat ctcccctgca 2340

gacccccact gaggacggat ctgaggaacc gggctctgaa acctctgatg ctaagagcac 2400

tccaacagcg gaagatgtga cagcaccctt agtggatgag ggagctcccg gcaagcaggc 2460

tgccgcgcag ccccacacgg agatcccaga aggaaccaca gctgaagaag caggcattgg 2520

agacaccccc agcctggaag acgaagctgc tggtcacgtg acccaagctc gcatggtcag 2580

taaaagcaaa gacgggactg gaagcgatga caaaaaagcc aaggggggctg atggtaaaac 2640

gaagatcgcc acaccgcggg gagcagcccc tccaggccag aagggccagg ccaacgccac 2700

caggattcca gcaaaaaccc cgcccgctcc aaagacacca cccagctctg gtgaacctcc 2760

aaaatcaggg gatcgcagcg gctacagcag ccccggctcc ccaggcactc ccggcagccg 2820

ctcccgcacc ccgtcccttc caaccccacc cacccgggag cccaagaagg tggcagtggt 2880

ccgtactcca cccaagtcgc cgtcttccgc caagagccgc ctgcagacag cccccgtgcc 2940

catgccagac ctgaagaatg tcaagtccaa gatcggctcc actgagaacc tgaagcacca 3000

gccgggaggc gggaaggtgc agataattaa taagaagctg gatcttagca acgtccagtc 3060

caagtgtggc tcaaaggata atatcaaaca cgtcccggga ggcggcagtg tgcaaatagt 3120

ctacaaacca gttgacctga gcaaggtgac ctccaagtgt ggctcattag gcaacatcca 3180

tcataaacca ggaggtggcc aggtggaagt aaaatctgag aagctagact tcaaggacag 3240

agtccagtcg aagattgggt ccctggacaa tatcacccac gtccctggcg gaggaaataa 3300

aaagattgaa acccacaagc tgaccttccg cgagaacgcc aaagccaaga cagaccacgg 3360

ggcggagatc gtgtacaagt cgccagtggt gtctggggac acgtctccac ggcatctcag 3420

caatgtctcc tccaccggca gcatcgacat ggtagactcg ccccagctcg ccacgctagc 3480

tgacgaggtg tctgcctccc tggccaagca gggtttgtga ctcgaggaga acttgtactt 3540

ccagggaagt ggtggcagtc atcaccatca ccatcaccat caccatcact gagaattcat 3600

tgatcataat cagccatacc acatttgtag aggttttact tgctttaaaa aacctcccac 3660

acctcccccc gaacctgaaa cataaaatga atgcaattgt tgttgttaac ttgtttattg 3720

cagcttataa tggttacaaa taaagcaata gcatcacaaa tttcacaaat aaagcatttt 3780

tttcactgca ttctagttgt ggtttgtcca aactcatcaa tgtatcttat catgtctgaa 3840

tcctctacgc cggacgcatc gtggccggca tcaccggcgc cacaggtgcg gttgctggcg 3900

cctatatcgc cgacatcacc gatggggaag atcgggctcg ccacttcggg ctcatgagcg 3960

cttgtttcgg cgtgggtatg gtggcaggcc ccgtggccgg gggactgttg ggcgccatct 4020

ccttgcatgc accattcctt gcggcggcgg tgctcaacgg cctcaaccta ctactgggct 4080

gcttcctaat gcaggagtcg cataagggag agcgtcgact ggggcgccct ctggtaaggt 4140

tgggaagccc tgcaaagtaa actggatggc tttctcgccg ccaagcatct gatggcgcag 4200

gggatcaagc tctgatcaag agacaggatg aggatcgttt cgcatgattg aacaagatgg 4260

attgcacgca ggttctccgg ccgcttgggt ggagaggcta ttcggctatg actgggcaca 4320

acagacaatc ggctgctctg atgccgccgt gttccggctg tcagcgcagg ggcgcccggt 4380

tctttttgtc aagaccgacc tgtccggtgc cctgaatgaa ctgcaagacg aggcagcgcg 4440

gctatcgtgg ctggccacga cgggcgttcc ttgcgcagca gtgctcgacg ttgtcactga 4500

agcgggaagg gactggctgc tattgggcga agtgccgggg caggatctcc tgtcatctca 4560

ccttgctcct gccgagaaag tatccatcat ggctgatgca atgcggcggc tgcatacgct 4620

tgatccggct acctgcccat tcgaccacca agcgaaacat cgcatcgagc gagcacgtac 4680

tcggatggaa gccggtcttg tcgatcagga tgatctggac gaagagcatc aggggctcgc 4740

gccagccgaa ctgttcgcca ggctcaaggc gagcatgccc gacggcgagg atctcgtcgt 4800

gacccacggc gatgcctgct tgccgaatat catggtggaa aatggccgct tttctggatt 4860

catcgactgt ggccggctgg gtgtggcgga ccgctatcag gacatagcgt tggctacccg 4920

tgatattgct gaagagcttg gcggcgaatg ggctgaccgc ttcctcgtgc tttacggtat 4980

cgccgctccc gattcgcagc gcatcgcctt ctatcgcctt cttgacgagt tcttctgaat 5040

tattaacgct tacaatttcc tgatgcggta ttttctcctt acgcatctgt gcggtatttc 5100

acaccgcatc aggtggcact tttcggggaa atgtgcgcgg aacccctatt tgtttatttt 5160

tctaaataca ttcaaatatg tatccgctca tgagacaata accctgataa atgcttcaat 5220

aatagcacgt gctaaaactt catttttaat ttaaaaggat ctaggtgaag atccttttg 5280

ataatctcat gaccaaaatc ccttaacgtg agttttcgtt ccactgagcg tcagaccccg 5340

tagaaaagat caaaggatct tcttgagatc ctttttttct gcgcgtaatc tgctgcttgc 5400

aaacaaaaaa accaccgcta ccagcggtgg tttgtttgcc ggatcaagag ctaccaactc 5460

tttttccgaa ggtaactggc ttcagcagag cgcagatacc aaatactgtt cttctagtgt 5520

agccgtagtt aggccaccac ttcaagaact ctgtagcacc gcctacatac ctcgctctgc 5580

taatcctgtt accagtggct gctgccagtg gcgataagtc gtgtcttacc gggttggact 5640

caagacgata gttaccggat aaggcgcagc ggtcgggctg aacgggggt tcgtgcacac 5700

agcccagctt ggagcgaacg acctacaccg aactgagata cctacagcgt gagctatgag 5760

aaagcgccac gcttcccgaa gggagaaagg cggacaggta tccggtaagc ggcagggtcg 5820

gaacaggaga gcgcacgagg gagcttccag ggggaaacgc ctggtatctt tatagtcctg 5880

tcgggtttcg ccacctctga cttgagcgtc gatttttgtg atgctcgtca gggggggcgga 5940

gcctatggaa aaacgccagc aacgcggcct ttttacggtt cctggccttt tgctggcctt 6000

ttgctcacat gttctt 6016

<210> 52
<211> 465
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 52

Met Gly Ser Ser His His His His His His His His His His Ser Ser
1 5 10 15

Gly Glu Asn Leu Tyr Phe Gln Gly Ser Ala Glu Pro Arg Gln Glu Phe
20 25 30

Glu Val Met Glu Asp His Ala Gly Thr Tyr Gly Leu Gly Asp Arg Lys
35 40 45

Asp Gln Gly Gly Tyr Thr Met His Gln Asp Gln Glu Gly Asp Thr Asp
50 55 60

```
Ala Gly Leu Lys Glu Ser Pro Leu Gln Thr Pro Thr Glu Asp Gly Ser
65                  70                  75                  80

Glu Glu Pro Gly Ser Glu Thr Ser Asp Ala Lys Ser Thr Pro Thr Ala
                85                  90                  95

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

Ala Ala Ala Gln Pro His Thr Glu Ile Pro Glu Gly Thr Thr Ala Glu
        115                 120                 125

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

His Val Thr Gln Ala Arg Met Val Ser Lys Ser Lys Asp Gly Thr Gly
145                 150                 155                 160

Ser Asp Asp Lys Lys Ala Lys Gly Ala Asp Gly Lys Thr Lys Ile Ala
                165                 170                 175

Thr Pro Arg Gly Ala Ala Pro Pro Gly Gln Lys Gly Gln Ala Asn Ala
            180                 185                 190

Thr Arg Ile Pro Ala Lys Thr Pro Pro Ala Pro Lys Thr Pro Pro Ser
        195                 200                 205

Ser Gly Glu Pro Pro Lys Ser Gly Asp Arg Ser Gly Tyr Ser Ser Pro
    210                 215                 220

Gly Ser Pro Gly Thr Pro Gly Ser Arg Ser Arg Thr Pro Ser Leu Pro
225                 230                 235                 240

Thr Pro Pro Thr Arg Glu Pro Lys Lys Val Ala Val Val Arg Thr Pro
                245                 250                 255

Pro Lys Ser Pro Ser Ser Ala Lys Ser Arg Leu Gln Thr Ala Pro Val
            260                 265                 270

Pro Met Pro Asp Leu Lys Asn Val Lys Ser Lys Ile Gly Ser Thr Glu
        275                 280                 285

Asn Leu Lys His Gln Pro Gly Gly Gly Lys Val Gln Ile Ile Asn Lys
    290                 295                 300

Lys Leu Asp Leu Ser Asn Val Gln Ser Lys Cys Gly Ser Lys Asp Asn
305                 310                 315                 320

Ile Lys His Val Pro Gly Gly Gly Ser Val Gln Ile Val Tyr Lys Pro
                325                 330                 335
```

Val Asp Leu Ser Lys Val Thr Ser Lys Cys Gly Ser Leu Gly Asn Ile
340 345 350

His His Lys Pro Gly Gly Gly Gln Val Glu Val Lys Ser Glu Lys Leu
355 360 365

Asp Phe Lys Asp Arg Val Gln Ser Lys Ile Gly Ser Leu Asp Asn Ile
370 375 380

Thr His Val Pro Gly Gly Gly Asn Lys Lys Ile Glu Thr His Lys Leu
385 390 395 400

Thr Phe Arg Glu Asn Ala Lys Ala Lys Thr Asp His Gly Ala Glu Ile
405 410 415

Val Tyr Lys Ser Pro Val Val Ser Gly Asp Thr Ser Pro Arg His Leu
420 425 430

Ser Asn Val Ser Ser Thr Gly Ser Ile Asp Met Val Asp Ser Pro Gln
435 440 445

Leu Ala Thr Leu Ala Asp Glu Val Ser Ala Ser Leu Ala Lys Gln Gly
450 455 460

Leu
465

<210> 53
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 53

Gly Ser Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala
1 5 10 15

Gly Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met
20 25 30

His Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro
35 40 45

Leu Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr
50 55 60

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

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

```
Glu Ile Pro Glu Gly Thr Thr Ala Glu Glu Ala Gly Ile Gly Asp Thr
            100                 105                 110

Pro Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Ala Arg Met
        115                 120                 125

Val Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Lys Ala Lys
    130                 135                 140

Gly Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala Ala Pro
145                 150                 155                 160

Pro Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala Lys Thr
                165                 170                 175

Pro Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro Lys Ser
            180                 185                 190

Gly Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro Gly
        195                 200                 205

Ser Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg Glu Pro
    210                 215                 220

Lys Lys Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser Ser Ala
225                 230                 235                 240

Lys Ser Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn
                245                 250                 255

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

Gly Gly Lys Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser Asn Val
        275                 280                 285

Gln Ser Lys Cys Gly Ser Lys Asp Asn Ile Lys His Val Pro Gly Gly
    290                 295                 300

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

Ser Lys Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gly
                325                 330                 335

Gln Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln
            340                 345                 350

Ser Lys Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Gly
        355                 360                 365
```

```
Asn Lys Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn Ala Lys
    370                 375                 380

Ala Lys Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro Val Val
385                 390                 395                 400

Ser Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser Thr Gly
                405                 410                 415

Ser Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu
            420                 425                 430

Val Ser Ala Ser Leu Ala Lys Gln Gly Leu
        435                 440


<210>  54
<211>  448
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  humanized

<400>  54

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asn
            20                  25                  30

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

Gly Thr Ile Trp Thr Asp Gly Ser Thr Asn Tyr Asn Ala Ala Val Gln
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

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

Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140
```

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

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

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

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

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

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

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335

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

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415
```

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 55
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized

<400> 55

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asn
20 25 30

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

Gly Thr Ile Trp Thr Asp Gly Ser Thr Asn Tyr Asn Thr Ala Val Gln
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

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

Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

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

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

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

```
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

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

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

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

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335

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

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 56
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>

<223> humanized

<400> 56
gaggtgcagc tgcaggaatc cggtcccggc ctcgtgaagc cttcagaaac cctgtcgctc 60

acatgcactg tgtccgggtt ctccctgacc tctaacgaca tcgcctggat tcggcagccg 120

ccaggaaagg gactggagtg gatgggcacc atttggaccg acgggtcaac caactacaat 180

gccgcggtgc aatccagagt gaccatcagc gtggacacgt ccaagaacca gttctcgctg 240

aaattgagct ccgtgactgc cgctgatact gccgtgtatt actgtgcccg gcaccgcctt 300

tactacggcg catttgacta ctggggacag ggaaccatgg tcactgtctc gagtgcctcc 360

accaagggcc cctccgtgtt cccgctcgct ccatcatcga agtctaccag cggaggcact 420

gcggctctcg gttgcctcgt gaaggactac ttcccggagc cggtgaccgt gtcgtggaac 480

agcggagccc tgaccagcgg ggtgcacacc tttccggccg tcttgcagtc aagcggcctt 540

tactccctgt catcagtggt gactgtcccg tccagctcat tgggaaccca aacctacatc 600

tgcaatgtga atcacaaacc tagcaacacc aaggttgaca agaaagtcga gcccaaatcg 660

tgtgacaaga ctcacacttg tccgccgtgc ccggcacccg aactgctggg aggtcccagc 720

gtctttctgt tccctccaaa gccgaaagac acgctgatga tctcccgcac cccggaggtc 780

acttgcgtgg tcgtggacgt gtcacatgag gacccagagg tgaagttcaa ttggtacgtg 840

gatggcgtcg aagtccacaa tgccaaaact aagcccagag aagaacagta caattcgacc 900

taccgcgtcg tgtccgtgct cacggtgttg catcaggatt ggctgaacgg gaaggaatac 960

aagtgcaaag tgtccaacaa ggcgctgccg gcaccgatcg agaaaactat ctccaaagcg 1020

aagggacagc ctagggaacc tcaagtctac acgctgccac catcacggga tgaactgact 1080

aagaatcaag tctcactgac ttgtctggtg aaggggtttt accctagcga cattgccgtg 1140

gagtgggaat ccaacggcca gccagagaac aactacaaga ctacccctcc agtgctcgac 1200

tcggatggat cgttcttcct ttactcgaag ctcaccgtgg ataagtcccg gtggcagcag 1260

ggaaacgtgt tctcctgctc ggtgatgcat gaagccctcc ataaccacta tacccaaaag 1320

tcgctgtccc tgtcgccggg aaag 1344

<210> 57
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized

<400> 57
gaggtgcaac tgcaggaatc cggtcccggc ctcgtgaagc cttcagaaac cctgtcgctc 60

acatgcactg tgtccgggtt ctccctgacc tctaacgaca tcgcctggat tcggcagccg 120

ccaggaaagg gactggagtg gatgggcacc atttggaccg acgggtcaac caactacaat 180

accgcggtgc aatccagagt gaccatcagc gtggacacgt ccaagaacca gttctcgctg 240

aaattgagct ccgtgactgc cgctgatact gccgtgtatt actgtgcccg gcaccgcctt 300

tactacggcg catttgacta ctggggacag ggaaccatgg tcactgtctc gagtgcctcc 360

accaagggcc cctccgtgtt cccgctcgct ccatcatcga agtctaccag cggaggcact 420

gcggctctcg gttgcctcgt gaaggactac ttcccggagc cggtgaccgt gtcgtggaac 480

agcggagccc tgaccagcgg ggtgcacacc tttccggccg tcttgcagtc aagcggcctt 540

tactccctgt catcagtggt gactgtcccg tccagctcat tgggaaccca aacctacatc 600

tgcaatgtga atcacaaacc tagcaacacc aaggttgaca agaaagtcga gcccaaatcg 660

tgtgacaaga ctcacacttg tccgccgtgc ccggcacccg aactgctggg aggtcccagc 720

gtctttctgt tccctccaaa gccgaaagac acgctgatga tctcccgcac cccggaggtc 780

acttgcgtgg tcgtggacgt gtcacatgag gacccagagg tgaagttcaa ttggtacgtg 840

gatggcgtcg aagtccacaa tgccaaaact aagcccagag aagaacagta caattcgacc 900

taccgcgtcg tgtccgtgct cacggtgttg catcaggatt ggctgaacgg gaaggaatac 960

aagtgcaaag tgtccaacaa ggcgctgccg gcaccgatcg agaaaactat ctccaaagcg 1020

aagggacagc ctagggaacc tcaagtctac acgctgccac catcacggga tgaactgact 1080

aagaatcaag tctcactgac ttgtctggtg aaggggtttt accctagcga cattgccgtg 1140

gagtgggaat ccaacggcca gccagagaac aactacaaga ctacccctcc agtgctcgac 1200

tcggatggat cgttcttcct ttactcgaag ctcaccgtgg ataagtcccg gtggcagcag 1260

ggaaacgtgt tctcctgctc ggtgatgcat gaagccctcc ataaccacta tacccaaaag 1320

tcgctgtccc tgtcgccggg aaag 1344