SEQUENCE LISTING

<110> CARISMA THERAPEUTICS INC.

<120> SELF-POLARIZING IMMUNE CELLS

<130> 2012851-0124

<140> PCT/US2022/014936
<141> 2022-02-02

<150> 63/144,860
<151> 2021-02-02

<160> 179

<170> PatentIn version 3.5

<210> 1
<211> 165
<212> PRT
<213> Homo sapiens

<400> 1

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Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
1               5                  10                  15


Leu Leu Ala Gln Met Arg Lys Ile Ser Leu Phe Ser Cys Leu Lys Asp
            20                  25                  30


Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
        35                  40                  45


Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
    50                  55                  60


Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
65                  70                  75                  80


Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
                85                  90                  95


Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
            100                 105                 110
```

```
Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
        115                 120                 125

Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
    130                 135                 140

Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
145                 150                 155                 160

Leu Arg Ser Lys Glu
                165
```

<210> 2
<211> 166
<212> PRT
<213> Homo sapiens

<400> 2

```
Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
1               5                   10                  15

Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu
            20                  25                  30

Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln
        35                  40                  45

Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
    50                  55                  60

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

Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
                85                  90                  95

His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr
            100                 105                 110
```

```
Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
        115                 120                 125


Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
    130                 135                 140


Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu
145                 150                 155                 160


Thr Gly Tyr Leu Arg Asn
                165
```

<210> 3
<211> 138
<212> PRT
<213> Homo sapiens

<400> 3

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


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


Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln
        35                  40                  45


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


Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val Lys
65                  70                  75                  80


Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp Phe Glu Lys Leu Thr
                85                  90                  95


Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg Lys Ala Ile His Glu
            100                 105                 110
```

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

Arg Lys Arg Ser Gln Met Leu Phe Arg Gly
    130                 135
```

<210> 4
<211> 157
<212> PRT
<213> Homo sapiens

<400> 4

```
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
1               5                   10                  15

Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
            20                  25                  30

Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
        35                  40                  45

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

Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
65                  70                  75                  80

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

Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
            100                 105                 110

Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
        115                 120                 125

Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
    130                 135                 140
```

```
Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145                 150                 155


<210> 5
<211> 153
<212> PRT
<213> Homo sapiens

<400> 5
Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg Asp Ser Gln Gln Lys
1               5                   10                  15


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


Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser Met Ser Phe Val Gln
        35                  40                  45


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


Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp Asp Lys Pro Thr Leu
65                  70                  75                  80


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


Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn Asn Lys Leu Glu Phe
            100                 105                 110


Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser Thr Ser Gln Ala Glu
        115                 120                 125


Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly Gly Gln Asp Ile Thr
    130                 135                 140


Asp Phe Thr Met Gln Phe Val Ser Ser
145                 150
```

<210> 6
<211> 183
<212> PRT
<213> Homo sapiens

<400> 6

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

Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu
            20                  25                  30

Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met
        35                  40                  45

Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro
    50                  55                  60

Lys Met Ala Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu
65                  70                  75                  80

Thr Cys Leu Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr
                85                  90                  95

Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg
            100                 105                 110

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

Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala
    130                 135                 140

Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp Met
145                 150                 155                 160

Thr Thr His Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser
                165                 170                 175
```

```
Leu Arg Ala Leu Arg Gln Met
            180


<210> 7
<211> 197
<212> PRT
<213> Homo sapiens

<400> 7
Arg Asn Leu Pro Val Ala Thr Pro Asp Pro Gly Met Phe Pro Cys Leu
1               5                   10                  15


His His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Met Leu Gln Lys
            20                  25                  30


Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr Ser Glu Glu Ile Asp
        35                  40                  45


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


Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn Ser Arg Glu Thr
65                  70                  75                  80


Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe
                85                  90                  95


Met Met Ala Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
            100                 105                 110


Gln Val Glu Phe Lys Thr Met Asn Ala Lys Leu Leu Met Asp Pro Lys
        115                 120                 125


Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Ala Val Ile Asp Glu Leu
    130                 135                 140


Met Gln Ala Leu Asn Phe Asn Ser Glu Thr Val Pro Gln Lys Ser Ser
145                 150                 155                 160
```

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
165 170 175

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Val Met Ser
180 185 190

Tyr Leu Asn Ala Ser
195

<210> 8
<211> 306
<212> PRT
<213> Homo sapiens

<400> 8
Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr
1 5 10 15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu
20 25 30

Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val Leu Gly
35 40 45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu
65 70 75 80

Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
85 90 95

Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys
100 105 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr
115 120 125

```
Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
    130                 135                 140

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

Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala
                165                 170                 175

Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala
            180                 185                 190

Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg
        195                 200                 205

Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu
    210                 215                 220

Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp
225                 230                 235                 240

Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln
                245                 250                 255

Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys Thr
            260                 265                 270

Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala
        275                 280                 285

Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro
    290                 295                 300

Cys Ser
305
```

<210> 9
<211> 129
<212> PRT
<213> Homo sapiens

<400> 9
His Lys Cys Asp Ile Thr Leu Gln Glu Ile Ile Lys Thr Leu Asn Ser
1   5   10   15

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

Phe Ala Ala Ser Lys Asn Thr Thr Glu Lys Glu Thr Phe Cys Arg Ala
        35   40   45

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

Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His Lys Gln Leu Ile
65   70   75   80

Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly Leu
                85   90   95

Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser Thr Leu Glu Asn Phe
            100   105   110

Leu Glu Arg Leu Lys Thr Ile Met Arg Glu Lys Tyr Ser Lys Cys Ser
        115   120   125

Ser

<210> 10
<211> 160
<212> PRT
<213> Homo sapiens

<400> 10
Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
1   5   10   15

```
Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
            20                  25                  30

Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
        35                  40                  45

Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
    50                  55                  60

Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65                  70                  75                  80

Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu
                85                  90                  95

Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
            100                 105                 110

Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
        115                 120                 125

Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
    130                 135                 140

Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
145                 150                 155                 160
```

<210> 11
<211> 122
<212> PRT
<213> Homo sapiens

<400> 11

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

Thr Ala Leu Arg Glu Leu Ile Glu Glu Leu Val Asn Ile Thr Gln Asn
            20                  25                  30
```

```
Gln Lys Ala Pro Leu Cys Asn Gly Ser Met Val Trp Ser Ile Asn Leu
        35                  40                  45

Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser Leu Ile Asn Val Ser
    50                  55                  60

Gly Cys Ser Ala Ile Glu Lys Thr Gln Arg Met Leu Ser Gly Phe Cys
65                  70                  75                  80

Pro His Lys Val Ser Ala Gly Gln Phe Ser Ser Leu His Val Arg Asp
                85                  90                  95

Thr Lys Ile Glu Val Ala Gln Phe Val Lys Asp Leu Leu Leu His Leu
            100                 105                 110

Lys Lys Leu Phe Arg Glu Gly Arg Phe Asn
        115                 120
```

<210> 12
<211> 157
<212> PRT
<213> Homo sapiens

<400> 12

```
Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn
1               5                   10                  15

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

Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile
        35                  40                  45

Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile
    50                  55                  60

Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn Lys Ile
65                  70                  75                  80
```

```
Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys
                85                  90                  95


Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys
            100                 105                 110


Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu
        115                 120                 125


Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu
    130                 135                 140


Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp
145                 150                 155


<210> 13
<211> 530
<212> PRT
<213> Homo sapiens

<400> 13
Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile Ile Asp Asp
1               5                   10                  15


Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val Gly Asn Val
            20                  25                  30


Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys
        35                  40                  45


Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn Phe Ser Ser
    50                  55                  60


Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu
65                  70                  75                  80


Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe
                85                  90                  95
```

```
Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp
            100                 105                 110

Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser Val Met
        115                 120                 125

Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Val Ile Trp Lys
    130                 135                 140

Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His
145                 150                 155                 160

Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys
                165                 170                 175

Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His
            180                 185                 190

Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile
        195                 200                 205

Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr
    210                 215                 220

Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys
225                 230                 235                 240

Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys
                245                 250                 255

Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln
            260                 265                 270

Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly Asn Asn Thr
        275                 280                 285
```

```
Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe
    290                 295                 300

Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His
305                 310                 315                 320

Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln
                325                 330                 335

Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn
            340                 345                 350

Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn
        355                 360                 365

Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg Ala His Thr Met
    370                 375                 380

Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu
385                 390                 395                 400

Lys Thr Lys Pro Gly Asn Thr Ser Lys Ile Trp Leu Ile Val Gly Ile
                405                 410                 415

Cys Ile Ala Leu Phe Ala Leu Pro Phe Val Ile Tyr Ala Ala Lys Val
            420                 425                 430

Phe Leu Arg Cys Ile Asn Tyr Val Phe Phe Pro Ser Leu Lys Pro Ser
        435                 440                 445

Ser Ser Ile Asp Glu Tyr Phe Ser Glu Gln Pro Leu Lys Asn Leu Leu
    450                 455                 460

Leu Ser Thr Ser Glu Glu Gln Ile Glu Lys Cys Phe Ile Ile Glu Asn
465                 470                 475                 480

Ile Ser Thr Ile Ala Thr Val Glu Glu Thr Asn Gln Thr Asp Glu Asp
                485                 490                 495
```

```
His Lys Lys Tyr Ser Ser Gln Thr Ser Gln Asp Ser Gly Asn Tyr Ser
            500                 505                 510

Asn Glu Asp Glu Ser Glu Ser Lys Thr Ser Glu Glu Leu Gln Gln Asp
        515                 520                 525

Phe Val
    530
```

<210> 14
<211> 489
<212> PRT
<213> Homo sapiens

<400> 14

```
Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser Cys Thr Phe Lys
1               5                   10                  15

Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp Glu Leu Lys Asn
            20                  25                  30

His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr Thr Ile Met Ser
        35                  40                  45

Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala Asn Thr Thr Arg
    50                  55                  60

Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr His Glu Ala Tyr
65                  70                  75                  80

Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr Leu Phe Ser Cys
                85                  90                  95

Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe Glu Pro Pro Glu
            100                 105                 110

Phe Glu Ile Val Gly Phe Thr Asn His Ile Asn Val Met Val Lys Phe
        115                 120                 125
```

```
Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu Ser Leu Val Ile
    130                 135                 140

Glu Glu Gln Ser Glu Gly Ile Val Lys Lys His Lys Pro Glu Ile Lys
145                 150                 155                 160

Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile Asp Lys Leu Ile Pro
                165                 170                 175

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

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

Glu Ser Glu Ser Ala Glu Ser Ala Lys Ile Gly Gly Ile Ile Thr Val
    210                 215                 220

Phe Leu Ile Ala Leu Val Leu Thr Ser Thr Ile Val Thr Leu Lys Trp
225                 230                 235                 240

Ile Gly Tyr Ile Cys Leu Arg Asn Ser Leu Pro Lys Val Leu Asn Phe
                245                 250                 255

His Asn Phe Leu Ala Trp Pro Phe Pro Asn Leu Pro Pro Leu Glu Ala
            260                 265                 270

Met Asp Met Val Glu Val Ile Tyr Ile Asn Arg Lys Lys Lys Val Trp
        275                 280                 285

Asp Tyr Asn Tyr Asp Asp Glu Ser Asp Ser Asp Thr Glu Ala Ala Pro
    290                 295                 300

Arg Thr Ser Gly Gly Gly Tyr Thr Met His Gly Leu Thr Val Arg Pro
305                 310                 315                 320
```

```
Leu Gly Gln Ala Ser Ala Thr Ser Thr Glu Ser Gln Leu Ile Asp Pro
                325                 330                 335

Glu Ser Glu Glu Glu Pro Asp Leu Pro Glu Val Asp Val Glu Leu Pro
            340                 345                 350

Thr Met Pro Lys Asp Ser Pro Gln Gln Leu Glu Leu Leu Ser Gly Pro
        355                 360                 365

Cys Glu Arg Arg Lys Ser Pro Leu Gln Asp Pro Phe Pro Glu Glu Asp
    370                 375                 380

Tyr Ser Ser Thr Glu Gly Ser Gly Gly Arg Ile Thr Phe Asn Val Asp
385                 390                 395                 400

Leu Asn Ser Val Phe Leu Arg Val Leu Asp Asp Glu Asp Ser Asp Asp
                405                 410                 415

Leu Glu Ala Pro Leu Met Leu Ser Ser His Leu Glu Glu Met Val Asp
            420                 425                 430

Pro Glu Asp Pro Asp Asn Val Gln Ser Asn His Leu Leu Ala Ser Gly
        435                 440                 445

Glu Gly Thr Gln Pro Thr Phe Pro Ser Pro Ser Ser Glu Gly Leu Trp
    450                 455                 460

Ser Glu Asp Ala Pro Ser Asp Gln Ser Asp Thr Ser Glu Ser Asp Val
465                 470                 475                 480

Asp Leu Gly Asp Gly Tyr Ile Met Arg
                485
```

<210> 15
<211> 472
<212> PRT
<213> Homo sapiens

<400> 15

```
Glu Met Gly Thr Ala Asp Leu Gly Pro Ser Ser Val Pro Thr Pro Thr
1               5                  10                  15

Asn Val Thr Ile Glu Ser Tyr Asn Met Asn Pro Ile Val Tyr Trp Glu
            20                  25                  30

Tyr Gln Ile Met Pro Gln Val Pro Val Phe Thr Val Glu Val Lys Asn
        35                  40                  45

Tyr Gly Val Lys Asn Ser Glu Trp Ile Asp Ala Cys Ile Asn Ile Ser
    50                  55                  60

His His Tyr Cys Asn Ile Ser Asp His Val Gly Asp Pro Ser Asn Ser
65                  70                  75                  80

Leu Trp Val Arg Val Lys Ala Arg Val Gly Gln Lys Glu Ser Ala Tyr
                85                  90                  95

Ala Lys Ser Glu Glu Phe Ala Val Cys Arg Asp Gly Lys Ile Gly Pro
            100                 105                 110

Pro Lys Leu Asp Ile Arg Lys Glu Glu Lys Gln Ile Met Ile Asp Ile
        115                 120                 125

Phe His Pro Ser Val Phe Val Asn Gly Asp Glu Gln Glu Val Asp Tyr
    130                 135                 140

Asp Pro Glu Thr Thr Cys Tyr Ile Arg Val Tyr Asn Val Tyr Val Arg
145                 150                 155                 160

Met Asn Gly Ser Glu Ile Gln Tyr Lys Ile Leu Thr Gln Lys Glu Asp
                165                 170                 175

Asp Cys Asp Glu Ile Gln Cys Gln Leu Ala Ile Pro Val Ser Ser Leu
            180                 185                 190

Asn Ser Gln Tyr Cys Val Ser Ala Glu Gly Val Leu His Val Trp Gly
        195                 200                 205
```

```
Val Thr Thr Glu Lys Ser Lys Glu Val Cys Ile Thr Ile Phe Asn Ser
    210                 215                 220

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

Phe Leu Val Leu Ser Leu Val Phe Ile Cys Phe Tyr Ile Lys Lys Ile
                245                 250                 255

Asn Pro Leu Lys Glu Lys Ser Ile Ile Leu Pro Lys Ser Leu Ile Ser
            260                 265                 270

Val Val Arg Ser Ala Thr Leu Glu Thr Lys Pro Glu Ser Lys Tyr Val
        275                 280                 285

Ser Leu Ile Thr Ser Tyr Gln Pro Phe Ser Leu Glu Lys Glu Val Val
    290                 295                 300

Cys Glu Glu Pro Leu Ser Pro Ala Thr Val Pro Gly Met His Thr Glu
305                 310                 315                 320

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

Glu Val Val Thr Thr Glu Glu Asn Ile Pro Asp Val Val Pro Gly Ser
            340                 345                 350

His Leu Thr Pro Ile Glu Arg Glu Ser Ser Ser Pro Leu Ser Ser Asn
        355                 360                 365

Gln Ser Glu Pro Gly Ser Ile Ala Leu Asn Ser Tyr His Ser Arg Asn
    370                 375                 380

Cys Ser Glu Ser Asp His Ser Arg Asn Gly Phe Asp Thr Asp Ser Ser
385                 390                 395                 400
```

```
Cys Leu Glu Ser His Ser Ser Leu Ser Asp Ser Glu Phe Pro Pro Asn
                405                 410                 415

Asn Lys Gly Glu Ile Lys Thr Glu Gly Gln Glu Leu Ile Thr Val Ile
            420                 425                 430

Lys Ala Pro Thr Ser Phe Gly Tyr Asp Lys Pro His Val Leu Val Asp
        435                 440                 445

Leu Leu Val Asp Asp Ser Gly Lys Glu Ser Leu Ile Gly Tyr Arg Pro
    450                 455                 460

Thr Glu Asp Ser Lys Glu Phe Ser
465                 470
```

<210> 16
<211> 316
<212> PRT
<213> Homo sapiens

<400> 16

```
Ala Pro Pro Asp Pro Leu Ser Gln Leu Pro Ala Pro Gln His Pro Lys
1               5                   10                  15

Ile Arg Leu Tyr Asn Ala Glu Gln Val Leu Ser Trp Glu Pro Val Ala
            20                  25                  30

Leu Ser Asn Ser Thr Arg Pro Val Val Tyr Gln Val Gln Phe Lys Tyr
        35                  40                  45

Thr Asp Ser Lys Trp Phe Thr Ala Asp Ile Met Ser Ile Gly Val Asn
    50                  55                  60

Cys Thr Gln Ile Thr Ala Thr Glu Cys Asp Phe Thr Ala Ala Ser Pro
65                  70                  75                  80

Ser Ala Gly Phe Pro Met Asp Phe Asn Val Thr Leu Arg Leu Arg Ala
                85                  90                  95
```

```
Glu Leu Gly Ala Leu His Ser Ala Trp Val Thr Met Pro Trp Phe Gln
            100                 105                 110

His Tyr Arg Asn Val Thr Val Gly Pro Pro Glu Asn Ile Glu Val Thr
        115                 120                 125

Pro Gly Glu Gly Ser Leu Ile Ile Arg Phe Ser Ser Pro Phe Asp Ile
    130                 135                 140

Ala Asp Thr Ser Thr Ala Phe Phe Cys Tyr Tyr Val His Tyr Trp Glu
145                 150                 155                 160

Lys Gly Gly Ile Gln Gln Val Lys Gly Pro Phe Arg Ser Asn Ser Ile
                165                 170                 175

Ser Leu Asp Asn Leu Lys Pro Ser Arg Val Tyr Cys Leu Gln Val Gln
            180                 185                 190

Ala Gln Leu Leu Trp Asn Lys Ser Asn Ile Phe Arg Val Gly His Leu
        195                 200                 205

Ser Asn Ile Ser Cys Tyr Glu Thr Met Ala Asp Ala Ser Thr Glu Leu
    210                 215                 220

Gln Gln Val Ile Leu Ile Ser Val Gly Thr Phe Ser Leu Leu Ser Val
225                 230                 235                 240

Leu Ala Gly Ala Cys Phe Phe Leu Val Leu Lys Tyr Arg Gly Leu Ile
                245                 250                 255

Lys Tyr Trp Phe His Thr Pro Pro Ser Ile Pro Leu Gln Ile Glu Glu
            260                 265                 270

Tyr Leu Lys Asp Pro Thr Gln Pro Ile Leu Glu Ala Leu Asp Lys Asp
        275                 280                 285

Ser Ser Pro Lys Asp Asp Val Trp Asp Ser Val Ser Ile Ile Ser Phe
    290                 295                 300
```

```
Pro Glu Lys Glu Gln Glu Asp Val Leu Gln Thr Leu
305                 310                 315


<210> 17
<211> 426
<212> PRT
<213> Homo sapiens

<400> 17
Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro
1               5                   10                  15


Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys
            20                  25                  30


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


Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu
    50                  55                  60


Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met
65                  70                  75                  80


Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys
                85                  90                  95


Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe
            100                 105                 110


Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser
        115                 120                 125


Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe
    130                 135                 140


Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu
145                 150                 155                 160
```

```
Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr
                165                 170                 175

Glu Asp Ser Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly
            180                 185                 190

Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln
        195                 200                 205

Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro
    210                 215                 220

Glu Lys Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro
225                 230                 235                 240

Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe
                245                 250                 255

Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro
            260                 265                 270

Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro
        275                 280                 285

Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro
    290                 295                 300

Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln
305                 310                 315                 320

Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn
                325                 330                 335

Val Pro Pro Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser
            340                 345                 350
```

```
Asp His Glu Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg
        355                 360                 365

Glu Ala Gln Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg
    370                 375                 380

Arg Glu Ala Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp
385                 390                 395                 400

Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala
                405                 410                 415

Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg
            420                 425
```

<210> 18
<211> 439
<212> PRT
<213> Homo sapiens

<400> 18

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

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
            20                  25                  30

Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr
        35                  40                  45

Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
    50                  55                  60

Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
65                  70                  75                  80

Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
                85                  90                  95
```

```
Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
            100                 105                 110

Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
        115                 120                 125

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
    130                 135                 140

Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
145                 150                 155                 160

Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
                165                 170                 175

Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
            180                 185                 190

His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr
        195                 200                 205

Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
    210                 215                 220

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

Gly Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val
                245                 250                 255

Val Asn Cys Val Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu
            260                 265                 270

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

Thr Gln Gly Pro Glu Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser
    290                 295                 300
```

```
Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala
305                 310                 315                 320

Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala
                325                 330                 335

Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly
            340                 345                 350

His Gly Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser
        355                 360                 365

Ser Asp His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly
    370                 375                 380

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

Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro Glu
                405                 410                 415

Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro
            420                 425                 430

Asp Ala Gly Met Lys Pro Ser
        435
```

<210> 19
<211> 552
<212> PRT
<213> Homo sapiens

<400> 19

```
Leu Glu Ala Asp Lys Cys Lys Glu Arg Glu Glu Lys Ile Ile Leu Val
1               5                   10                  15

Ser Ser Ala Asn Glu Ile Asp Val Arg Pro Cys Pro Leu Asn Pro Asn
            20                  25                  30
```

```
Glu His Lys Gly Thr Ile Thr Trp Tyr Lys Asp Asp Ser Lys Thr Pro
        35                  40                  45

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

Trp Phe Val Pro Ala Lys Val Glu Asp Ser Gly His Tyr Tyr Cys Val
65                  70                  75                  80

Val Arg Asn Ser Ser Tyr Cys Leu Arg Ile Lys Ile Ser Ala Lys Phe
                85                  90                  95

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

Gln Lys Leu Pro Val Ala Gly Asp Gly Gly Leu Val Cys Pro Tyr Met
        115                 120                 125

Glu Phe Phe Lys Asn Glu Asn Asn Glu Leu Pro Lys Leu Gln Trp Tyr
    130                 135                 140

Lys Asp Cys Lys Pro Leu Leu Leu Asp Asn Ile His Phe Ser Gly Val
145                 150                 155                 160

Lys Asp Arg Leu Ile Val Met Asn Val Ala Glu Lys His Arg Gly Asn
                165                 170                 175

Tyr Thr Cys His Ala Ser Tyr Thr Tyr Leu Gly Lys Gln Tyr Pro Ile
            180                 185                 190

Thr Arg Val Ile Glu Phe Ile Thr Leu Glu Glu Asn Lys Pro Thr Arg
        195                 200                 205

Pro Val Ile Val Ser Pro Ala Asn Glu Thr Met Glu Val Asp Leu Gly
    210                 215                 220
```

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

Ala Tyr Trp Lys Trp Asn Gly Ser Val Ile Asp Glu Asp Asp Pro Val
                245                 250                 255

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

Ser Thr Leu Ile Thr Val Leu Asn Ile Ser Glu Ile Glu Ser Arg Phe
        275                 280                 285

Tyr Lys His Pro Phe Thr Cys Phe Ala Lys Asn Thr His Gly Ile Asp
    290                 295                 300

Ala Ala Tyr Ile Gln Leu Ile Tyr Pro Val Thr Asn Phe Gln Lys His
305                 310                 315                 320

Met Ile Gly Ile Cys Val Thr Leu Thr Val Ile Ile Val Cys Ser Val
                325                 330                 335

Phe Ile Tyr Lys Ile Phe Lys Ile Asp Ile Val Leu Trp Tyr Arg Asp
            340                 345                 350

Ser Cys Tyr Asp Phe Leu Pro Ile Lys Ala Ser Asp Gly Lys Thr Tyr
        355                 360                 365

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

Asp Cys Asp Ile Phe Val Phe Lys Val Leu Pro Glu Val Leu Glu Lys
385                 390                 395                 400

Gln Cys Gly Tyr Lys Leu Phe Ile Tyr Gly Arg Asp Asp Tyr Val Gly
                405                 410                 415

Glu Asp Ile Val Glu Val Ile Asn Glu Asn Val Lys Lys Ser Arg Arg
            420                 425                 430
```

```
Leu Ile Ile Ile Leu Val Arg Glu Thr Ser Gly Phe Ser Trp Leu Gly
        435                 440                 445

Gly Ser Ser Glu Glu Gln Ile Ala Met Tyr Asn Ala Leu Val Gln Asp
    450                 455                 460

Gly Ile Lys Val Val Leu Leu Glu Leu Glu Lys Ile Gln Asp Tyr Glu
465                 470                 475                 480

Lys Met Pro Glu Ser Ile Lys Phe Ile Lys Gln Lys His Gly Ala Ile
                485                 490                 495

Arg Trp Ser Gly Asp Phe Thr Gln Gly Pro Gln Ser Ala Lys Thr Arg
            500                 505                 510

Phe Trp Lys Asn Val Arg Tyr His Met Pro Val Gln Arg Arg Ser Pro
        515                 520                 525

Ser Ser Lys His Gln Leu Leu Ser Pro Ala Thr Lys Glu Lys Leu Gln
    530                 535                 540

Arg Glu Ala His Val Pro Leu Gly
545                 550


<210> 20
<211> 550
<212> PRT
<213> Homo sapiens

<400> 20
Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met Arg Gln Ile Gln
1               5                   10                  15

Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro Leu Phe Glu His
            20                  25                  30

Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser Ala Gly Leu Thr Leu
        35                  40                  45
```

```
Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu Glu Pro Ile Asn
    50                  55                  60

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

Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr Thr Cys Met Leu
                85                  90                  95

Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro Leu Glu Val Val
            100                 105                 110

Gln Lys Asp Ser Cys Phe Asn Ser Pro Met Lys Leu Pro Val His Lys
        115                 120                 125

Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile Thr Cys Pro Asn Val Asp
    130                 135                 140

Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr Ile Thr Trp Tyr Met Gly
145                 150                 155                 160

Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val Ile Pro Glu Gly Met Asn
                165                 170                 175

Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn Asn Gly Asn Tyr Thr Cys
            180                 185                 190

Val Val Thr Tyr Pro Glu Asn Gly Arg Thr Phe His Leu Thr Arg Thr
        195                 200                 205

Leu Thr Val Lys Val Val Gly Ser Pro Lys Asn Ala Val Pro Pro Val
    210                 215                 220

Ile His Ser Pro Asn Asp His Val Val Tyr Glu Lys Glu Pro Gly Glu
225                 230                 235                 240
```

```
Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe Ser Phe Leu Met Asp Ser
                245                 250                 255

Arg Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys Pro Asp Asp Ile
            260                 265                 270

Thr Ile Asp Val Thr Ile Asn Glu Ser Ile Ser His Ser Arg Thr Glu
        275                 280                 285

Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys Val Thr Ser Glu
    290                 295                 300

Asp Leu Lys Arg Ser Tyr Val Cys His Ala Arg Ser Ala Lys Gly Glu
305                 310                 315                 320

Val Ala Lys Ala Ala Lys Val Lys Gln Lys Val Pro Ala Pro Arg Tyr
                325                 330                 335

Thr Val Glu Leu Ala Cys Gly Phe Gly Ala Thr Val Leu Leu Val Val
            340                 345                 350

Ile Leu Ile Val Val Tyr His Val Tyr Trp Leu Glu Met Val Leu Phe
        355                 360                 365

Tyr Arg Ala His Phe Gly Thr Asp Glu Thr Ile Leu Asp Gly Lys Glu
    370                 375                 380

Tyr Asp Ile Tyr Val Ser Tyr Ala Arg Asn Ala Glu Glu Glu Glu Phe
385                 390                 395                 400

Val Leu Leu Thr Leu Arg Gly Val Leu Glu Asn Glu Phe Gly Tyr Lys
                405                 410                 415

Leu Cys Ile Phe Asp Arg Asp Ser Leu Pro Gly Gly Ile Val Thr Asp
            420                 425                 430

Glu Thr Leu Ser Phe Ile Gln Lys Ser Arg Arg Leu Leu Val Val Leu
        435                 440                 445
```

```
Ser Pro Asn Tyr Val Leu Gln Gly Thr Gln Ala Leu Leu Glu Leu Lys
    450                 455                 460

Ala Gly Leu Glu Asn Met Ala Ser Arg Gly Asn Ile Asn Val Ile Leu
465                 470                 475                 480

Val Gln Tyr Lys Ala Val Lys Glu Thr Lys Val Lys Glu Leu Lys Arg
                485                 490                 495

Ala Lys Thr Val Leu Thr Val Ile Lys Trp Lys Gly Glu Lys Ser Lys
            500                 505                 510

Tyr Pro Gln Gly Arg Phe Trp Lys Gln Leu Gln Val Ala Met Pro Val
        515                 520                 525

Lys Lys Ser Pro Arg Arg Ser Ser Ser Asp Glu Gln Gly Leu Ser Tyr
    530                 535                 540

Ser Ser Leu Lys Asn Val
545                 550
```

<210> 21
<211> 449
<212> PRT
<213> Homo sapiens

<400> 21

```
Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg Gly Val Leu
1               5                   10                  15

Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro Gly Val Glu
            20                  25                  30

Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys Pro Ala Ala
        35                  40                  45

Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg Leu Leu Leu
    50                  55                  60
```

```
Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys Tyr Arg Ala
65                  70                  75                  80

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

Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser Asn Val Val
            100                 105                 110

Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr Lys Ala Val
        115                 120                 125

Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp Phe Gln Glu
    130                 135                 140

Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys Gln Leu Ala
145                 150                 155                 160

Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met Cys Val Ala
                165                 170                 175

Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe Gln Gly Cys
            180                 185                 190

Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val Thr Ala Val
        195                 200                 205

Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp Pro His Ser
    210                 215                 220

Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg Tyr Arg Ala
225                 230                 235                 240

Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp Leu Gln His
                245                 250                 255
```

```
His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His Val Val Gln
            260                 265                 270

Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser Glu Trp Ser
        275                 280                 285

Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser Pro Pro Ala
    290                 295                 300

Glu Asn Glu Val Ser Thr Pro Met Gln Ala Leu Thr Thr Asn Lys Asp
305                 310                 315                 320

Asp Asp Asn Ile Leu Phe Arg Asp Ser Ala Asn Ala Thr Ser Leu Pro
                325                 330                 335

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

Gly Ser Leu Ala Phe Gly Thr Leu Leu Cys Ile Ala Ile Val Leu Arg
        355                 360                 365

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

Met His Pro Pro Tyr Ser Leu Gly Gln Leu Val Pro Glu Arg Pro Arg
385                 390                 395                 400

Pro Thr Pro Val Leu Val Pro Leu Ile Ser Pro Pro Val Ser Pro Ser
                405                 410                 415

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

Asp Pro Arg Ser Pro Tyr Asp Ile Ser Asn Thr Asp Tyr Phe Phe Pro
        435                 440                 445

Arg
```

<210> 22
<211> 896
<212> PRT
<213> Homo sapiens

<400> 22
Glu Leu Leu Asp Pro Cys Gly Tyr Ile Ser Pro Glu Ser Pro Val Val
1 5 10 15

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

Met Asp Tyr Phe His Val Asn Ala Asn Tyr Ile Val Trp Lys Thr Asn
35 40 45

His Phe Thr Ile Pro Lys Glu Gln Tyr Thr Ile Ile Asn Arg Thr Ala
50 55 60

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

Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu Gln Asn Val Tyr Gly Ile
85 90 95

Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys Pro Lys Asn Leu Ser Cys
100 105 110

Ile Val Asn Glu Gly Lys Lys Met Arg Cys Glu Trp Asp Gly Gly Arg
115 120 125

Glu Thr His Leu Glu Thr Asn Phe Thr Leu Lys Ser Glu Trp Ala Thr
130 135 140

His Lys Phe Ala Asp Cys Lys Ala Lys Arg Asp Thr Pro Thr Ser Cys
145 150 155 160

Thr Val Asp Tyr Ser Thr Val Tyr Phe Val Asn Ile Glu Val Trp Val
165 170 175

```
Glu Ala Glu Asn Ala Leu Gly Lys Val Thr Ser Asp His Ile Asn Phe
            180                 185                 190

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

Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu Lys Leu Thr Trp Thr Asn
    210                 215                 220

Pro Ser Ile Lys Ser Val Ile Ile Leu Lys Tyr Asn Ile Gln Tyr Arg
225                 230                 235                 240

Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile Pro Pro Glu Asp Thr Ala
                245                 250                 255

Ser Thr Arg Ser Ser Phe Thr Val Gln Asp Leu Lys Pro Phe Thr Glu
            260                 265                 270

Tyr Val Phe Arg Ile Arg Cys Met Lys Glu Asp Gly Lys Gly Tyr Trp
        275                 280                 285

Ser Asp Trp Ser Glu Glu Ala Ser Gly Ile Thr Tyr Glu Asp Arg Pro
    290                 295                 300

Ser Lys Ala Pro Ser Phe Trp Tyr Lys Ile Asp Pro Ser His Thr Gln
305                 310                 315                 320

Gly Tyr Arg Thr Val Gln Leu Val Trp Lys Thr Leu Pro Pro Phe Glu
                325                 330                 335

Ala Asn Gly Lys Ile Leu Asp Tyr Glu Val Thr Leu Thr Arg Trp Lys
            340                 345                 350

Ser His Leu Gln Asn Tyr Thr Val Asn Ala Thr Lys Leu Thr Val Asn
        355                 360                 365
```

```
Leu Thr Asn Asp Arg Tyr Leu Ala Thr Leu Thr Val Arg Asn Leu Val
    370                 375                 380

Gly Lys Ser Asp Ala Ala Val Leu Thr Ile Pro Ala Cys Asp Phe Gln
385                 390                 395                 400

Ala Thr His Pro Val Met Asp Leu Lys Ala Phe Pro Lys Asp Asn Met
                405                 410                 415

Leu Trp Val Glu Trp Thr Thr Pro Arg Glu Ser Val Lys Lys Tyr Ile
            420                 425                 430

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

Gln Gln Glu Asp Gly Thr Val His Arg Thr Tyr Leu Arg Gly Asn Leu
    450                 455                 460

Ala Glu Ser Lys Cys Tyr Leu Ile Thr Val Thr Pro Val Tyr Ala Asp
465                 470                 475                 480

Gly Pro Gly Ser Pro Glu Ser Ile Lys Ala Tyr Leu Lys Gln Ala Pro
                485                 490                 495

Pro Ser Lys Gly Pro Thr Val Arg Thr Lys Lys Val Gly Lys Asn Glu
            500                 505                 510

Ala Val Leu Glu Trp Asp Gln Leu Pro Val Asp Val Gln Asn Gly Phe
        515                 520                 525

Ile Arg Asn Tyr Thr Ile Phe Tyr Arg Thr Ile Ile Gly Asn Glu Thr
    530                 535                 540

Ala Val Asn Val Asp Ser Ser His Thr Glu Tyr Thr Leu Ser Ser Leu
545                 550                 555                 560

Thr Ser Asp Thr Leu Tyr Met Val Arg Met Ala Ala Tyr Thr Asp Glu
                565                 570                 575
```

```
Gly Gly Lys Asp Gly Pro Glu Phe Thr Phe Thr Thr Pro Lys Phe Ala
            580                 585                 590

Gln Gly Glu Ile Glu Ala Ile Val Val Pro Val Cys Leu Ala Phe Leu
        595                 600                 605

Leu Thr Thr Leu Leu Gly Val Leu Phe Cys Phe Asn Lys Arg Asp Leu
    610                 615                 620

Ile Lys Lys His Ile Trp Pro Asn Val Pro Asp Pro Ser Lys Ser His
625                 630                 635                 640

Ile Ala Gln Trp Ser Pro His Thr Pro Pro Arg His Asn Phe Asn Ser
                645                 650                 655

Lys Asp Gln Met Tyr Ser Asp Gly Asn Phe Thr Asp Val Ser Val Val
            660                 665                 670

Glu Ile Glu Ala Asn Asp Lys Lys Pro Phe Pro Glu Asp Leu Lys Ser
        675                 680                 685

Leu Asp Leu Phe Lys Lys Glu Lys Ile Asn Thr Glu Gly His Ser Ser
    690                 695                 700

Gly Ile Gly Gly Ser Ser Cys Met Ser Ser Ser Arg Pro Ser Ile Ser
705                 710                 715                 720

Ser Ser Asp Glu Asn Glu Ser Ser Gln Asn Thr Ser Ser Thr Val Gln
                725                 730                 735

Tyr Ser Thr Val Val His Ser Gly Tyr Arg His Gln Val Pro Ser Val
            740                 745                 750

Gln Val Phe Ser Arg Ser Glu Ser Thr Gln Pro Leu Leu Asp Ser Glu
        755                 760                 765
```

```
Glu Arg Pro Glu Asp Leu Gln Leu Val Asp His Val Asp Gly Gly Asp
    770                 775                 780

Gly Ile Leu Pro Arg Gln Gln Tyr Phe Lys Gln Asn Cys Ser Gln His
785                 790                 795                 800

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

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

His Ile Ser Gln Ser Cys Gly Ser Gly Gln Met Lys Met Phe Gln Glu
        835                 840                 845

Val Ser Ala Ala Asp Ala Phe Gly Pro Gly Thr Glu Gly Gln Val Glu
    850                 855                 860

Arg Phe Glu Thr Val Gly Met Glu Ala Ala Thr Asp Glu Gly Met Pro
865                 870                 875                 880

Lys Ser Tyr Leu Pro Gln Thr Val Arg Gln Gly Gly Tyr Met Pro Gln
                885                 890                 895
```

<210> 23
<211> 639
<212> PRT
<213> Homo sapiens

<400> 23

```
Cys Arg Thr Ser Glu Cys Cys Phe Gln Asp Pro Pro Tyr Pro Asp Ala
1               5                   10                  15

Asp Ser Gly Ser Ala Ser Gly Pro Arg Asp Leu Arg Cys Tyr Arg Ile
            20                  25                  30

Ser Ser Asp Arg Tyr Glu Cys Ser Trp Gln Tyr Glu Gly Pro Thr Ala
        35                  40                  45
```

```
Gly Val Ser His Phe Leu Arg Cys Cys Leu Ser Ser Gly Arg Cys Cys
    50                  55                  60

Tyr Phe Ala Ala Gly Ser Ala Thr Arg Leu Gln Phe Ser Asp Gln Ala
65                  70                  75                  80

Gly Val Ser Val Leu Tyr Thr Val Thr Leu Trp Val Glu Ser Trp Ala
                85                  90                  95

Arg Asn Gln Thr Glu Lys Ser Pro Glu Val Thr Leu Gln Leu Tyr Asn
            100                 105                 110

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

Ala Gly Gln Leu Arg Met Glu Trp Glu Thr Pro Asp Asn Gln Val Gly
    130                 135                 140

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

Gly Asp Cys Gly Pro Gln Asp Asp Asp Thr Glu Ser Cys Leu Cys Pro
                165                 170                 175

Leu Glu Met Asn Val Ala Gln Glu Phe Gln Leu Arg Arg Arg Gln Leu
            180                 185                 190

Gly Ser Gln Gly Ser Ser Trp Ser Lys Trp Ser Ser Pro Val Cys Val
        195                 200                 205

Pro Pro Glu Asn Pro Pro Gln Pro Gln Val Arg Phe Ser Val Glu Gln
    210                 215                 220

Leu Gly Gln Asp Gly Arg Arg Arg Leu Thr Leu Lys Glu Gln Pro Thr
225                 230                 235                 240

Gln Leu Glu Leu Pro Glu Gly Cys Gln Gly Leu Ala Pro Gly Thr Glu
                245                 250                 255
```

```
Val Thr Tyr Arg Leu Gln Leu His Met Leu Ser Cys Pro Cys Lys Ala
            260                 265                 270

Lys Ala Thr Arg Thr Leu His Leu Gly Lys Met Pro Tyr Leu Ser Gly
        275                 280                 285

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

Leu Asn Gln Thr Trp His Ile Pro Ala Asp Thr His Thr Glu Pro Val
305                 310                 315                 320

Ala Leu Asn Ile Ser Val Gly Thr Asn Gly Thr Thr Met Tyr Trp Pro
                325                 330                 335

Ala Arg Ala Gln Ser Met Thr Tyr Cys Ile Glu Trp Gln Pro Val Gly
            340                 345                 350

Gln Asp Gly Gly Leu Ala Thr Cys Ser Leu Thr Ala Pro Gln Asp Pro
        355                 360                 365

Asp Pro Ala Gly Met Ala Thr Tyr Ser Trp Ser Arg Glu Ser Gly Ala
    370                 375                 380

Met Gly Gln Glu Lys Cys Tyr Tyr Ile Thr Ile Phe Ala Ser Ala His
385                 390                 395                 400

Pro Glu Lys Leu Thr Leu Trp Ser Thr Val Leu Ser Thr Tyr His Phe
                405                 410                 415

Gly Gly Asn Ala Ser Ala Ala Gly Thr Pro His His Val Ser Val Lys
            420                 425                 430

Asn His Ser Leu Asp Ser Val Ser Val Asp Trp Ala Pro Ser Leu Leu
        435                 440                 445
```

```
Ser Thr Cys Pro Gly Val Leu Lys Glu Tyr Val Val Arg Cys Arg Asp
    450                 455                 460

Glu Asp Ser Lys Gln Val Ser Glu His Pro Val Gln Pro Thr Glu Thr
465                 470                 475                 480

Gln Val Thr Leu Ser Gly Leu Arg Ala Gly Val Ala Tyr Thr Val Gln
                485                 490                 495

Val Arg Ala Asp Thr Ala Trp Leu Arg Gly Val Trp Ser Gln Pro Gln
            500                 505                 510

Arg Phe Ser Ile Glu Val Gln Val Ser Asp Trp Leu Ile Phe Phe Ala
        515                 520                 525

Ser Leu Gly Ser Phe Leu Ser Ile Leu Leu Val Gly Val Leu Gly Tyr
    530                 535                 540

Leu Gly Leu Asn Arg Ala Ala Arg His Leu Cys Pro Pro Leu Pro Thr
545                 550                 555                 560

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

Gln Trp Ile Asn Pro Val Asp Phe Gln Glu Glu Ala Ser Leu Gln Glu
            580                 585                 590

Ala Leu Val Val Glu Met Ser Trp Asp Lys Gly Glu Arg Thr Glu Pro
        595                 600                 605

Leu Glu Lys Thr Glu Leu Pro Glu Gly Ala Pro Glu Leu Ala Leu Asp
    610                 615                 620

Thr Glu Leu Ser Leu Glu Asp Gly Asp Arg Cys Lys Ala Lys Met
625                 630                 635
```

<210> 24
<211> 839

<212> PRT
<213> Homo sapiens

<400> 24
Lys Ile Asp Ala Cys Lys Arg Gly Asp Val Thr Val Lys Pro Ser His
1   5   10   15

Val Ile Leu Leu Gly Ser Thr Val Asn Ile Thr Cys Ser Leu Lys Pro
            20   25   30

Arg Gln Gly Cys Phe His Tyr Ser Arg Arg Asn Lys Leu Ile Leu Tyr
        35   40   45

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

Gln Val Thr Gly Leu Pro Leu Gly Thr Thr Leu Phe Val Cys Lys Leu
65   70   75   80

Ala Cys Ile Asn Ser Asp Glu Ile Gln Ile Cys Gly Ala Glu Ile Phe
                85   90   95

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

Gly Glu Gln Gly Thr Val Ala Cys Thr Trp Glu Arg Gly Arg Asp Thr
        115   120   125

His Leu Tyr Thr Glu Tyr Thr Leu Gln Leu Ser Gly Pro Lys Asn Leu
    130   135   140

Thr Trp Gln Lys Gln Cys Lys Asp Ile Tyr Cys Asp Tyr Leu Asp Phe
145   150   155   160

Gly Ile Asn Leu Thr Pro Glu Ser Pro Glu Ser Asn Phe Thr Ala Lys
                165   170   175

Val Thr Ala Val Asn Ser Leu Gly Ser Ser Ser Ser Leu Pro Ser Thr
            180   185   190

```
Phe Thr Phe Leu Asp Ile Val Arg Pro Leu Pro Pro Trp Asp Ile Arg
        195                 200                 205

Ile Lys Phe Gln Lys Ala Ser Val Ser Arg Cys Thr Leu Tyr Trp Arg
    210                 215                 220

Asp Glu Gly Leu Val Leu Leu Asn Arg Leu Arg Tyr Arg Pro Ser Asn
225                 230                 235                 240

Ser Arg Leu Trp Asn Met Val Asn Val Thr Lys Ala Lys Gly Arg His
                245                 250                 255

Asp Leu Leu Asp Leu Lys Pro Phe Thr Glu Tyr Glu Phe Gln Ile Ser
            260                 265                 270

Ser Lys Leu His Leu Tyr Lys Gly Ser Trp Ser Asp Trp Ser Glu Ser
        275                 280                 285

Leu Arg Ala Gln Thr Pro Glu Glu Glu Pro Thr Gly Met Leu Asp Val
    290                 295                 300

Trp Tyr Met Lys Arg His Ile Asp Tyr Ser Arg Gln Gln Ile Ser Leu
305                 310                 315                 320

Phe Trp Lys Asn Leu Ser Val Ser Glu Ala Arg Gly Lys Ile Leu His
                325                 330                 335

Tyr Gln Val Thr Leu Gln Glu Leu Thr Gly Gly Lys Ala Met Thr Gln
            340                 345                 350

Asn Ile Thr Gly His Thr Ser Trp Thr Thr Val Ile Pro Arg Thr Gly
        355                 360                 365

Asn Trp Ala Val Ala Val Ser Ala Ala Asn Ser Lys Gly Ser Ser Leu
    370                 375                 380
```

```
Pro Thr Arg Ile Asn Ile Met Asn Leu Cys Glu Ala Gly Leu Leu Ala
385                 390                 395                 400

Pro Arg Gln Val Ser Ala Asn Ser Glu Gly Met Asp Asn Ile Leu Val
                405                 410                 415

Thr Trp Gln Pro Pro Arg Lys Asp Pro Ser Ala Val Gln Glu Tyr Val
            420                 425                 430

Val Glu Trp Arg Glu Leu His Pro Gly Gly Asp Thr Gln Val Pro Leu
        435                 440                 445

Asn Trp Leu Arg Ser Arg Pro Tyr Asn Val Ser Ala Leu Ile Ser Glu
    450                 455                 460

Asn Ile Lys Ser Tyr Ile Cys Tyr Glu Ile Arg Val Tyr Ala Leu Ser
465                 470                 475                 480

Gly Asp Gln Gly Gly Cys Ser Ser Ile Leu Gly Asn Ser Lys His Lys
                485                 490                 495

Ala Pro Leu Ser Gly Pro His Ile Asn Ala Ile Thr Glu Glu Lys Gly
            500                 505                 510

Ser Ile Leu Ile Ser Trp Asn Ser Ile Pro Val Gln Glu Gln Met Gly
        515                 520                 525

Cys Leu Leu His Tyr Arg Ile Tyr Trp Lys Glu Arg Asp Ser Asn Ser
    530                 535                 540

Gln Pro Gln Leu Cys Glu Ile Pro Tyr Arg Val Ser Gln Asn Ser His
545                 550                 555                 560

Pro Ile Asn Ser Leu Gln Pro Arg Val Thr Tyr Val Leu Trp Met Thr
                565                 570                 575

Ala Leu Thr Ala Ala Gly Glu Ser Ser His Gly Asn Glu Arg Glu Phe
            580                 585                 590
```

```
Cys Leu Gln Gly Lys Ala Asn Trp Met Ala Phe Val Ala Pro Ser Ile
        595                 600                 605

Cys Ile Ala Ile Ile Met Val Gly Ile Phe Ser Thr His Tyr Phe Gln
    610                 615                 620

Gln Lys Val Phe Val Leu Leu Ala Ala Leu Arg Pro Gln Trp Cys Ser
625                 630                 635                 640

Arg Glu Ile Pro Asp Pro Ala Asn Ser Thr Cys Ala Lys Lys Tyr Pro
                645                 650                 655

Ile Ala Glu Glu Lys Thr Gln Leu Pro Leu Asp Arg Leu Leu Ile Asp
            660                 665                 670

Trp Pro Thr Pro Glu Asp Pro Glu Pro Leu Val Ile Ser Glu Val Leu
        675                 680                 685

His Gln Val Thr Pro Val Phe Arg His Pro Pro Cys Ser Asn Trp Pro
    690                 695                 700

Gln Arg Glu Lys Gly Ile Gln Gly His Gln Ala Ser Glu Lys Asp Met
705                 710                 715                 720

Met His Ser Ala Ser Ser Pro Pro Pro Pro Arg Ala Leu Gln Ala Glu
                725                 730                 735

Ser Arg Gln Leu Val Asp Leu Tyr Lys Val Leu Glu Ser Arg Gly Ser
            740                 745                 750

Asp Pro Lys Pro Glu Asn Pro Ala Cys Pro Trp Thr Val Leu Pro Ala
        755                 760                 765

Gly Asp Leu Pro Thr His Asp Gly Tyr Leu Pro Ser Asn Ile Asp Asp
    770                 775                 780
```

```
Leu Pro Ser His Glu Ala Pro Leu Ala Asp Ser Leu Glu Glu Leu Glu
785                 790                 795                 800

Pro Gln His Ile Ser Leu Ser Val Phe Pro Ser Ser Ser Leu His Pro
                805                 810                 815

Leu Thr Phe Ser Cys Gly Asp Lys Leu Thr Leu Asp Gln Leu Lys Met
            820                 825                 830

Arg Cys Asp Ser Leu Met Leu
        835
```

<210> 25
<211> 800
<212> PRT
<213> Homo sapiens

<400> 25

```
Met Lys Val Leu Gln Glu Pro Thr Cys Val Ser Asp Tyr Met Ser Ile
1               5                   10                  15

Ser Thr Cys Glu Trp Lys Met Asn Gly Pro Thr Asn Cys Ser Thr Glu
            20                  25                  30

Leu Arg Leu Leu Tyr Gln Leu Val Phe Leu Leu Ser Glu Ala His Thr
        35                  40                  45

Cys Ile Pro Glu Asn Asn Gly Gly Ala Gly Cys Val Cys His Leu Leu
    50                  55                  60

Met Asp Asp Val Val Ser Ala Asp Asn Tyr Thr Leu Asp Leu Trp Ala
65                  70                  75                  80

Gly Gln Gln Leu Leu Trp Lys Gly Ser Phe Lys Pro Ser Glu His Val
                85                  90                  95

Lys Pro Arg Ala Pro Gly Asn Leu Thr Val His Thr Asn Val Ser Asp
            100                 105                 110
```

```
Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp Asn Tyr Leu
        115                 120                 125

Tyr Asn His Leu Thr Tyr Ala Val Asn Ile Trp Ser Glu Asn Asp Pro
    130                 135                 140

Ala Asp Phe Arg Ile Tyr Asn Val Thr Tyr Leu Glu Pro Ser Leu Arg
145                 150                 155                 160

Ile Ala Ala Ser Thr Leu Lys Ser Gly Ile Ser Tyr Arg Ala Arg Val
                165                 170                 175

Arg Ala Trp Ala Gln Cys Tyr Asn Thr Thr Trp Ser Glu Trp Ser Pro
            180                 185                 190

Ser Thr Lys Trp His Asn Ser Tyr Arg Glu Pro Phe Glu Gln His Leu
        195                 200                 205

Leu Leu Gly Val Ser Val Ser Cys Ile Val Ile Leu Ala Val Cys Leu
    210                 215                 220

Leu Cys Tyr Val Ser Ile Thr Lys Ile Lys Lys Glu Trp Trp Asp Gln
225                 230                 235                 240

Ile Pro Asn Pro Ala Arg Ser Arg Leu Val Ala Ile Ile Ile Gln Asp
                245                 250                 255

Ala Gln Gly Ser Gln Trp Glu Lys Arg Ser Arg Gly Gln Glu Pro Ala
            260                 265                 270

Lys Cys Pro His Trp Lys Asn Cys Leu Thr Lys Leu Leu Pro Cys Phe
        275                 280                 285

Leu Glu His Asn Met Lys Arg Asp Glu Asp Pro His Lys Ala Ala Lys
    290                 295                 300

Glu Met Pro Phe Gln Gly Ser Gly Lys Ser Ala Trp Cys Pro Val Glu
305                 310                 315                 320
```

```
Ile Ser Lys Thr Val Leu Trp Pro Glu Ser Ile Ser Val Val Arg Cys
                325                 330                 335

Val Glu Leu Phe Glu Ala Pro Val Glu Cys Glu Glu Glu Glu Glu Val
            340                 345                 350

Glu Glu Glu Lys Gly Ser Phe Cys Ala Ser Pro Glu Ser Ser Arg Asp
        355                 360                 365

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

Leu Phe Leu Asp Leu Leu Gly Glu Glu Asn Gly Gly Phe Cys Gln Gln
385                 390                 395                 400

Asp Met Gly Glu Ser Cys Leu Leu Pro Pro Ser Gly Ser Thr Ser Ala
                405                 410                 415

His Met Pro Trp Asp Glu Phe Pro Ser Ala Gly Pro Lys Glu Ala Pro
            420                 425                 430

Pro Trp Gly Lys Glu Gln Pro Leu His Leu Glu Pro Ser Pro Pro Ala
        435                 440                 445

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

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

Gln Ser Pro Cys Pro Arg Glu Leu Gly Pro Asp Pro Leu Leu Ala Arg
                485                 490                 495

His Leu Glu Glu Val Glu Pro Glu Met Pro Cys Val Pro Gln Leu Ser
            500                 505                 510
```

```
Glu Pro Thr Thr Val Pro Gln Pro Glu Pro Glu Thr Trp Glu Gln Ile
        515                 520                 525

Leu Arg Arg Asn Val Leu Gln His Gly Ala Ala Ala Ala Pro Val Ser
    530                 535                 540

Ala Pro Thr Ser Gly Tyr Gln Glu Phe Val His Ala Val Glu Gln Gly
545                 550                 555                 560

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

Gly Tyr Lys Ala Phe Ser Ser Leu Leu Ala Ser Ser Ala Val Ser Pro
            580                 585                 590

Glu Lys Cys Gly Phe Gly Ala Ser Ser Gly Glu Glu Gly Tyr Lys Pro
        595                 600                 605

Phe Gln Asp Leu Ile Pro Gly Cys Pro Gly Asp Pro Ala Pro Val Pro
    610                 615                 620

Val Pro Leu Phe Thr Phe Gly Leu Asp Arg Glu Pro Pro Arg Ser Pro
625                 630                 635                 640

Gln Ser Ser His Leu Pro Ser Ser Ser Pro Glu His Leu Gly Leu Glu
                645                 650                 655

Pro Gly Glu Lys Val Glu Asp Met Pro Lys Pro Pro Leu Pro Gln Glu
            660                 665                 670

Gln Ala Thr Asp Pro Leu Val Asp Ser Leu Gly Ser Gly Ile Val Tyr
        675                 680                 685

Ser Ala Leu Thr Cys His Leu Cys Gly His Leu Lys Gln Cys His Gly
    690                 695                 700

Gln Glu Asp Gly Gly Gln Thr Pro Val Met Ala Ser Pro Cys Cys Gly
705                 710                 715                 720
```

```
Cys Cys Cys Gly Asp Arg Ser Ser Pro Pro Thr Thr Pro Leu Arg Ala
                725                 730                 735

Pro Asp Pro Ser Pro Gly Gly Val Pro Leu Glu Ala Ser Leu Cys Pro
            740                 745                 750

Ala Ser Leu Ala Pro Ser Gly Ile Ser Glu Lys Ser Lys Ser Ser Ser
        755                 760                 765

Ser Phe His Pro Ala Pro Gly Asn Ala Gln Ser Ser Ser Gln Thr Pro
    770                 775                 780

Lys Ile Val Asn Phe Val Ser Val Gly Pro Thr Tyr Met Arg Val Ser
785                 790                 795                 800
```

<210> 26
<211> 347
<212> PRT
<213> Homo sapiens

<400> 26

```
Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly Asn Glu Asp Thr Thr Ala
1               5                   10                  15

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

Leu Pro Leu Pro Glu Val Gln Cys Phe Val Phe Asn Val Glu Tyr Met
        35                  40                  45

Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro Gln Pro Thr Asn Leu Thr
    50                  55                  60

Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn Asp Lys Val Gln Lys Cys
65                  70                  75                  80

Ser His Tyr Leu Phe Ser Glu Glu Ile Thr Ser Gly Cys Gln Leu Gln
                85                  90                  95
```

```
Lys Lys Glu Ile His Leu Tyr Gln Thr Phe Val Val Gln Leu Gln Asp
            100                 105                 110

Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln Met Leu Lys Leu Gln Asn
        115                 120                 125

Leu Val Ile Pro Trp Ala Pro Glu Asn Leu Thr Leu His Lys Leu Ser
    130                 135                 140

Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn Arg Phe Leu Asn His Cys
145                 150                 155                 160

Leu Glu His Leu Val Gln Tyr Arg Thr Asp Trp Asp His Ser Trp Thr
                165                 170                 175

Glu Gln Ser Val Asp Tyr Arg His Lys Phe Ser Leu Pro Ser Val Asp
            180                 185                 190

Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg Ser Arg Phe Asn Pro Leu
        195                 200                 205

Cys Gly Ser Ala Gln His Trp Ser Glu Trp Ser His Pro Ile His Trp
    210                 215                 220

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

Val Val Ile Ser Val Gly Ser Met Gly Leu Ile Ile Ser Leu Leu Cys
                245                 250                 255

Val Tyr Phe Trp Leu Glu Arg Thr Met Pro Arg Ile Pro Thr Leu Lys
            260                 265                 270

Asn Leu Glu Asp Leu Val Thr Glu Tyr His Gly Asn Phe Ser Ala Trp
        275                 280                 285
```

```
Ser Gly Val Ser Lys Gly Leu Ala Glu Ser Leu Gln Pro Asp Tyr Ser
    290                 295                 300

Glu Arg Leu Cys Leu Val Ser Glu Ile Pro Pro Lys Gly Gly Ala Leu
305                 310                 315                 320

Gly Glu Gly Pro Gly Ala Ser Pro Cys Asn Gln His Ser Pro Tyr Trp
                325                 330                 335

Ala Pro Pro Cys Tyr Thr Leu Lys Pro Glu Thr
            340                 345
```

<210> 27
<211> 406
<212> PRT
<213> Homo sapiens

<400> 27

```
Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn
1               5                   10                  15

Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn
            20                  25                  30

Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp Tyr Phe Ser His
        35                  40                  45

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

Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln
65                  70                  75                  80

Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu Val Glu Lys Cys
                85                  90                  95

Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln
            100                 105                 110
```

```
Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp Leu Pro Gly
        115                 120                 125

Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr Tyr Trp His Arg
    130                 135                 140

Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe Arg Glu Gly Gln
145                 150                 155                 160

Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys Asp Ser Ser Phe
                165                 170                 175

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

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

Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp Asp Leu Tyr Val
    210                 215                 220

Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys Leu Phe Tyr Glu
225                 230                 235                 240

Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn Val Phe Tyr Val
                245                 250                 255

Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg Asn Val Glu Asn
            260                 265                 270

Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr
        275                 280                 285

Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys
    290                 295                 300

Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly Lys Lys Arg Asn
305                 310                 315                 320
```

```
Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro Val Ile Val Ala
                325                 330                 335

Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg Leu Lys Ile Ile
            340                 345                 350

Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu Met Phe
        355                 360                 365

Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys Tyr Asp Ile Tyr
    370                 375                 380

Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val Leu Ile Glu Asn
385                 390                 395                 400

Leu Lys Lys Ala Ser Gln
                405
```

<210> 28
<211> 557
<212> PRT
<213> Homo sapiens

<400> 28

```
His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe Glu Ala Glu
1               5                   10                  15

Phe Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn Gln Ser Glu
            20                  25                  30

Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile Glu Ser Trp
        35                  40                  45

Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp Leu Thr Ala
    50                  55                  60

Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala Arg Val Arg
65                  70                  75                  80
```

```
Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr Asn Thr Arg
                85                  90                  95

Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val Asn Leu Glu
            100                 105                 110

Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro Arg Pro Lys
        115                 120                 125

Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser His Phe Arg
    130                 135                 140

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

His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr Ser Gly Glu
                165                 170                 175

Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala Ser Arg Ser
            180                 185                 190

Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu Thr Arg Gln
        195                 200                 205

Tyr Phe Thr Val Thr Asn Val Ile Ile Phe Phe Ala Phe Val Leu Leu
    210                 215                 220

Leu Ser Gly Ala Leu Ala Tyr Cys Leu Ala Leu Gln Leu Tyr Val Arg
225                 230                 235                 240

Arg Arg Lys Lys Leu Pro Ser Val Leu Leu Phe Lys Lys Pro Ser Pro
                245                 250                 255

Phe Ile Phe Ile Ser Gln Arg Pro Ser Pro Glu Thr Gln Asp Thr Ile
            260                 265                 270
```

```
His Pro Leu Asp Glu Glu Ala Phe Leu Lys Val Ser Pro Glu Leu Lys
        275                 280                 285

Asn Leu Asp Leu His Gly Ser Thr Asp Ser Gly Phe Gly Ser Thr Lys
    290                 295                 300

Pro Ser Leu Gln Thr Glu Glu Pro Gln Phe Leu Leu Pro Asp Pro His
305                 310                 315                 320

Pro Gln Ala Asp Arg Thr Leu Gly Asn Arg Glu Pro Pro Val Leu Gly
                325                 330                 335

Asp Ser Cys Ser Ser Gly Ser Ser Asn Ser Thr Asp Ser Gly Ile Cys
            340                 345                 350

Leu Gln Glu Pro Ser Leu Ser Pro Ser Thr Gly Pro Thr Trp Glu Gln
        355                 360                 365

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

Val Gln Asn Ser Glu Gly Arg Ala Gly Asp Thr Gln Gly Gly Ser Ala
385                 390                 395                 400

Leu Gly His His Ser Pro Pro Glu Pro Glu Val Pro Gly Glu Glu Asp
                405                 410                 415

Pro Ala Ala Val Ala Phe Gln Gly Tyr Leu Arg Gln Thr Arg Cys Ala
            420                 425                 430

Glu Glu Lys Ala Thr Lys Thr Gly Cys Leu Glu Glu Glu Ser Pro Leu
        435                 440                 445

Thr Asp Gly Leu Gly Pro Lys Phe Gly Arg Cys Leu Val Asp Glu Ala
    450                 455                 460

Gly Leu His Pro Pro Ala Leu Ala Lys Gly Tyr Leu Lys Gln Asp Pro
465                 470                 475                 480
```

Leu Glu Met Thr Leu Ala Ser Ser Gly Ala Pro Thr Gly Gln Trp Asn
485 490 495

Gln Pro Thr Glu Glu Trp Ser Leu Leu Ala Leu Ser Ser Cys Ser Asp
500 505 510

Leu Gly Ile Ser Asp Trp Ser Phe Ala His Asp Leu Ala Pro Leu Gly
515 520 525

Cys Val Ala Ala Pro Gly Gly Leu Leu Gly Ser Phe Asn Ser Asp Leu
530 535 540

Val Thr Leu Pro Leu Ile Ser Ser Leu Gln Ser Ser Glu
545 550 555

<210> 29
<211> 306
<212> PRT
<213> Homo sapiens

<400> 29
Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val Asn Phe Lys
1 5 10 15

Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly Asn Leu Thr
20 25 30

Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp Lys Cys Met
35 40 45

Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly
50 55 60

Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp
65 70 75 80

Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro
85 90 95

```
Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe
            100                 105                 110

Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn
        115                 120                 125

Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr
    130                 135                 140

Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg
145                 150                 155                 160

Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu
                165                 170                 175

Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln
            180                 185                 190

Thr Thr His Asp Glu Thr Val Pro Ser Trp Met Val Ala Val Ile Leu
        195                 200                 205

Met Ala Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly Cys Phe Ala
    210                 215                 220

Leu Leu Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala Phe Ser Pro Arg
225                 230                 235                 240

Asn Ser Leu Pro Gln His Leu Lys Glu Phe Leu Gly His Pro His His
                245                 250                 255

Asn Thr Leu Leu Phe Phe Ser Phe Pro Leu Ser Asp Glu Asn Asp Val
            260                 265                 270

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

Asn Pro Gly Asp Ser Cys Ser Leu Gly Thr Pro Pro Gly Gln Gly Pro
290 295 300

Gln Ser
305

<210> 30
<211> 523
<212> PRT
<213> Homo sapiens

<400> 30
Ala Glu Ser Cys Thr Ser Arg Pro His Ile Thr Val Val Glu Gly Glu
1 5 10 15

Pro Phe Tyr Leu Lys His Cys Ser Cys Ser Leu Ala His Glu Ile Glu
20 25 30

Thr Thr Thr Lys Ser Trp Tyr Lys Ser Ser Gly Ser Gln Glu His Val
35 40 45

Glu Leu Asn Pro Arg Ser Ser Ser Arg Ile Ala Leu His Asp Cys Val
50 55 60

Leu Glu Phe Trp Pro Val Glu Leu Asn Asp Thr Gly Ser Tyr Phe Phe
65 70 75 80

Gln Met Lys Asn Tyr Thr Gln Lys Trp Lys Leu Asn Val Ile Arg Arg
85 90 95

Asn Lys His Ser Cys Phe Thr Glu Arg Gln Val Thr Ser Lys Ile Val
100 105 110

Glu Val Lys Lys Phe Phe Gln Ile Thr Cys Glu Asn Ser Tyr Tyr Gln
115 120 125

Thr Leu Val Asn Ser Thr Ser Leu Tyr Lys Asn Cys Lys Lys Leu Leu
130 135 140

```
Leu Glu Asn Asn Lys Asn Pro Thr Ile Lys Lys Asn Ala Glu Phe Glu
145                 150                 155                 160

Asp Gln Gly Tyr Tyr Ser Cys Val His Phe Leu His His Asn Gly Lys
                165                 170                 175

Leu Phe Asn Ile Thr Lys Thr Phe Asn Ile Thr Ile Val Glu Asp Arg
            180                 185                 190

Ser Asn Ile Val Pro Val Leu Leu Gly Pro Lys Leu Asn His Val Ala
        195                 200                 205

Val Glu Leu Gly Lys Asn Val Arg Leu Asn Cys Ser Ala Leu Leu Asn
    210                 215                 220

Glu Glu Asp Val Ile Tyr Trp Met Phe Gly Glu Glu Asn Gly Ser Asp
225                 230                 235                 240

Pro Asn Ile His Glu Glu Lys Glu Met Arg Ile Met Thr Pro Glu Gly
                245                 250                 255

Lys Trp His Ala Ser Lys Val Leu Arg Ile Glu Asn Ile Gly Glu Ser
            260                 265                 270

Asn Leu Asn Val Leu Tyr Asn Cys Thr Val Ala Ser Thr Gly Gly Thr
        275                 280                 285

Asp Thr Lys Ser Phe Ile Leu Val Arg Lys Ala Asp Met Ala Asp Ile
    290                 295                 300

Pro Gly His Val Phe Thr Arg Gly Met Ile Ile Ala Val Leu Ile Leu
305                 310                 315                 320

Val Ala Val Val Cys Leu Val Thr Val Cys Val Ile Tyr Arg Val Asp
                325                 330                 335

Leu Val Leu Phe Tyr Arg His Leu Thr Arg Arg Asp Glu Thr Leu Thr
            340                 345                 350
```

```
Asp Gly Lys Thr Tyr Asp Ala Phe Val Ser Tyr Leu Lys Glu Cys Arg
        355                 360                 365

Pro Glu Asn Gly Glu Glu His Thr Phe Ala Val Glu Ile Leu Pro Arg
    370                 375                 380

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

Val Val Pro Gly Gly Ala Val Val Asp Glu Ile His Ser Leu Ile Glu
                405                 410                 415

Lys Ser Arg Arg Leu Ile Ile Val Leu Ser Lys Ser Tyr Met Ser Asn
            420                 425                 430

Glu Val Arg Tyr Glu Leu Glu Ser Gly Leu His Glu Ala Leu Val Glu
        435                 440                 445

Arg Lys Ile Lys Ile Ile Leu Ile Glu Phe Thr Pro Val Thr Asp Phe
    450                 455                 460

Thr Phe Leu Pro Gln Ser Leu Lys Leu Leu Lys Ser His Arg Val Leu
465                 470                 475                 480

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

Asn Leu Leu Tyr Leu Met Pro Ala Lys Thr Val Lys Pro Gly Arg Asp
            500                 505                 510

Glu Pro Glu Val Leu Pro Val Leu Ser Glu Ser
        515                 520
```

<210> 31
<211> 580
<212> PRT
<213> Homo sapiens

<400> 31
Phe Asn Ile Ser Gly Cys Ser Thr Lys Lys Leu Leu Trp Thr Tyr Ser
1 5 10 15

Thr Arg Ser Glu Glu Glu Phe Val Leu Phe Cys Asp Leu Pro Glu Pro
20 25 30

Gln Lys Ser His Phe Cys His Arg Asn Arg Leu Ser Pro Lys Gln Val
35 40 45

Pro Glu His Leu Pro Phe Met Gly Ser Asn Asp Leu Ser Asp Val Gln
50 55 60

Trp Tyr Gln Gln Pro Ser Asn Gly Asp Pro Leu Glu Asp Ile Arg Lys
65 70 75 80

Ser Tyr Pro His Ile Ile Gln Asp Lys Cys Thr Leu His Phe Leu Thr
85 90 95

Pro Gly Val Asn Asn Ser Gly Ser Tyr Ile Cys Arg Pro Lys Met Ile
100 105 110

Lys Ser Pro Tyr Asp Val Ala Cys Cys Val Lys Met Ile Leu Glu Val
115 120 125

Lys Pro Gln Thr Asn Ala Ser Cys Glu Tyr Ser Ala Ser His Lys Gln
130 135 140

Asp Leu Leu Leu Gly Ser Thr Gly Ser Ile Ser Cys Pro Ser Leu Ser
145 150 155 160

Cys Gln Ser Asp Ala Gln Ser Pro Ala Val Thr Trp Tyr Lys Asn Gly
165 170 175

Lys Leu Leu Ser Val Glu Arg Ser Asn Arg Ile Val Val Asp Glu Val
180 185 190

```
Tyr Asp Tyr His Gln Gly Thr Tyr Val Cys Asp Tyr Thr Gln Ser Asp
        195                 200                 205

Thr Val Ser Ser Trp Thr Val Arg Ala Val Val Gln Val Arg Thr Ile
    210                 215                 220

Val Gly Asp Thr Lys Leu Lys Pro Asp Ile Leu Asp Pro Val Glu Asp
225                 230                 235                 240

Thr Leu Glu Val Glu Leu Gly Lys Pro Leu Thr Ile Ser Cys Lys Ala
                245                 250                 255

Arg Phe Gly Phe Glu Arg Val Phe Asn Pro Val Ile Lys Trp Tyr Ile
            260                 265                 270

Lys Asp Ser Asp Leu Glu Trp Glu Val Ser Val Pro Glu Ala Lys Ser
        275                 280                 285

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

Glu Lys Val Thr Gln Arg Asp Leu Arg Arg Lys Phe Val Cys Phe Val
305                 310                 315                 320

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

Arg Gly Val Val Leu Leu Tyr Ile Leu Leu Gly Thr Ile Gly Thr Leu
            340                 345                 350

Val Ala Val Leu Ala Ala Ser Ala Leu Leu Tyr Arg His Trp Ile Glu
        355                 360                 365

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

Asp Lys Lys Asp Phe Asp Ala Phe Val Ser Tyr Ala Lys Trp Ser Ser
385                 390                 395                 400
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Phe Pro Ser Glu Ala Thr Ser Ser Leu Ser Glu Glu His Leu Ala Leu
                405                 410                 415

Ser Leu Phe Pro Asp Val Leu Glu Asn Lys Tyr Gly Tyr Ser Leu Cys
            420                 425                 430

Leu Leu Glu Arg Asp Val Ala Pro Gly Gly Val Tyr Ala Glu Asp Ile
        435                 440                 445

Val Ser Ile Ile Lys Arg Ser Arg Arg Gly Ile Phe Ile Leu Ser Pro
    450                 455                 460

Asn Tyr Val Asn Gly Pro Ser Ile Phe Glu Leu Gln Ala Ala Val Asn
465                 470                 475                 480

Leu Ala Leu Asp Asp Gln Thr Leu Lys Leu Ile Leu Ile Lys Phe Cys
                485                 490                 495

Tyr Phe Gln Glu Pro Glu Ser Leu Pro His Leu Val Lys Lys Ala Leu
            500                 505                 510

Arg Val Leu Pro Thr Val Thr Trp Arg Gly Leu Lys Ser Val Pro Pro
        515                 520                 525

Asn Ser Arg Phe Trp Ala Lys Met Arg Tyr His Met Pro Val Lys Asn
    530                 535                 540

Ser Gln Gly Phe Thr Trp Asn Gln Leu Arg Ile Thr Ser Arg Ile Phe
545                 550                 555                 560

Gln Trp Lys Gly Leu Ser Arg Thr Glu Thr Thr Gly Arg Ser Ser Gln
                565                 570                 575

Pro Lys Glu Trp
            580
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<210> 32
<211> 495
<212> DNA
<213> Artificial Sequence

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

<400> 32
tgcgaccttc cacagaccca ttccctcggc tctcgaagaa ctctgatgtt gctggcccag 60

atgcggaaga tttctctttt ctcatgtctg aaagacaggc acgactttgg ttttccccag 120

gaggagttcg gaaaccagtt ccagaaagcg gaaaccattc ctgtgctgca cgaaatgatc 180

caacaaattt tcaacctgtt ttcaactaaa gatagctccg ctgcatggga cgagacactc 240

ctcgataagt tttatacaga gctttaccag cagttaaatg atctggaagc ttgtgtcatc 300

caaggggtcg gcgtaaccga gacgcccctg atgaaggagg atagcatact ggcagtgcgg 360

aagtacttcc agaggatcac cctctatcta aaggaaaaaa agtacagtcc gtgcgcctgg 420

gaagtggtta gagccgaaat catgcgtagc ttttccttat ctacaaattt gcaggagtcg 480

ttgcgcagta aagag 495

<210> 33
<211> 498
<212> DNA
<213> Artificial Sequence

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

<400> 33
atgagttata atttactcgg atttctacag cggtctagca acttccaatg tcagaagctg 60

ctgtggcaac tcaacggcag gctggagtac tgcctcaaag atagaatgaa ctttgatatt 120

cccgaagaaa tcaagcagct tcagcagttc cagaaagagg acgccgcact aaccatatac 180

gagatgctgc agaacatttt cgctatattc agacaggact cgtcctctac tggatggaat 240

gagaccatcg tcgagaattt gctggccaat gtgtatcatc aaattaacca cctcaagacg 300

gtgcttgaag aaaagttgga aaaagaggac ttcactagag gcaaactgat gtcatccctt 360

cacctcaaac gctactatgg gaggatcctg cactacttaa aggcgaagga gtatagccat 420

tgcgcttgga caatcgttcg cgtagagatt ctgcggaatt tttactttat caatcgtttg 480

acaggttacc tgcgaaac 498

<210> 34
<211> 414
<212> DNA
<213> Artificial Sequence

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

<400> 34
caggatccct acgtgaagga agcagaaaat ctcaaaaagt atttcaatgc gggccatagc 60

gatgtggccg ataacggcac cctgtttctg gggattctta agaattggaa agaggagtct 120

gataggaaga ttatgcagtc ccagatcgtg agcttctatt tcaagctgtt caaaaacttc 180

aaagacgacc agtcgatcca aaaatctgtt gagacaataa aagaggacat gaatgtgaag 240

ttttttaatt caaacaaaaa gaagcgcgac gattttgaga aattaacgaa ctactccgtc 300

accgacttga acgtacaacg aaaggctatt cacgaactaa tccaggtcat ggctgaactg 360

agtcctgccg ccaagactgg taagcgtaaa cggagtcaga tgctctttag agga 414

<210> 35
<211> 471
<212> DNA
<213> Artificial Sequence

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

<400> 35
gtgcgatctt caagccggac accctcagac aagccagtgg cacacgtggt agcgaaccca 60

caagctgagg ggcagctcca gtggctcaat cggcgtgcca acgccctgtt agccaatggg 120

gtcgagctta gggacaacca acttgtggta ccctcggaag gattatactt gatttacagt 180

caggtgctgt tcaaaggaca gggctgccct tccacacatg ttctgctcac tcacacgatc 240

tcccgcattg cagtgtctta tcagaccaag gtcaacttgc taagcgctat caaaagtcca 300

tgtcagagag agaccccgga gggtgctgag gctaagcctt ggtacgaacc tatttatctg 360

ggcggagtct ttcaactgga aaaaggtgat agactgagcg cagagatcaa taggcccgat 420

tacctggact tcgccgaatc cggccaggtt tattttggga taatcgccct c 471

<210> 36
<211> 459
<212> DNA
<213> Artificial Sequence

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

<400> 36
gcgcctgtca gaagcctcaa ctgcacgctg agggactcac agcaaaagag cctggtcatg 60

agtggcccct acgagctgaa agcactccac cttcaggggc aggacatgga acaacaggtg 120

gttttctcca tgtctttcgt acagggagag gagtctaacg ataagatccc cgtggctttg 180

ggcttaaaag agaaaaacct gtatctgagc tgtgtgctaa aggacgataa gcccacactt 240

cagctcgagt ccgttgatcc aaaaaattat ccaaagaaga aaatggaaaa gcggtttgtg 300

tttaacaaga ttgagattaa taacaaattg gaattcgaat cagcccagtt ccctaattgg 360

tacatcagta cctctcaagc cgaaaatatg ccggtgtttc tgggagggac caagggtggc 420

caggatataa cagacttcac tatgcagttt gtctcgtcc 459

<210> 37
<211> 549
<212> DNA
<213> Artificial Sequence

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

<400> 37
gtgccgcccg gggaagatag caaggatgtg gctgctcctc acaggcagcc actgacaagc 60

agcgagagaa tcgacaagca aataaggtat attcttgatg gaatcagcgc gctgcgaaag 120

gagacatgta acaagtcgaa tatgtgcgag tcttccaaag aagcacttgc tgaaaataat 180

ctgaacctcc caaaaatggc cgagaaagac ggctgctttc agtccggttt taacgaggag 240

acttgtttag taaagattat aacgggcttg ttggaattcg aagtctacct agaatacctc 300

caaaatagat tcgagagtag tgaggaacag gcccgcgctg ttcagatgtc aacaaaagtg 360

ttgatccaat tcctgcagaa aaaagccaag aacttagatg caatcaccac acctgacccc 420

actaccaatg cctctctgct caccaagctg caagcccaga accagtggct gcaggacatg 480

actacccatc taattctgcg gtcttttaag gagttcctcc agtcatccct gcgtgcactt 540

cggcagatg 549

<210> 38
<211> 591
<212> DNA
<213> Artificial Sequence

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

<400> 38
cgaaatctgc cagtggctac ccccgacccg ggcatgtttc cctgcctcca tcatagccag 60

aatctgctca gagcggtcag caacatgcta cagaaggccc gccagacctt agagttttac 120

ccttgcacct ctgaggaaat cgatcacgaa gacatcacca aagataagac tagcaccgtt 180

gaagcctgtc tcccattgga acttacaaaa aatgaatctt gtctgaattc cagagagaca 240

tcttttatca ctaatggaag ttgcctcgcc agtcggaaaa cttccttcat gatggccctg 300

tgtctgagtt caatctacga ggatcttaag atgtatcaag tggaattcaa aacgatgaac 360

gcaaaactgt tgatggatcc taagaggcag atatttttgg atcagaacat gttagctgtg 420

atcgacgagc tgatgcaagc actcaacttc aactcagaga cagtccccca gaagtcctcc 480

ctggaggagc ctgacttcta caagacgaaa attaagctat gcattctgct tcacgcattc 540

aggatacggg ccgtaacaat tgaccgtgtg atgagctatc tgaacgcttc g 591

<210> 39

<211> 918
<212> DNA
<213> Artificial Sequence

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

<400> 39
atctgggagc tcaaaaagga tgtttatgtg gtcgaacttg actggtaccc ggacgcacca 60

ggggagatgg tggtgttgac ctgcgacacc cccgaagagg acgggattac atggactttg 120

gaccagtcca gtgaagtcct gggctcggga aagaccctga ctatccaggt gaaggagttc 180

ggagatgctg gacaatatac atgccacaag ggcggggaag ttttgagcca ttccctcctg 240

ctgctgcata aaaaagagga tggtatttgg agcactgata ttctgaaaga ccagaaggaa 300

cccaagaaca aaacttttct gcggtgtgag gccaagaatt acagtggaag attcacctgt 360

tggtggttaa ccacaatctc taccgatctt acctttccg tcaaatcaag tcgcggcagc 420

agcgatccac agggcgtgac gtgcggcgct gccacactaa gcgcggagag agtgcggggt 480

gacaacaagg aatacgagta ctccgttgag tgtcaagaag actctgcatg ccctgccgca 540

gaggaatcat taccgatcga agtaatggtg gatgctgttc acaaactgaa gtatgaaaac 600

tacacttctt catttttcat aagggacatt atcaagcctg atcctccaaa gaacctccaa 660

cttaaaccac tcaagaatag ccgtcaggta gaggtgtcct gggagtaccc cgatacctgg 720

tcaacgcccc actcatattt ctccctgacg ttctgtgtgc aggtgcaggg gaaatccaag 780

agggagaaga aagacagggt ctttacagat aagacatctg ccactgtcat ctgcagaaaa 840

aatgcctcta tatccgtgcg agcccaggac cgctactatt ctagtagctg gagcgagtgg 900

gctagtgtac cttgttcg 918

<210> 40
<211> 387
<212> DNA
<213> Artificial Sequence

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

<400> 40
cacaagtgtg atattacact ccaagaaata atcaagaccc tgaacagcct aaccgagcag 60

aaaactctct gtacggaatt gaccgttacc gatatcttcg cagctagtaa gaatacaact 120

gaaaaagaga cgttttgtcg tgccgccaca gtcctgaggc agttttattc acatcacgag 180

aaagacaccc ggtgccttgg ggcaactgcc caacagtttc atcgccacaa acagctgatc 240

agattcttga agcggctgga caggaatctc tggggattag ctggcctgaa ttcttgcccc 300

gtgaaggagg cgaaccagag cactctggag aacttcctgg aacgacttaa gacaattatg 360

agagagaagt actccaaatg ctcctct 387

<210> 41
<211> 480
<212> DNA
<213> Artificial Sequence

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

<400> 41
tcacccggac agggtactca atctgaaaat agttgcaccc attttccagg aaatctgcct 60

aacatgctga gggacttacg cgatgcattt tcgcgtgtaa aaacattctt tcagatgaaa 120

gatcaactgg ataacctgtt gctaaaagag agcctgcttg aggatttcaa gggctatctg 180

ggctgtcagg cgctctccga aatgattcaa ttctacctcg aagaggtgat gccccaggcc 240

gagaaccagg acccagacat caaggcccac gtgaattctc tgggggagaa tctgaaaacg 300

ctcagattgc gactcagacg gtgccacagg tttttacctt gtgaaaacaa gagcaaagcc 360

gttgagcagg tcaagaacgc ttttaataag cttcaggaaa aagggatcta taaggcaatg 420

tccgagttcg acatattcat taattacatt gaggcttaca tgaccatgaa gatccggaac 480

<210> 42
<211> 366
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 42
ttaacatgtc tgggcgggtt cgcctcacct ggaccagttc ccccttcaac cgctctcaga 60

gaactgattg aggagctcgt caatatcacc cagaaccaaa aagccccact ctgcaatgga 120

agtatggtgt ggtctattaa cttgactgcc ggcatgtact gtgccgcact ggagtctttg 180

atcaacgtgt ccgggtgcag tgcaatcgaa aagacgcagc ggatgctgag cggcttttgc 240

ccccacaagg tgagcgctgg tcagttttcc agccttcacg tgcgagatac aaagatagaa 300

gtagcgcagt tcgtcaagga cctgctgctg catcttaaaa aactatttcg cgagggtagg 360

ttcaat 366

<210> 43
<211> 471
<212> DNA
<213> Artificial Sequence

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

<400> 43
tattttggca aactcgaaag taagctgagc gtgattcgga atcttaacga tcaggtgtta 60

ttcatcgatc aaggcaacag accactcttt gaagatatga cagattcaga ctgtagggat 120

aatgccccta ggaccatctt tattataagc atgtataagg actctcagcc ccgcggtatg 180

gcagtaacga ttagcgttaa gtgcgagaag atttctacac tttcatgcga aaacaaaatc 240

atctccttca aagagatgaa ccctcccgat aatatcaaag ataccaagtc ggacataatt 300

ttctttcaga gatccgtccc aggacacgac aataagatgc aattcgaatc cagcagttac 360

gagggatact ttctggcttg tgagaaggaa cgtgacttgt tcaaactgat cctgaagaaa 420

gaggacgagc taggggaccg atctatcatg ttcactgtgc agaacgagga c 471

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

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

<400> 44
aagaacctga aatccccaca gaaagtcgag gtggacatca tcgatgacaa tttcatctta 60

agatggaacc gtagcgatga gtccgtcgga aatgtcacat tttcttttga ttatcagaag 120

accgggatgg acaactggat taagctgtcc ggttgccaga acataaccag taccaagtgt 180

aacttcagca gcctcaaact caatgtatat gaggaaatca agctgaggat ccgggccgag 240

aaggaaaaca caagctcctg gtatgaagtt gattcattta ctccatttcg aaaagcgcaa 300

ataggacccc cggaagttca cctcgaggct gaagataaag caattgtaat acacatatcg 360

cctggcacca aggactctgt gatgtgggct ttagatgggc tgtcattcac gtacagcctg 420

gtgatctgga agaacagttc tggggtggag gagagaatag aaaacattta tagtcgccac 480

aaaatctaca aattgtcacc cgaaacaacc tattgcctga aggtcaaggc ggcactattg 540

acgtcctgga agatcggcgt gtactcacca gtgcattgta taaagacaac agtggaaaac 600

gagcttcccc cgccggagaa tattgaggtt tccgtgcaga atcagaatta tgtgttgaag 660

tgggactaca catatgccaa tatgaccttc caggttcaat ggcttcatgc atttctgaaa 720

agaaaccctg gtaaccacct ttacaaatgg aagcagattc ctgactgcga gaatgtcaag 780

accacacagt gcgtgtttcc tcaaaacgtt ttccagaaag gcatctatct gctacgggtc 840

caggcttccg atggcaataa tacctcattt tggagcgagg aaattaaatt cgacactgaa 900

atccaagcct tcctactccc tcccgtattt aacatcagga gtctgtctga tagcttccat 960

atttacatcg gtgctcccaa gcagtctgga aacactcccg tgatccagga ttacccccctc 1020

atctacgaga tcattttctg ggaaaacacc tctaacgccg aacggaagat tatagagaag 1080

aaaactgacg tcactgtgcc taacctgaaa ccattaactg tctattgcgt caaagctagg 1140

gcccacacca tggatgaaaa actgaacaag tctagcgtgt tcagcgacgc agtttgtgag 1200

aaaacgaagc caggaaatac ttctaagatt tggcttatcg tgggcatttg tatcgctctg 1260

ttcgcactgc cctttgtaat ctacgccgcc aaggtttttc tccgctgtat taattatgtg 1320

ttttcccat ccctgaagcc atcatcgtcg attgacgagt acttctctga gcaacctctt 1380

aaaaacctgt tgttgtccac cagtgaagag cagattgaga aatgcttcat tatcgaaaat 1440

atttcaacaa tcgccacagt ggaggagacg aatcagaccg acgaggacca taagaagtac 1500

agcagtcaga catctcagga ttccgggaat tacagcaatg aagatgaaag tgaatccaaa 1560

actagcgagg agctccaaca ggactttgtg 1590

<210> 45
<211> 1467
<212> DNA
<213> Artificial Sequence

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

<400> 45
atcagctacg actcccccga ttacaccgac gagtcctgta cctttaaaat ctccctacgt 60

aacttcaggt ccattctctc ctgggaactg aaaaaccata gcattgtgcc gactcactat 120

acactgctgt ataccataat gtctaaaccc gaggatctga aggtggtgaa gaactgtgcg 180

aacaccacaa gatccttctg cgacctgaca gatgagtggc gatctaccca tgaagcctac 240

gtcacggtcc tcgagggctt cagcggtaat accacacttt tcagctgctc acataacttt 300

tggttggcca tcgatatgtc ctttgaacca cccgagttcg agattgtcgg tttcacaaac 360

cacatcaatg tcatggtgaa atttccttct attgtcgagg aagaactcca gtttgatttg 420

agcctcgtga ttgaggagca gtcagaggga atcgtgaaga agcataagcc cgaaataaag 480

ggaaatatga gtgggaactt cacttacata atcgacaagc tcatccccaa cacgaattat 540

tgtgtgtcag tgtatctcga gcactcggat gagcaagccg tgatcaagtc tccacttaag 600

tgcactctcc tgccgccagg ccaggagtca gagagcgctg aatcggctaa gataggcggg 660

atcattaccg tcttcctcat cgcactggtg ttgacttcta ctattgttac cctgaagtgg 720

atcggataca tctgcttgcg caactctctg ccaaaagttc taaactttca caattttctg 780

gcctggccct tccccaatct tcctcctctg gaggccatgg acatggttga ggttatctat 840

ataaatcgga aaaaaaaagt ctgggactac aattacgatg acgaaagtga ctcagacacg 900

gaggccgcac caaggacctc tggaggggc tatactatgc acggccttac cgtgagacct 960

ttaggacagg catctgctac aagcactgaa agccagctga ttgacccaga gagcgaggaa 1020

gagcctgatc taccagaagt ggatgtagag ctgccgacaa tgcctaagga ctccccccaa 1080

cagctcgaac tgttgagcgg cccttgtgaa aggcgcaaaa gtcccttgca agatccgttc 1140

cctgaagaag actatagcag taccgaagga tccggcggtc ggattacatt caacgtggat 1200

ttaaatagtg tatttttacg ggttctggac gatgaggaca gtgatgatct ggaggcgccc 1260

cttatgctgt cctcccatct ggaggagatg gtagaccccg aagatccaga taacgtgcag 1320

tctaatcacc ttctggcttc cggggaaggt actcagccaa cctttcctag tccttcttca 1380

gagggcttat ggtcagaaga cgcaccaagc gatcagtcag acacaagtga gagcgacgta 1440

gacctcgggg acgggtacat tatgaga 1467

<210> 46
<211> 1416
<212> DNA
<213> Artificial Sequence

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

<400> 46
gaaatgggga ctgccgactt gggacctagc agtgtcccca ctcccaccaa cgtgaccatc 60

gagtcttata atatgaatcc tattgtttat tgggaatatc agatcatgcc tcaggttcca 120

gtgttcactg ttgaagtgaa aaattacgga gtgaagaact cagagtggat agacgcttgc 180

ataaacatat ctcaccatta ctgcaatatt tccgaccacg tgggcgaccc cagcaacagt 240

ttgtgggtca gagtgaaagc tcgcgtgggc cagaaggaga gtgcttatgc caaaagcgaa 300

gaattcgccg tttgtagaga tggcaagatc gggcccccca aattagacat tcgcaaagaa 360

gaaaaacaaa ttatgatcga tatcttccat ccctctgtct tcgtcaacgg cgacgaacag 420

gaggtagatt atgatccaga gacaacgtgt tacatcaggg tatacaacgt ttacgtgagg 480

atgaatgggt cagagatcca gtataagatc ctcactcaaa aggaggacga ctgtgacgaa 540

attcagtgtc aactcgccat cccagtgtct tcgctgaata gccagtactg cgtgtctgcc 600

gagggtgtgc ttcacgtttg gggagtcaca actgaaaagt ccaaagaagt ttgtattacc 660

atttttaaca gctctatcaa gggctccctg tggataccag tggtggcggc actgctgctg 720

ttccttgtac tcagcctggt cttcatctgc ttctatatta agaagatcaa ccctctgaag 780

gagaagagca tcatactacc caagtcgctt atctcagtcg tgcggtccgc caccctagaa 840

actaagcccg aatcaaaata tgtatccctg atcacaagct accagccatt ttcattagag 900

aaagaagtcg tgtgcgagga gcctctgtcc ccagcaactg tgccaggtat gcatacggag 960

gacaatccgg gtaaagtaga gcacaccgag gagctgtcca gcattacaga ggtcgtcacc 1020

acagaggaga acatacccga tgtggtgcct ggaagtcatc tcacacctat tgagcgtgaa 1080

tctagcagtc ccttgtcttc taatcagagt gaaccgggga gtattgcatt aaactcctac 1140

cactcccgga attgcagcga aagcgaccac tcgagaaatg ggtttgatac cgatagttct 1200

tgtctggaat cccactcatc actgagcgat tctgagtttc cgccaaacaa caagggcgaa 1260

attaaaacgg agggacaaga gctcatcacc gtcatcaagg ctccaaccag ttttggttac 1320

gacaagcctc atgttttggt ggatctgctt gtggatgact caggcaagga gtccctcatt 1380

ggataccgac ctacagagga ttccaaagag tttagc 1416

<210> 47
<211> 948
<212> DNA
<213> Artificial Sequence

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

<400> 47
gccccccctg atcctctctc acagctaccc gccccacagc atcccaagat aagactgtac 60

aatgccgagc aggtgcttag ctgggagccc gtggcactat caaacagtac gagacccgtg 120

gtgtaccagg tacagttcaa gtacacagac agcaagtggt ttaccgctga cattatgagc 180

attggagtca attgcactca gatcaccgca accgagtgtg actttacagc agcttcaccc 240

tccgccggat tccctatgga cttcaacgtc actctgcggc ttcgtgcaga actgggcgct 300

cttcattccg cctgggtgac aatgccttgg ttccagcact atcggaacgt caccgtaggg 360

ccccctgaaa atatcgaagt aacccctgga gaaggttcgc tgataataag gttcagctct 420

ccgtttgaca ttgctgatac atccactgcg ttcttctgct actatgtgca ctactgggag 480

aagggcggga ttcaacaagt gaaagggcca ttcaggagca acagtatcag tctcgacaac 540

ctgaaacctt ctcgcgtcta ttgcctccaa gtgcaggctc aactgctgtg gaacaaaagt 600

aatattttcc gagttggcca cctgtctaat atctcctgtt atgagaccat ggccgacgca 660

tctacggagt tgcagcaggt catcctcatt tctgtgggca cattttccct gctgtcggtt 720

ctggccggtg cctgtttttt tctcgttttg aaataccgcg gcttgatcaa atactggttt 780

cataccccac catcaatacc attacagatc gaagagtatc ttaaagatcc aactcagcca 840

attttagagg cgctcgataa ggactctagc ccgaaggacg atgtgtggga ttccgtgtcc 900

atcatcagct ttcccgaaaa ggagcaggaa gatgttctgc aaactttg 948

<210> 48
<211> 1278
<212> DNA
<213> Artificial Sequence

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

<400> 48
ttggtacccc atcttggcga ccgagagaaa cgggatagtg tctgtcccca agggaaatat 60

atacacccac agaataactc tatctgctgc actaagtgcc ataaaggaac gtacctttat 120

aacgactgcc caggccccgg ccaagatact gactgcagag agtgcgagtc tgggagcttc 180

accgcctccg agaatcactt gagacattgc ctgagttgta gcaagtgcag gaaggagatg 240

gggcaggttg agatctcatc atgtaccgtt gatcgggaca ccgtctgtgg atgccgcaaa 300

aatcagtatc ggcattattg gtccgaaaac ctatttcagt gttttaactg ttctttgtgc 360

ctgaacggaa cagtccacct gagttgccag gaaaaacaga atacagtttg cacttgccac 420

gctggctttt ttctccgcga gaacgaatgt gtgtcctgtt ccaattgtaa gaagtctcta 480

gaatgtacaa agctgtgtct gccccaaatc gagaacgtga aaggaactga ggacagtggt 540

acaaccgtgt tgctgcctct ggtgatcttc ttcgggctct gcctcctcag tctgcttttc 600

attgggctaa tgtaccggta ccagcgttgg aaatctaagt tatactcaat tgtctgtggg 660

aagtccaccc ctgagaagga aggagaactg gaaggtacta ccaccaaacc actggctcca 720

aacccctcct tctctcctac acccggcttt actcctaccc tgggcttctc accggtgccc 780

agctcaacgt tcaccagctc gagcacatac acccctggcg attgtcccaa cttcgcagca 840

ccaaggcgtg aagtggcccc accctaccag ggtgctgatc caatacttgc caccgcatta 900

gccagcgatc cgattcctaa tcctttacag aagtgggagg attcggccca caaaccccag 960

agcctggaca ctgacgaccc cgccacgctg tatgctgtgg tcgagaatgt accgcctctc 1020

agatggaagg aatttgtgag gcgactgggc ctgtccgatc acgagatcga cagactggag 1080

ttgcaaaatg gtcgatgcct ccgggaggcc cagtacagca tgctggctac atggaggagg 1140

cgcacacctc gcagggaggc gactcttgaa ttgctgggac gcgtgctcag agatatggac 1200

ttactcggat gtcttgaaga cattgaagag gcgctctgcg gcccagcagc cctgcctccg 1260

gcaccatccc tgctcaga 1278

<210> 49
<211> 1317
<212> DNA
<213> Artificial Sequence

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

<400> 49
ctgcctgccc aggtcgcttt tacaccatat gcacctgagc ctggttccac gtgtaggctt 60

agggagtact acgatcaaac cgctcagatg tgttgctcca agtgtagtcc aggccagcac 120

gcaaaagtct tttgtacaaa gacgtcagat accgtgtgcg acagctgcga agatagcacc 180

tatacccagc tgtggaattg ggttcccgaa tgtttgtctt gtggctcccg ctgctctagt 240

gaccaggtgg aaacacaggc ctgcactcgg gaacagaacc gtatttgtac ctgcaggccc 300

ggttggtact gcgcactgtc caaacaagag gggtgtagac tgtgtgcccc tttgcgcaag 360

tgtcgtccag gcttcggtgt ggcaagacct ggaacagaga cttcagacgt cgtttgtaag 420

ccctgcgccc ctggcacatt ctccaatacc acctcatcta ccgacatatg cagaccccac 480

caaatatgca acgtggtggc tatccctggg aacgcctcca tggacgctgt ttgcacttcc 540

acttctccca ctcggtctat ggctcccggt gccgtgcatt taccccaacc cgtgagcact 600

cggagccaac acacacagcc aacacccgag ccaagtaccg ccccgagtac cagcttccta 660

ctccccatgg gcccatctcc accggctgag ggatctaccg gggattttgc tctgcctgtc 720

gggctaatcg tcggggtgac ggcgctcgga ttgctcatta tcggagtggt aaactgcgtg 780

attatgactc aggtgaaaaa gaagccttta tgcctccaga gagaagcgaa agttccccac 840

ctgcctgcag acaaggccag gggtacacag ggcccggaac agcaacatct gctgatcacc 900

gccccctctt caagctccag cagcctggaa tccagtgcca gtgcacttga tcggcgcgca 960

ccaacgcgaa accagcccca ggcccctggg gtagaggcat caggcgctgg agaagcgcgc 1020

gctagcacag gcagttccga ttccagccct ggagggcatg gaacacaggt aaatgtcacc 1080

tgcatcgtta atgtgtgctc gtcctcggac cacagctctc aatgttcaag ccaggcctca 1140

agcactatgg gcgacactga tagctctccc tccgagtcac cgaaggacga gcaggtccca 1200

tttagtaaag aggagtgtgc cttccgaagt cagctggaga caccagaaac cctgcttggg 1260

tctactgaag agaaaccact ccctcttggc gtgccagatg cgggaatgaa gccgtcg 1317

<210> 50
<211> 1656
<212> DNA
<213> Artificial Sequence

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

<400> 50
ctcgaggccg ataagtgcaa agaaagagag gaaaaaatca ttctggtttc tagcgccaac 60

gaaatcgatg tccgcccctg tccactgaat cctaacgagc ataaggggac tataacatgg 120

tataaggacg acagcaagac ccctgtgtct acagaacaag caagcaggat acaccagcac 180

aaagaaaagc tttggtttgt accagcaaag gtcgaggaca gcgggcatta ttattgcgtg 240

gtacgaaaca gttcttactg cctcagaatc aagatttccg ctaagtttgt cgagaacgaa 300

cctaacttat gttacaacgc acaggctatt tttaaacaga agctcccagt tgctggggat 360

ggcggcctgg tgtgtcccta catggagttt tttaaaaatg agaataatga gctacctaaa 420

ctgcaatggt acaaggactg caaacccctt ttgctcgaca atattcactt cagcggagtg 480

aaagatcggc tgattgtgat gaacgtggct gagaaacacc gcgggaacta tacatgccac 540

gcctcttata cgtacctggg caagcagtac ccgatcacta gagtgattga atttataaca 600

ctggaagaga acaagccaac tcgtcctgtc atagtatccc ccgcaaacga aaccatggag 660

gtggacttgg gttctcagat ccagctgatt tgcaatgtta ccgggcaatt gagtgatatc 720

gcctattgga agtggaatgg ttctgtcatt gacgaagacg atccagtgtt aggagaggac 780

tattatagcg tagaaaatcc tgcgaacaag aggcggtcga ctctgataac tgtcctgaac 840

atcagtgaga tcgagagccg attttataaa catccattca catgtttcgc caaaaataca 900

cacgggatcg acgccgccta cattcagctg atctaccccg taaccaattt ccagaagcac 960

atgatcggga tatgcgtgac gctaaccgtg atcattgttt gctcagtgtt catttacaag 1020

atcttcaaga tcgacatcgt cctttggtat agggatagct gttacgactt tctgcccatt 1080

aaggcatcgg atggcaaaac ctacgacgct tacatcttgt acccaaagac cgtgggagaa 1140

ggctcaacct ccgactgtga cattttcgtc tttaaggtgc tccctgaggt cctcgagaaa 1200

cagtgtggct ataaactgtt catctatggc cgggatgact acgtgggcga ggatatagtt 1260

gaagtcataa atgaaaatgt taagaaatca cggaggctga tcatcattct agtgcgggag 1320

acctcaggtt tttcctggct cggcggctcc tcagaggagc agattgcgat gtacaacgct 1380

ctggtgcaag atggaatcaa ggtggttctg ttggagctcg aaaagatcca ggattacgag 1440

aaaatgcccg agagcattaa gttcatcaaa caaaaacacg gagccattag atggagtggt 1500

gatttcacgc aaggaccgca gtccgccaag acacgtttct ggaaaaacgt gcgctatcat 1560

atgcccgtgc agaggagatc cccctccagt aaacatcagc tgttatctcc ggcgactaag 1620

gaaaagcttc agcgcgaagc ccatgttcct cttgga 1656

<210> 51
<211> 1650
<212> DNA
<213> Artificial Sequence

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

<400> 51
tccgagcggt gcgatgattg gggcttagat accatgcggc agattcaggt gttcgaagac 60

gagcctgctc gcattaaatg cccgctcttt gagcacttcc tgaagtttaa ttacagcact 120

gctcactccg caggactcac actgatctgg tattggacac gccaagacag agatctggag 180

gagcccatta attttaggct ccccgagaac aggatctcta aggagaagga cgtgctgtgg 240

tttcggccga cactactgaa cgatactggg aattacacat gtatgcttcg aaatactacc 300

tattgctcca aggtggcttt tccacttgag gtggtgcaga aagacagctg ttttaatagc 360

ccaatgaaac tgcccgtgca caagctgtac atcgaatatg gcatacagag aatcacatgc 420

cctaacgtcg acggctactt ccctagctca gttaagccga ccataacttg gtatatgggc 480

tgctataaaa tacagaactt caataatgta atccccgagg gtatgaactt gagtttcctg 540

atcgcactga tatctaacaa cgggaactac acctgtgtgg tgacttatcc cgagaacgga 600

cgcacattcc atttgacaag gacgttaact gtcaaggtag tgggtagtcc taagaatgca 660

gttcctcccg tgattcacag ccctaatgat cacgtggtgt atgaaaaaga accaggtgaa 720

gaactcctga tcccctgcac ggtgtacttc tctttttaa tggactcccg taatgaagtt 780

tggtggacca tcgacggcaa aaaacctgat gatattacca tcgacgtgac aatcaacgag 840

agcatttcac atagtcggac cgaagatgag acaagaaccc agattcttag cataaaaaaa 900

gtgacttctg aagacctgaa gcgcagttac gtatgtcacg cgcgatccgc aaaaggggaa 960

gttgccaagg ctgccaaggt gaagcagaaa gtccctgccc cacggtacac cgtagagctg 1020

gcctgtggct tcggagctac ggttttgctg gttgttatcc ttatcgtcgt ctatcatgtg 1080

tactggttgg agatggtgct tttttatcgg gcccatttcg ggaccgatga gacgattcta 1140

gacggaaagg agtacgatat ttacgtctcg tacgccagaa atgcggagga agaggaattc 1200

gtgctcttaa ccctgagggg agtactggaa aacgagtttg gctacaagtt gtgtattttt 1260

gacagagatt cactgccagg aggaattgtc actgacgaga cactctcatt catccagaaa 1320

tctaggaggt tgctcgttgt cctgagtcca aattatgtgc tccaaggcac ccaggccttg 1380

ctagaactga aggcggggct tgaaaacatg gcctctcgcg ggaacatcaa cgtaattctg 1440

gtgcagtaca aagcagtgaa ggagaccaaa gttaaagagc tgaaacgagc caagacagtc 1500

ctcactgtca tcaagtggaa aggtgaaaaa tcaaagtatc cacaagggag attctggaag 1560

cagcttcaag tcgctatgcc cgtgaagaag tccccccgtc gttcctcctc ggacgagcag 1620

ggcctgagct acagctctct caagaatgtc 1650

<210> 52
<211> 1347
<212> DNA
<213> Artificial Sequence

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

<400> 52
cttgcaccaa gacgctgtcc ggctcaggag gtcgctaggg gagtgctgac ctcgctgccg 60

ggcgactccg tgaccctgac atgtcctgga gtggagcctg aggacaacgc aacagttcac 120

tgggtgctac ggaagcccgc cgctggctcc catccttcca ggtgggccgg gatggggcgc 180

agactgcttc tcagatcagt gcagttacat gatagcggta attacagctg ctaccgcgct 240

ggaaggccgg caggcactgt gcacctccta gtggatgttc cacctgagga gccacagttg 300

agctgctttc gaaaaagtcc cttgtctaac gtcgtatgcg agtggggccc tagatcaact 360

ccctccctca ccaccaaagc ggttctcctc gtacgtaagt tccaaaactc tcctgccgaa 420

gattttcaag agccatgtca gtatagccag gagagtcaga agttctcatg ccagcttgca 480

gtcccggagg gtgactcatc cttctatatt gttagtatgt gcgtcgcctc gtctgtgggg 540

tctaagttta gcaagactca aacttttcag ggctgcggca tcctccaacc agacccccct 600

gccaacatta cagtgaccgc agttgccaga aaccctaggt ggttgagcgt gacgtggcag 660

gatccccatt cctggaattc atcattctac agactgcggt tcgagctccg atacagggcg 720

gaacgtagca agacattcac cacgtggatg gtcaaagacc tgcagcacca ctgtgtaatc 780

catgacgctt ggagcggtct gcgccacgtg gtccagctgc gggcacaaga ggaattcgga 840

cagggtgaat ggagtgaatg gtctcctgag gctatgggca ctccgtggac cgaatctcgg 900

tctccaccag ccgaaaacga agtgtccacc cctatgcagg ctctgactac taataaggat 960

gacgataata tcttgtttag ggactccgca aatgctacat cactgcctgt acaggattcc 1020

agtagtgttc ccctaccaac ctttttagtc gccggagggt ctctggcgtt cgggacgttg 1080

ctctgtatag ccattgtgct gcgtttcaaa aagacctgga aactgcgcgc cttaaaggag 1140

ggaaaaacaa gcatgcaccc cccatattct cttgggcagc tggtgcccga acggcccaga 1200

ccaacaccag tcctggtgcc tcttatatcc ccccccgtga gcccctctag cctgggcagt 1260

gacaatacca gtagccataa taggcccgac gcccgagacc ctcgctcccc atacgatatc 1320

tcaaacacag attatttttt tccccgg 1347

<210> 53
<211> 2688
<212> DNA
<213> Artificial Sequence

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

<400> 53
gaactcctgg acccctgcgg gtatattagc cccgagtctc ccgtggtgca actgcattct 60

aacttcaccg cagtttgtgt gctcaaagaa aagtgtatgg attacttcca tgttaacgcc 120

aactacattg tgtggaaaac taatcatttt acgataccaa aggagcagta cacaattatc 180

aacagaaccg catcatccgt cacatttacc gatatcgcct ccttgaacat tcagctgaca 240

tgtaatatct taacattcgg tcaactggaa caaaacgtgt atggcatcac catcatctct 300

ggacttcctc cagaaaaacc caaaaatttg tcgtgtatcg tgaatgaggg aaaaaaaatg 360

cgctgtgaat gggacggggg ccgggagact cacctcgaga cgaacttcac ccttaagtca 420

gagtgggcga cacataaatt tgccgactgc aaagcaaaga gagatacccc cacttcctgc 480

accgtcgact attcaactgt gtacttcgtc aacattgagg tgtgggtgga ggcggagaat 540

gcccttggca aggttacttc cgaccacatc aactttgatc ccgtctacaa ggtgaaaccg 600

aacccacccc acaacctgtc cgtcattaat tcagaggagc taagttctat actcaagtta 660

acttggacga atccctccat aaagagtgta attattctca agtataacat ccaatatagg 720

actaaagatg cttcaacctg gtcacagatc ccaccggagg acaccgcctc tacaaggtca 780

tcgttcaccg tgcaggatct taagcctttc accgagtatg tgttcagaat ccgatgcatg 840

aaagaggacg gcaaggggta ttggagcgat tggagcgaag aagcttccgg cattacctac 900

gaggacaggc cttcgaaagc accttctttc tggtacaaaa tcgatccttc tcacactcag 960

ggctaccgga ccgtgcagct tgtgtggaag actttgccac cattcgaggc aaatggaaag 1020

atactggatt atgaggtcac actgacccgc tggaaaagtc acttgcagaa ctatacagta 1080

aacgccacca aactgacagt caatctcact aacgatagat atttagcaac cctgactgta 1140

cgaaacctgg tgggaaaatc tgacgccgcg gtactgacta tccctgcttg tgactttcag 1200

gctacccacc ctgttatgga tctgaaggcc ttccctaagg ataacatgct atgggtcgag 1260

tggaccacac caagggaaag cgtcaaaaag tatattctcg agtggtgcgt tctgagcgac 1320

aaggccccat gtattacaga ctggcaacag gaggacggga cagttcatcg gacatatctg 1380

cgcggcaatc tagctgaaag taaatgctac cttatcaccg tcacgccagt ctacgccgac 1440

ggcccgggct ctccagagtc aatcaaggct tacctaaagc aggcccctcc ctctaagggg 1500

ccaactgtga gaacaaaaaa ggtaggtaag aatgaagccg tcctggagtg ggatcaactg 1560

ccagtggacg tacagaacgg tttcattcgc aactacacca tcttttacag gacgatcatt 1620

gggaatgaga cagcagtgaa cgtggattct tcccataccg aatacacgct cagcagtctg 1680

acgtcggaca cattgtacat ggtcaggatg gctgcatata cagacgaagg agggaaggat 1740

gggcctgagt tcacctttac cacccctaag ttcgctcagg gcgagattga agcaattgtg 1800

gtgcccgtat gcctggcctt tctccttacg acactgctgg gtgttctctt ttgctttaat 1860

aagcgggacc tcatcaagaa acacatttgg cctaatgtgc ccgaccccag caaaagtcac 1920

atagcccagt ggagccctca tactcccccc cgtcataatt ttaatagcaa ggatcagatg 1980

tacagcgacg gcaattttac agacgtgtcc gtcgtcgaaa tagaagctaa tgataagaag 2040

ccctttcctg aagacctgaa atccttggac ttattcaaaa aggagaagat caataccgaa 2100

gggcactcct cagggatagg gggcagcagt tgcatgtcct catcccgtcc ctctatcagc 2160

tccagcgatg agaacgagag cagccagaat actagttcca ctgttcagta cagcactgta 2220

gttcacagtg gctatagaca tcaggtcccg agtgttcagg tgttctccag gagtgaatct 2280

acccagccgt tgttagactc agaagaacgc ccagaagacc tgcagctggt ggaccacgtg 2340

gatggaggtg atggcattct gccgcgccag caatacttta agcagaactg ttctcagcat 2400

gaatccagcc ctgacatctc tcactttgag cgaagcaaac aggtgtcaag cgtgaacgaa 2460

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ggacaaatga agatgtttca ggaggttagt gcggccgatg ctttcggccc tggcactgag 2580

ggtcaggtgg aaagattcga gacagtgggt atggaagccg ctacagatga gggaatgccc 2640

aaaagctacc tcccacaaac cgtgcggcag ggaggatata tgccacag 2688

<210> 54
<211> 1917
<212> DNA
<213> Artificial Sequence

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

<400> 54
tgcagaacta gcgaatgttg tttccaggac cccccgtatc ccgacgccga ttccggaagc 60

gcatccggac cacgtgacct gcggtgctat cggatttcta gcgataggta cgaatgctca 120

tggcagtacg aggggcccac tgctggggtg agtcacttct taagatgctg tttaagttcc 180

gggaggtgct gctatttcgc cgcagggtca gctactcgac tacagttttc tgaccaggct 240

ggagtaagcg tgctttatac agtgacactg tgggtcgaat cctgggccag gaaccaaacg 300

gagaagtcac ccgaggtgac cctgcaactg tataactcag tcaaatacga gcctcctctg 360

ggtgacatta aagtgtcgaa actcgccgga cagcttagaa tggagtggga gacccccgat 420

aaccaggttg gcgcagaggt gcagttccgg caccgaacac cctcatctcc ttggaaactg 480

ggcgattgtg gtccgcagga cgacgatacc gagagttgct tgtgtcccct agagatgaat 540

gtcgcacagg agtttcagct gaggaggcgt cagctcggca gccaaggcag ttcttggtca 600

aaatggtcct cccccgtctg cgttccccct gaaaatcctc cacagccgca ggttcgattc 660

agcgtggaac aactcgggca ggacgggaga cgccgcttga ctcttaagga gcaaccaacg 720

cagctcgaac tcccagaagg ttgccagggc ctggcacctg gcaccgaggt gacctaccgt 780

ttgcagttac atatgcttag ttgcccttgt aaggccaagg ctacacggac ccttcaccta 840

ggcaaaatgc catacctaag cggtgctgca tacaacgtgg cggtcatttc ttccaaccag 900

ttcggacccg gtctgaatca gacctggcac atccccgcag atacccatac cgaacctgtg 960

gcgctgaata tcagcgtggg cacaaatggc actacgatgt attggccggc ccgcgctcaa 1020

tctatgactt actgcatcga atggcagcct gttgggcaag atggaggact cgcgacatgc 1080

agccttactg ccccgcagga ccctgatcca gcaggtatgg ccacttattc ttggagccgc 1140

gagtccgggg ccatgggaca ggagaagtgt tactacatca ccatatttgc gtcagctcat 1200

ccagaaaagc tgaccctgtg gtcaaccgtt ctgagcacat accacttcgg gggcaatgcg 1260

tccgctgcag gcaccccaca ccacgtgtcg gtgaaaaacc actctctgga cagtgtgagt 1320

gttgactggg ccccaagcct gttgtccaca tgtcccgggg tgctcaagga atatgttgtc 1380

cgctgtcgag acgaggactc caaacaagtg tcggaacatc ccgtacagcc aacggagacc 1440

caagtcactc tgtctggact gagagccggc gtggcctaca cagtccaagt gcgggcagat 1500

acagcttggt tacggggcgt atggagccag ccacaaaggt tcagcattga ggtacaggtc 1560

tctgattggt tgatttttt tgccagtctg ggcagttttc tctctatcct gttggtcgga 1620

gtgttgggct atctgggact gaatcgcgcc gccagacatc tgtgcccccc actcccaacc 1680

ccatgtgcct cctccgccat agaatttcct gggggtaaag agacatggca gtggatcaac 1740

cctgtagact tccaggagga ggctagcctc caggaagccc tggttgtgga aatgtcatgg 1800

gataagggcg agagaacgga acctctcgag aagactgaac ttcccgaggg agctcctgag 1860

ctcgcacttg acacagaact gtctttagag gatggggata ggtgtaaggc taagatg 1917

<210> 55
<211> 2517
<212> DNA
<213> Artificial Sequence

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

<400> 55
aaaattgatg cgtgcaaacg cggcgatgtg accgtgaaac cgagccatgt gattctgctg 60

ggcagcaccg tgaacattac ctgcagcctg aaaccgcgcc agggctgctt tcattatagc 120

cgccgcaaca aactgattct gtataaattt gatcgccgca ttaactttca tcatggccat 180

agcctgaaca gccaggtgac cggcctgccg ctgggcacca ccctgtttgt gtgcaaactg 240

gcgtgcatta acagcgatga attcagatt tgcggcgcgg aaatttttgt gggcgtggcg 300

ccggaacagc cgcagaacct gagctgcatt cagaaaggcg aacagggcac cgtggcgtgc 360

acctgggaac gcggccgcga tacccatctg tataccgaat ataccctgca gctgagcggc 420

ccgaaaaacc tgacctggca gaaacagtgc aaagatattt attgcgatta tctggatttt 480

ggcattaacc tgaccccgga aagcccggaa agcaacttta ccgcgaaagt gaccgcggtg 540

aacagcctgg gcagcagcag cagcctgccg agcaccttta cctttctgga tattgtgcgc 600

ccgctgccgc cgtgggatat tcgcattaaa tttcagaaag cgagcgtgag ccgctgcacc 660

ctgtattggc gcgatgaagg cctggtgctg ctgaaccgcc tgcgctatcg cccgagcaac 720

agccgcctgt ggaacatggt gaacgtgacc aaagcgaaag gccgccatga tctgctggat 780

ctgaaaccgt ttaccgaata tgaatttcag attagcagca aactgcatct gtataaaggc 840

agctggagcg attggagcga aagcctgcgc gcgcagaccc cggaagaaga accgaccggc 900

atgctggatg tgtggtatat gaaacgccat attgattata gccgccagca gattagcctg 960

ttttggaaaa acctgagcgt gagcgaagcg cgcggcaaaa ttctgcatta tcaggtgacc 1020

ctgcaggaac tgaccggcgg caaagcgatg acccagaaca ttaccggcca taccagctgg 1080

accaccgtga ttccgcgcac cggcaactgg gcggtggcgg tgagcgcggc gaacagcaaa 1140

ggcagcagcc tgccgacccg cattaacatt atgaacctgt gcgaagcggg cctgctggcg 1200

ccgcgccagg tgagcgcgaa cagcgaaggc atggataaca ttctggtgac ctggcagccg 1260

ccgcgcaaag atccgagcgc ggtgcaggaa tatgtggtgg aatggcgcga actgcatccg 1320

ggcggcgata cccaggtgcc gctgaactgg ctgcgcagcc gcccgtataa cgtgagcgcg 1380

ctgattagcg aaaacattaa aagctatatt tgctatgaaa ttcgcgtgta tgcgctgagc 1440

ggcgatcagg gcggctgcag cagcattctg ggcaacagca aacataaagc gccgctgagc 1500

ggcccgcata ttaacgcgat taccgaagaa aaaggcagca ttctgattag ctggaacagc 1560

attccggtgc aggaacagat gggctgcctg ctgcattatc gcatttattg gaaagaacgc 1620

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cattattttc agcagaaagt gtttgtgctg ctggcggcgc tgcgcccgca gtggtgcagc 1920

cgcgaaattc cggatccggc gaacagcacc tgcgcgaaaa aatatccgat tgcggaagaa 1980

aaaacccagc tgccgctgga tcgcctgctg attgattggc cgaccccgga agatccggaa 2040

ccgctggtga ttagcgaagt gctgcatcag gtgaccccgg tgtttcgcca tccgccgtgc 2100

agcaactggc cgcagcgcga aaaaggcatt cagggccatc aggcgagcga aaaagatatg 2160

atgcatagcg cgagcagccc gccgccgccg cgcgcgctgc aggcggaaag ccgccagctg 2220

gtggatctgt ataaagtgct ggaaagccgc ggcagcgatc cgaaaccgga aaacccggcg 2280

tgcccgtgga ccgtgctgcc ggcgggcgat ctgccgaccc atgatggcta tctgccgagc 2340

aacattgatg atctgccgag ccatgaagcg ccgctggcgg atagcctgga agaactggaa 2400

ccgcagcata ttagcctgag cgtgtttccg agcagcagcc tgcatccgct gacctttagc 2460

tgcggcgata aactgaccct ggatcagctg aaaatgcgct gcgatagcct gatgctg 2517

<210> 56
<211> 2400
<212> DNA
<213> Artificial Sequence

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

<400> 56
atgaaagtgc tgcaggaacc gacctgcgtg agcgattata tgagcattag cacctgcgaa 60

tggaaaatga acggcccgac caactgcagc accgaactgc gcctgctgta tcagctggtg 120

tttctgctga gcgaagcgca tacctgcatt ccggaaaaca acggcggcgc gggctgcgtg 180

tgccatctgc tgatggatga tgtggtgagc gcggataact ataccctgga tctgtgggcg 240

ggccagcagc tgctgtggaa aggcagcttt aaaccgagcg aacatgtgaa accgcgcgcg 300

ccgggcaacc tgaccgtgca taccaacgtg agcgataccc tgctgctgac ctggagcaac 360

ccgtatccgc cggataacta tctgtataac catctgacct atgcggtgaa catttggagc 420

gaaaacgatc cggcggattt tcgcatttat aacgtgacct atctggaacc gagcctgcgc 480

attgcggcga gcaccctgaa aagcggcatt agctatcgcg cgcgcgtgcg cgcgtgggcg 540

cagtgctata acaccacctg gagcgaatgg agcccgagca ccaaatggca taacagctat 600

cgcgaaccgt ttgaacagca tctgctgctg ggcgtgagcg tgagctgcat tgtgattctg 660

gcggtgtgcc tgctgtgcta tgtgagcatt accaaaatta aaaaagaatg gtgggatcag 720

attccgaacc cggcgcgcag ccgcctggtg gcgattatta ttcaggatgc gcagggcagc 780

cagtgggaaa aacgcagccg cggccaggaa ccggcgaaat gcccgcattg gaaaaactgc 840

ctgaccaaac tgctgccgtg ctttctggaa cataacatga aacgcgatga agatccgcat 900

aaagcggcga aagaaatgcc gtttcagggc agcggcaaaa gcgcgtggtg cccggtggaa 960

attagcaaaa ccgtgctgtg gccggaaagc attagcgtgg tgcgctgcgt ggaactgttt 1020

gaagcgccgg tggaatgcga agaagaagaa gaagtggaag aagaaaaagg cagcttttgc 1080

gcgagcccgg aaagcagccg cgatgatttt caggaaggcc gcgaaggcat tgtggcgcgc 1140

ctgaccgaaa gcctgtttct ggatctgctg ggcgaagaaa acggcggctt ttgccagcag 1200

gatatgggcg aaagctgcct gctgccgccg agcggcagca ccagcgcgca tatgccgtgg 1260

gatgaatttc cgagcgcggg cccgaaagaa gcgccgccgt ggggcaaaga acagccgctg 1320

catctggaac cgagcccgcc ggcgagcccg acccagagcc cggataacct gacctgcacc 1380

gaaaccccgc tggtgattgc gggcaacccg gcgtatcgca gctttagcaa cagcctgagc 1440

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gcgccggtgc cggtgccgct gtttaccttt ggcctggatc gcgaaccgcc gcgcagcccg 1920

cagagcagcc atctgccgag cagcagcccg gaacatctgg gcctggaacc gggcgaaaaa 1980

gtggaagata tgccgaaacc gccgctgccg caggaacagg cgaccgatcc gctggtggat 2040

agcctgggca gcggcattgt gtatagcgcg ctgacctgcc atctgtgcgg ccatctgaaa 2100

cagtgccatg gccaggaaga tggcggccag accccggtga tggcgagccc gtgctgcggc 2160

tgctgctgcg gcgatcgcag cagcccgccg accaccccgc tgcgcgcgcc ggatccgagc 2220

ccgggcggcg tgccgctgga agcgagcctg tgcccggcga gcctggcgcc gagcggcatt 2280

agcgaaaaaa gcaaaagcag cagcagcttt catccggcgc cgggcaacgc gcagagcagc 2340

agccagaccc cgaaaattgt gaactttgtg agcgtgggcc cgacctatat gcgcgtgagc 2400

<210> 57
<211> 1041
<212> DNA
<213> Artificial Sequence

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

<400> 57
ctgaacacaa caattctcac ccctaacggc aacgaagaca ctaccgcaga ttttttcctc 60

actactatgc ccactgattc cctttccgtg tcgaccttgc cgctgccaga agtgcagtgc 120

ttcgtcttta atgttgagta tatgaattgt acatggaatt ctagcagcga accgcagcca 180

accaatttga cattgcacta ctggtataaa aactcagata acgacaaagt gcagaagtgt 240

tcccactact tatttagcga ggaaataacc tctgggtgcc agctgcagaa gaaggagatc 300

catctgtacc agaccttcgt cgtgcagctc caggatccac gggaaccacg ccggcaagct 360

acccaaatgc taaagctgca aaatctcgtt atcccatggg cacctgagaa tttgacactt 420

cataagctgt cggaatccca gctggagctc aattggaaca accgtttcct caaccattgt 480

ctggagcacc tggtgcagta cagaaccgac tgggaccata gttggacgga gcagagtgtc 540

gattatagac acaaattctc actaccctca gtggacgggc agaagaggta cacatttaga 600

gtaaggagtc ggttcaatcc cctgtgcggg tccgcccaac actggagtga gtggtctcat 660

cctattcact ggggcagcaa cacgtccaag gagaaccctt tcttgtttgc tctggaagct 720

gttgtgattt cagtaggctc tatgggatta atcatcagcc tcctgtgtgt ctatttttgg 780

ctggagcgaa caatgcccag gatccccact ctcaaaaatc tggaagacct tgtgacggag 840

tatcacggca acttcagcgc gtggtctggc gtctctaaag gtcttgccga gagcctgcag 900

cctgattaca gtgagcgctt atgcctggtg agcgagatac cacctaaagg aggagccctt 960

ggtgaaggac cgggggcatc cccctgtaat caacactcac catactgggc ccccccctgc 1020

tataccctaa agcctgaaac t 1041

<210> 58
<211> 1218
<212> DNA
<213> Artificial Sequence

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

<400> 58
ggcggcggcg gcgcggcgcc gaccgaaacc cagccgccgg tgaccaacct gagcgtgagc 60

gtggaaaacc tgtgcaccgt gatttggacc tggaacccgc cggaaggcgc gagcagcaac 120

tgcagcctgt ggtattttag ccattttggc gataaacagg ataaaaaaat tgcgccggaa 180

acccgccgca gcattgaagt gccgctgaac gaacgcattt gcctgcaggt gggcagccag 240

tgcagcacca acgaaagcga aaaaccgagc attctggtgg aaaaatgcat tagcccgccg 300

gaaggcgatc cggaaagcgc ggtgaccgaa ctgcagtgca tttggcataa cctgagctat 360

atgaaatgca gctggctgcc gggccgcaac accagcccgg ataccaacta taccctgtat 420

tattggcatc gcagcctgga aaaaattcat cagtgcgaaa acatttttcg cgaaggccag 480

tattttggct gcagctttga tctgaccaaa gtgaaagata gcagctttga acagcatagc 540

gtgcagatta tggtgaaaga taacgcgggc aaaattaaac cgagctttaa cattgtgccg 600

ctgaccagcc gcgtgaaacc ggatccgccg catattaaaa acctgagctt tcataacgat 660

gatctgtatg tgcagtggga aaacccgcag aactttatta gccgctgcct gttttatgaa 720

gtggaagtga acaacagcca gaccgaaacc cataacgtgt tttatgtgca ggaagcgaaa 780

tgcgaaaacc cggaatttga acgcaacgtg gaaaacacca gctgctttat ggtgccgggc 840

gtgctgccgg ataccctgaa caccgtgcgc attcgcgtga aaaccaacaa actgtgctat 900

gaagatgata aactgtggag caactggagc caggaaatga gcattggcaa aaaacgcaac 960

agcaccctgt atattaccat gctgctgatt gtgccggtga ttgtggcggg cgcgattatt 1020

gtgctgctgc tgtatctgaa acgcctgaaa attattattt ttccgccgat tccggatccg 1080

ggcaaaattt ttaaagaaat gtttggcgat cagaacgatg ataccctgca ttggaaaaaa 1140

tatgatattt atgaaaaaca gaccaaagaa gaaaccgata gcgtggtgct gattgaaaac 1200

ctgaaaaaag cgagccag 1218

<210> 59
<211> 1671
<212> DNA
<213> Artificial Sequence

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

<400> 59
catgggaccg agctccccag tcctccttct gtttggttcg aagccgaatt ctttcaccat 60

attctgcact ggactcctat cccaaatcaa tcagaatcaa catgttacga ggtggcactg 120

ctgaggtacg gaatcgagtc ttggaatagc atttcaaact gtagccaaac cctgtcttac 180

gatcttaccg ctgtgacgct ggacctgtat catagcaacg gctaccgtgc cagggttagg 240

gcagttgatg gcagcagaca ctccaattgg acagttacga atacccgatt cagtgtcgac 300

gaggtgactt taactgtcgg gagtgttaac cttgaaattc acaacgggtt catattggga 360

aagatccagc tcccccggcc aaaaatggcc ccagccaacg acacatacga gagtatattt 420

tctcatttta gagagtatga gatcgcaatc cgcaaggtgc ctgggaattt cacatttact 480

cataagaagg taaaacacga gaacttctcc ttgctcacct ccggcgaagt gggggagttc 540

tgcgtgcagg tgaagccctc ggtggcttca cgctccaata aaggcatgtg gagcaaagaa 600

gaatgtattt ctctgactcg gcagtacttt accgtgacta acgtaatcat atttttgcc 660

ttcgtgctcc tgctgtctgg tgccctggcc tattgcctgg cgcttcaact ttatgtgcgg 720

aggaggaaga agctgccgtc cgtgctgttg tttaagaaac cgtctccctt cattttatc 780

agccagcgcc cctcacccga aacacaggat actattcacc cccttgacga agaagccttc 840

cttaaagtgt cccccgagct aaaaaacctc gacctgcacg ggtccaccga tagcgggttt 900

ggtagcacca aaccatcctt gcaaaccgag gagccccagt tcttgctccc tgatccacac 960

ccacaggctg acagaacgtt gggaaacaga gagcccccag tcctgggggа ttcctgttcg 1020

tcagggtcta gtaatagtac cgatagcggg atttgcctgc aggagccgag cctgtcaccc 1080

tcaaccggtc cgacctggga gcagcaagta ggatctaact cccgcgggca ggatgactcc 1140

ggcatagacc tcgtacagaa ttcggaaggc cgggcgggtg acacacaggg cggctccgct 1200

ctgggccacc attccccacc agagcccgag gtccctggcg aggaggaccc tgcagccgtc 1260

gcttttcaag gctatctgcg tcagacacga tgtgctgaag agaaagctac taagacggga 1320

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gtggatgagg cgggactaca tcctcccgca ttagcaaagg gctacctgaa gcaggatcca 1440

ctagaaatga cactggcctc atctggcgcc cctacaggac agtggaacca gccaaccgaa 1500

gagtggtcct tgctcgcttt aagctcttgc agtgacctgg gtatctcaga ttggagtttt 1560

gcacacgacc tcgcccctct gggttgcgtc gccgctcctg gtggactctt aggaagtttc 1620

aatagcgatc tcgtcactct gcctctcatc agtagcttac agagcagcga a 1671

<210> 60
<211> 918
<212> DNA
<213> Artificial Sequence

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

<400> 60
atggtaccac cacctgaaaa tgtgaggatg aactctgtga attttaagaa cattctccag 60

tgggaaagtc ccgcttttgc taaggggaac ctgaccttca cagcccaata cttatcctac 120

cgaatcttcc aagacaagtg catgaatacc actttaactg aatgcgactt ctcaagcctg 180

tctaagtatg gcgatcatac actgcgggtt cgtgccgagt ttgccgacga gcactctgac 240

tgggtgaata taaccttctg ccccgtcgat gatactataa ttgggccacc aggtatgcaa 300

gttgaagtgt tggcagattc gctgcacatg aggtttctcg cccccaaaat cgagaacgag 360

tacgagacct ggacgatgaa gaatgtctac aactcttgga catataatgt tcagtattgg 420

aaaaacggaa ccgacgagaa gtttcagatc actccgcagt atgatttcga agtcctgaga 480

aacctcgagc cttggacaac ttactgtgtc caagtgcgcg gctttctccc tgaccggaac 540

aaggcaggag agtggtcaga accggtgtgt gagcagacca cccacgacga gacagtaccc 600

agctggatgg tagctgtgat ccttatggcc tccgtgttca tggtttgtct agctttgttg 660

ggctgttttg cccttctatg gtgcgtctat aaaaagacca aatacgcgtt ttcacctaga 720

aacagccttc cacagcacct caaggagttc ctggggcatc ctcatcacaa tacactgctg 780

ttcttctcct tccccctgag tgacgaaaac gatgtgtttg ataaactgtc cgtgattgca 840

gaagacagtg agtccggcaa acagaatcca ggagatagtt gcagcctggg tacgcctccc 900

ggacagggcc cccagagc 918

<210> 61
<211> 1569
<212> DNA

<213> Artificial Sequence

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

<400> 61
gccgagagct gcactagccg gccccatata actgtggtcg aaggggagcc attctatctg 60

aaacattgtt cctgctccct tgcccatgaa attgaaacca caaccaagag ctggtacaaa 120

tctagtgggt ctcaagagca cgtcgagttg aacccaagat catctagtag gatcgccctg 180

catgactgcg ttctagagtt ttggccggtg gaattaaatg acaccggatc ttacttcttc 240

cagatgaaga attacaccca gaaatggaag ctgaacgtga tacgacgcaa caagcactca 300

tgcttcacag aacgtcaggt gacctcgaaa atcgtggaag tgaaaaagtt ctttcagatt 360

acatgcgaga acagttacta tcaaacgcta gtgaatagca cgagcctgta caaaaactgt 420

aagaaacttc tgctggagaa caataaaaac cctactatca aaaaaaatgc agaattcgag 480

gatcagggct attacagttg tgtgcatttt ctccaccaca atggtaagct attcaatatc 540

accaagacgt tcaacatcac cattgtggag gatcgctcca acatagtacc tgtgttattg 600

ggtcctaaac ttaaccacgt ggcagtggag ctggggaaaa acgtgagact caattgctca 660

gccttgctga acgaagagga tgttatttat tggatgtttg gggaagaaaa tggaagtgac 720

ccgaacattc acgaagagaa ggagatgcga atcatgacac cagaggggaa atggcacgcg 780

agtaaggtcc tcagaattga aaatattggc gaatcaaatc tcaacgtcct ctataactgt 840

accgtagcat ccacaggcgg cactgatact aagtccttta tccttgtgcg taaggccgat 900

atggctgaca tccccggcca cgtattcaca cggggaatga tcattgctgt tctgatcctg 960

gtggcagtag tgtgtttggt tactgtatgt gttatctacc gcgtggactt agttctgttt 1020

tataggcacc tgacccgaag agacgaaacc cttacagatg gcaagactta tgacgcgttc 1080

gtgtcgtatc ttaaagaatg ccggcccgag aatggagagg agcacacgtt tgctgtcgaa 1140

attctcccca gagtcctgga gaagcatttt ggttacaagc tgtgcatctt cgaaagagac 1200

gtcgtgcccg gtggcgccgt ggtcgacgag atacattccc tgatcgagaa gtcccgcagg 1260

ttgatcatag tcctctcaaa gtcttacatg agcaatgagg tgcggtacga actcgagagc 1320

ggactgcatg aggctttagt cgagaggaag attaagatta ttttgatcga gtttacacct 1380

gtgactgact ttaccttcct ccctcagtca ctgaaactcc ttaagtctca cagggtactg 1440

aagtggaaag ctgataaatc cctctcttat aatagccggt tttggaagaa cctattgtac 1500

ctgatgccag ccaaaacagt caagcctgga cgcgatgagc ccgaagttct gccagttctg 1560

agcgagtcc 1569

<210> 62
<211> 1740
<212> DNA
<213> Artificial Sequence

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

<400> 62
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gaagagttcg tgcttttctg cgatttacca gaaccacaga aatcccattt ttgtcacaga 120

aatcgtcttt ctcctaagca ggttcccgaa cacctgccct tcatgggctc caacgacctt 180

agtgacgttc aatggtacca gcaaccaagc aatggcgacc ctctggaaga catacgcaag 240

agttaccccc atattatcca ggataaatgc acgctacatt tcctgacccc aggcgtcaac 300

aacagtggat cttatatatg taggcctaag atgatcaaat ccccctacga cgtggcttgt 360

tgcgtcaaga tgattctcga ggtgaagccc cagaccaatg cctcatgtga gtactccgcc 420

tctcacaaac aggaccttct gctggggtcg accggcagta taagctgccc atcgctctct 480

tgtcagagtg atgcgcagag ccctgctgtg acatggtaca aaaacggaaa gctactgtca 540

gtggagcgct caaaccgtat tgtagtagac gaagtctacg actatcacca aggcacctac 600

gtgtgcgatt atacacagtc tgatacggtc tccagttgga ctgtgcgggc cgtggtgcag 660

gtacggacca tcgtgggggа cacaaaactg aagcccgaca tccttgatcc agttgaggac 720

accctggagg tggagctcgg gaagcccctg actatctcct gtaaagcaag atttggcttc 780

gagcgagtat ttaaccctgt tatcaagtgg tatattaaag atagcgatct cgagtgggag 840

gtatcagtgc ctgaagccaa atccatcaaa tcaactctga aggatgaaat cattgagcga 900

aatattattc ttgagaaggt tacccagcgc gatctccgcc gcaaatttgt ctgcttcgtg 960

caaaacagca taggcaatac tactcagagc gtgcagctga aagagaagcg tggtgtcgtc 1020

ttgttgtaca tcctgctcgg aacaattggt acactcgtag ccgtgttggc cgcctcagcc 1080

ctgctctaca ggcattggat tgaaatcgtg ttgctttaca ggacatatca gagcaaggac 1140

cagactctgg gcgacaaaaa ggatttcgat gcattcgtta gctatgctaa atggtcttca 1200

tttcctagcg aagctacatc ctccctgagc gaggaacact tagccttatc actgtttcca 1260

gatgtgttag aaaataaata tggctatagc ctgtgtttgc tggagcgcga cgttgcacca 1320

gggggggtgt atgctgaaga catcgtcagc atcatcaagc ggtccaggag gggaatattt 1380

atattaagcc ctaactacgt caacggtcca tcgattttcg aactgcaggc tgcagtgaac 1440

ttggcgctcg atgaccagac gctcaagctg attctcatca agttctgcta ctttcaagag 1500

cccgagtctc ttcctcacct agtcaagaag gcgctgagag tcctgccgac cgtgacatgg 1560

cgaggactaa agtctgtgcc gccgaattcc agattctggg caaagatgcg gtatcatatg 1620

cccgttaaaa attcccaagg ttttacttgg aaccagctgc ggattaccag tcggatcttc 1680

cagtggaagg ggctgtctag aaccgagacc accggaagat ccagtcaacc caaagaatgg 1740

<210> 63
<211> 262
<212> PRT
<213> Artificial Sequence

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

<400> 63
Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe Asn
1 5 10 15

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

Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln

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        35                  40                  45

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

Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val Lys
65                  70                  75                  80

Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp Phe Glu Lys Leu Thr
                85                  90                  95

Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg Lys Ala Ile His Glu
            100                 105                 110

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

Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser
    130                 135                 140

Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp
145                 150                 155                 160

Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe
                165                 170                 175

Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys
            180                 185                 190

Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser
        195                 200                 205

Asn Lys Lys Lys Arg Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val
    210                 215                 220

Thr Asp Leu Asn Val Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val
225                 230                 235                 240
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Met Ala Glu Leu Ser Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser
245 250 255

Gln Met Leu Phe Arg Gly
260

<210> 64
<211> 168
<212> PRT
<213> Artificial Sequence

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

<400> 64
Asn Tyr Pro Lys Lys Lys Met Glu Lys Arg Phe Val Phe Asn Lys Ile
1 5 10 15

Glu Ile Asn Asn Lys Leu Glu Phe Glu Ser Ala Gln Phe Pro Asn Trp
20 25 30

Tyr Ile Ser Thr Ser Gln Ala Glu Asn Met Pro Val Phe Leu Gly Gly
35 40 45

Thr Lys Gly Gly Gln Asp Ile Thr Asp Phe Thr Met Gln Phe Val Ser
50 55 60

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
65 70 75 80

Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg Asp Ser Gln Gln Lys
85 90 95

Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys Ala Leu His Leu Gln
100 105 110

Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser Met Ser Phe Val Gln
115 120 125

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

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

Gln Leu Glu Ser Val Asp Pro Lys
165

<210> 65
<211> 521
<212> PRT
<213> Artificial Sequence

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

<400> 65
Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr
1 5 10 15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu
20 25 30

Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val Leu Gly
35 40 45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu
65 70 75 80

Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
85 90 95

Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys
100 105 110

```
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr
        115                 120                 125

Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
    130                 135                 140

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

Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala
                165                 170                 175

Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala
            180                 185                 190

Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg
        195                 200                 205

Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu
    210                 215                 220

Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp
225                 230                 235                 240

Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln
                245                 250                 255

Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys Thr
            260                 265                 270

Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala
        275                 280                 285

Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro
    290                 295                 300

Cys Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
```

305 310 315 320

Ser Thr Lys Gly Arg Asn Leu Pro Val Ala Thr Pro Asp Pro Gly Met
325 330 335

Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn
340 345 350

Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr Ser
355 360 365

Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val
370 375 380

Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn
385 390 395 400

Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg
405 410 415

Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr Glu Asp
420 425 430

Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys Leu Leu
435 440 445

Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Ala Val
450 455 460

Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr Val Pro
465 470 475 480

Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys
485 490 495

Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp
500 505 510

Arg Val Met Ser Tyr Leu Asn Ala Ser
515 520

<210> 66
<211> 134
<212> PRT
<213> Artificial Sequence

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

<400> 66
Asn Thr Thr Glu Lys Glu Thr Phe Cys Arg Ala Ala Thr Val Leu Arg
1 5 10 15

Gln Phe Tyr Ser His His Glu Lys Asp Thr Arg Cys Leu Gly Ala Thr
20 25 30

Ala Gln Gln Phe His Arg His Lys Gln Leu Ile Arg Phe Leu Lys Arg
35 40 45

Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly Leu Asn Ser Cys Pro Val
50 55 60

Lys Glu Ala Asn Gln Ser Thr Leu Glu Asn Phe Leu Glu Arg Leu Lys
65 70 75 80

Thr Ile Met Arg Glu Lys Tyr Ser Lys Cys Ser Ser Gly Gly Asn Gly
85 90 95

Gly His Lys Cys Asp Ile Thr Leu Gln Glu Ile Ile Lys Thr Leu Asn
100 105 110

Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu Thr Val Thr Asp
115 120 125

Ile Phe Ala Ala Ser Lys
130

<210> 67
<211> 166
<212> PRT
<213> Artificial Sequence

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

<400> 67

```
Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
1               5                  10                  15

Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
            20                  25                  30

Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
        35                  40                  45

Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
    50                  55                  60

Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65                  70                  75                  80

Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu
                85                  90                  95

Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
            100                 105                 110

Pro Cys Glu Asn Gly Gly Gly Ser Gly Gly Lys Ser Lys Ala Val Glu
        115                 120                 125

Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys
    130                 135                 140

Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met
145                 150                 155                 160
```

Thr Met Lys Ile Arg Asn
165

<210> 68
<211> 175
<212> PRT
<213> Artificial Sequence

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

<400> 68
Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu
1 5 10 15

Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala
20 25 30

His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu
35 40 45

Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val
50 55 60

Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr
65 70 75 80

Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr
85 90 95

Met Thr Met Lys Ile Arg Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Ser Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn
115 120 125

Ser Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu
130 135 140

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

Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys
165 170 175

<210> 69
<211> 335
<212> PRT
<213> Artificial Sequence

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

<400> 69
Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
1 5 10 15

Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
20 25 30

Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
35 40 45

Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
50 55 60

Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65 70 75 80

Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu
85 90 95

Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
100 105 110

Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
115 120 125

```
Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
    130                 135                 140

Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
                165                 170                 175

Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly
            180                 185                 190

Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val
        195                 200                 205

Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys
    210                 215                 220

Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu
225                 230                 235                 240

Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu
                245                 250                 255

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

Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro
        275                 280                 285

Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn
    290                 295                 300

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

Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
```

325 330 335

<210> 70
<211> 127
<212> PRT
<213> Artificial Sequence

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

<400> 70
Val Ser Ala Gly Gln Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile
1 5 10 15

Glu Val Ala Gln Phe Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu
20 25 30

Phe Arg Glu Gly Arg Phe Asn Gly Gly Gly Gly Ser Leu Thr Cys Leu
35 40 45

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

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

Leu Cys Asn Gly Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met
85 90 95

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

Ile Glu Lys Thr Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys
115 120 125

<210> 71
<211> 786
<212> DNA
<213> Artificial Sequence

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

<400> 71
caggatccct acgtgaaaga agccgagaac ttaaagaaat atttcaacgc aggccattca 60

gacgtcgctg ataatggaac actttttttg ggcattctga aaaattggaa ggaagaatcg 120

gaccgaaaaa ttatgcagag ccagatagta tccttttatt tcaagttatt taaaaacttc 180

aaagacgatc agtctatcca aaaaagtgtg gagactatca aggaggacat gaatgtgaag 240

ttcttcaaca gcaataaaaa gaaacgggat gactttgaaa agctcaccaa ttactcagtc 300

actgatctga acgtgcagag aaaggcgatt catgagctaa tccaagtgat ggctgagctc 360

ggagccaacg tgagcggaga gtttgtgaag gaagccgaga atctgaagaa gtatttcaac 420

gctggtcact ctgacgtggc agataacggc acgctgttcc tggggatcct gaagaattgg 480

aaagaagagt ccgacaggaa gattatgcaa tcccagatcg tcagtttcta ctttaagctt 540

ttcaagaatt tcaaagacga tcagagtatc cagaagtctg tcgagaccat aaaagaagac 600

atgaatgtaa agtttttaa ttcaaacaaa aagaagcgtg acgatttcga aaaactcacc 660

aactactccg ttacagatct gaacgttcag agaaaagcca ttcacgagtt gatccaagtt 720

atggccgagc tctctcctgc agctaagaca ggtaagagga aacggagcca gatgctgttt 780

cgcggg 786

<210> 72
<211> 504
<212> DNA
<213> Artificial Sequence

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

<400> 72
aactacccca aaaaaaagat ggagaagcgg tttgttttta acaagattga gatcaacaat 60

aagctggaat tcgagtctgc gcagttccca aactggtata ttagcacatc gcaagcagaa 120

aatatgcccg tgttcctcgg cggaaccaaa ggcgggcagg atatcacaga ctttacgatg 180

cagttcgtgt catctggtgg tggtggaagc ggcgggggag gcagtggggg aggcgggtcc 240

gccccagtga ggtccctgaa ctgtacctta agagactcac agcaaaagtc cctggtcatg 300

tctggcccct acgaactgaa agcccttcac ctgcaggggc aagatatgga gcagcaggtg 360

gttttcagca tgagttttgt acagggcgaa gagagtaatg acaagatacc tgtggctcta 420

ggactcaagg aaaagaattt gtatctcagc tgcgtcctga aggacgataa acctactctt 480

cagttggagt ccgtcgatcc gaaa 504

<210> 73
<211> 1563
<212> DNA
<213> Artificial Sequence

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

<400> 73
atctgggagc tcaaaaagga tgtttatgtg gtcgaacttg actggtaccc ggacgcacca 60

ggggagatgg tggtgttgac ctgcgacacc cccgaagagg acgggattac atggactttg 120

gaccagtcca gtgaagtcct gggctcggga aagaccctga ctatccaggt gaaggagttc 180

ggagatgctg gacaatatac atgccacaag ggcggggaag ttttgagcca ttccctcctg 240

ctgctgcata aaaaagagga tggtatttgg agcactgata ttctgaaaga ccagaaggaa 300

cccaagaaca aaacttttct gcggtgtgag gccaagaatt acagtggaag attcacctgt 360

tggtggttaa ccacaatctc taccgatctt acctttttccg tcaaatcaag tcgcggcagc 420

agcgatccac agggcgtgac gtgcggcgct gccacactaa gcgcggagag agtgcggggt 480

gacaacaagg aatacgagta ctccgttgag tgtcaagaag actctgcatg ccctgccgca 540

gaggaatcat taccgatcga agtaatggtg gatgctgttc acaaactgaa gtatgaaaac 600

tacacttctt catttttcat aagggacatt atcaagcctg atcctccaaa gaacctccaa 660

cttaaaccac tcaagaatag ccgtcaggta gaggtgtcct gggagtaccc cgatacctgg 720

tcaacgcccc actcatattt ctccctgacg ttctgtgtgc aggtgcaggg gaaatccaag 780

agggagaaga aagacagggt ctttacagat aagacatctg ccactgtcat ctgcagaaaa 840

aatgcctcta tatccgtgcg agcccaggac cgctactatt ctagtagctg gagcgagtgg 900

gctagtgtac cttgttcggg ctcaaccagc ggatccggga aacccggttc tggcgagggg 960

agtacaaagg gacgaaatct gccagtggct acccccgacc cgggcatgtt tccctgcctc 1020

catcatagcc agaatctgct cagagcggtc agcaacatgc tacagaaggc ccgccagacc 1080

ttagagtttt acccttgcac ctctgaggaa atcgatcacg aagacatcac caaagataag 1140

actagcaccg ttgaagcctg tctcccattg gaacttacaa aaaatgaatc ttgtctgaat 1200

tccagagaga catcttttat cactaatgga agttgcctcg ccagtcggaa aacttccttc 1260

atgatggccc tgtgtctgag ttcaatctac gaggatctta agatgtatca agtggaattc 1320

aaaacgatga acgcaaaact gttgatggat cctaagaggc agatattttt ggatcagaac 1380

atgttagctg tgatcgacga gctgatgcaa gcactcaact tcaactcaga gacagtcccc 1440

cagaagtcct ccctggagga gcctgacttc tacaagacga aaattaagct atgcattctg 1500

cttcacgcat tcaggatacg ggccgtaaca attgaccgtg tgatgagcta tctgaacgct 1560

tcg 1563

<210> 74
<211> 402
<212> DNA
<213> Artificial Sequence

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

<400> 74
aatacgactg agaaagagac cttttgtagg gctgccacag tcctgcggca gttctatagt 60

caccatgaga aagacaccag atgtctgggg gcaaccgctc agcaattcca tagacacaag 120

cagttaatcc gatttctgaa gcggcttgat cgtaacttgt ggggactagc cggcctgaac 180

tcatgccccg tgaaagaagc gaatcagtcc actcttgaga acttcctcga aaggctcaag 240

acaattatgc gcgaaaagta cagcaagtgc agctctggcg gaaacggtgg gcacaagtgt 300

gatattacgc tccaagaaat catcaagact ctgaactccc tgaccgagca gaaaacactt 360

tgcactgagt tgacagtgac cgacatattc gccgctagca aa 402

<210> 75
<211> 498
<212> DNA
<213> Artificial Sequence

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

<400> 75
tcgcctggcc agggaacgca gagtgaaaat agctgtaccc actttcccgg caacctacca 60

aatatgctca gagatctgcg ggatgcattc tcccgggtga agacattttt ccaaatgaag 120

gatcagttgg acaaccttct gttgaaggag tcactcttag aggacttcaa gggatacctg 180

gggtgccaag ccctgtctga gatgattcag ttctacctcg aagaggtaat gccacaggcc 240

gaaaaccagg accctgatat aaaagctcat gtcaatagtt taggcgagaa tctgaaaact 300

ctcaggctgc gtctgcgaag atgccaccgc tttctgccct gtgagaacgg gggagggtct 360

ggtggcaaaa gcaaagctgt ggagcaagtt aaaaatgcat tcaacaaact tcaggagaag 420

ggtatttata aggcgatgtc cgaatttgac atctttatta attacatcga agcctatatg 480

accatgaaga tcaggaac 498

<210> 76
<211> 525
<212> DNA
<213> Artificial Sequence

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

<400> 76
ggttacttgg gctgtcaggc tctgagtgaa atgattcagt tctatcttga agaggttatg 60

cctcaggcgg agaaccaaga cccagacatc aaggcccatg tgaactctct cggggagaat 120

ctgaaaacac tgcgactgcg gttaagacgt tgccacaggt tcctaccctg cgaaaataaa 180

agcaaggccg tcgagcaagt gaaaaacgca ttcaataaac tccaggaaaa gggaatttac 240

aaggccatgt ccgagtttga tatctttata aactatattg aggcttacat gaccatgaag 300

atccgcaatg gtggtggtgg aagcggcggg ggaggcagtg ggggaggcgg gtcctcccct 360

ggccagggaa ctcagtcaga aaatagctgc acacactttc cagggaatct ccccaacatg 420

ttgagagatc tgagggacgc cttctctcgg gtgaaaacct ttttccaaat gaaagaccag 480

ctggacaacc tccttctgaa ggagagttta ctagaggatt tcaag 525

<210> 77
<211> 1005
<212> DNA
<213> Artificial Sequence

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

<400> 77
tctccgggac agggaaccca gagcgaaaac tcctgcactc attttcctgg caacctcccc 60

aatatgctgc gagacttgcg cgacgcattc tcaagggtga agacgttctt ccagatgaag 120

gatcaactgg acaacttatt gctgaaagaa tctctgctcg aggatttcaa aggatacctg 180

ggatgtcagg cactgagcga gatgatccaa ttttacctgg aggaggtcat gcctcaggct 240

gagaatcagg atcctgacat caaggcccac gtgaacagtc ttggagagaa tcttaagacc 300

cttaggctga gacttagacg gtgtcaccgc tttctgccct gcgaaaataa atcaaaagcg 360

gtggaacagg ttaagaacgc ttttaataag ctgcaggaaa agggcattta taaagctatg 420

agtgaatttg acattttcat taactatatc gaggcctata tgacaatgaa aattaggaac 480

gggggaggcg ggagcggggg cggcggctca ggcggtgggg ggtcctctcc aggtcaagga 540

acacaatctg agaactcctg cacacacttc cccggcaatc taccaaacat gctcagagat 600

ctcagggacg cgttcagtcg agtgaaaact ttcttccaga tgaaggatca gctggacaat 660

ctactgctga aagaaagctt gcttgaggat tttaaaggct atctgggttg tcaggcctta 720

tcggagatga tccagtttta cttggaggaa gttatgcctc aggcagaaaa ccaagacccc 780

gatatcaagg ctcatgtgaa ttccctcggt gaaaacctaa agaccttacg cctgcgtctc 840

agacggtgtc atcggttttt gccatgcgag aataagtcca aagccgtaga gcaggtcaag 900

aatgccttca ataagctcca ggagaagggg atatacaaag caatgagcga atttgacatt 960

ttcatcaact acatagaggc ctacatgacc atgaagatcc ggaac 1005

<210> 78
<211> 381
<212> DNA
<213> Artificial Sequence

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

<400> 78
gtgagcgcgg gccagtttag cagcctgcat gtgcgcgata ccaaaattga agtggcgcag 60

tttgtgaaag atctgctgct gcatctgaaa aaactgtttc gcgaaggccg ctttaacgga 120

ggaggtggat ctctgacctg cctgggcggc tttgcgagcc cgggcccggt gccgccgagc 180

accgcgctgc gcgaactgat tgaagaactg gtgaacatta cccagaacca gaaagcgccg 240

ctgtgcaacg gcagcatggt gtggagcatt aacctgaccg cgggcatgta ttgcgcggcg 300

ctggaaagcc tgattaacgt gagcggctgc agcgcgattg aaaaaaccca gcgcatgctg 360

agcggctttt gcccgcataa a 381

<210> 79
<211> 45
<212> DNA
<213> Artificial Sequence

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

<400> 79
ggtggtggtg gaagcggcgg gggaggcagt gggggaggcg ggtcc 45

<210> 80
<211> 54
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 80
ggctcaacca gcggatccgg gaaacccggt tctggcgagg ggagtacaaa ggga 54

<210> 81
<211> 78
<212> DNA
<213> Artificial Sequence

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

<400> 81
tctggaggcg gaagcggggg tggcggcagc ggcggtggag gatcaggtgg cgggggtcc 60

gggggcggaa gtctgcag 78

<210> 82
<211> 63
<212> DNA
<213> Artificial Sequence

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

<400> 82
atggccttgc ctgtgaccgc attactgctt ccactcgccc tgctcctgca cgctgcgaga 60

ccc 63

<210> 83
<211> 742
<212> PRT
<213> Artificial Sequence

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

<400> 83
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

```
His Ala Ala Arg Pro Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser
            20                  25                  30

Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Lys Ile Ser Leu Phe
        35                  40                  45

Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe
    50                  55                  60

Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His Glu Met
65                  70                  75                  80

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

Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln
            100                 105                 110

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

Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe
    130                 135                 140

Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala
145                 150                 155                 160

Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr
                165                 170                 175

Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu Ser Gly Gly Gly Ser Gly
            180                 185                 190

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        195                 200                 205

Gly Ser Leu Gln Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp
```

```
    210                 215                 220

Ile Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser
225                 230                 235                 240

Val Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp
                245                 250                 255

Asn Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys
            260                 265                 270

Asn Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg
        275                 280                 285

Ile Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser
    290                 295                 300

Phe Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu
305                 310                 315                 320

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

Asp Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu
            340                 345                 350

Val Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile
        355                 360                 365

Tyr Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys
    370                 375                 380

Leu Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr
385                 390                 395                 400

Ser Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro
                405                 410                 415
```

```
Pro Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys
            420                 425                 430

Trp Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu His
        435                 440                 445

Ala Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys Gln
    450                 455                 460

Ile Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln
465                 470                 475                 480

Asn Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp
                485                 490                 495

Gly Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu
            500                 505                 510

Ile Gln Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser
        515                 520                 525

Asp Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr
    530                 535                 540

Pro Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp Glu
545                 550                 555                 560

Asn Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp Val
                565                 570                 575

Thr Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala Arg
            580                 585                 590

Ala His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp
        595                 600                 605

Ala Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Ile Trp Leu
```

610 615 620

Ile Val Gly Ile Cys Ile Ala Leu Phe Ala Leu Pro Phe Val Ile Tyr
625 630 635 640

Ala Ala Lys Val Phe Leu Arg Cys Ile Asn Tyr Val Phe Phe Pro Ser
645 650 655

Leu Lys Pro Ser Ser Ser Ile Asp Glu Tyr Phe Ser Glu Gln Pro Leu
660 665 670

Lys Asn Leu Leu Leu Ser Thr Ser Glu Glu Gln Ile Glu Lys Cys Phe
675 680 685

Ile Ile Glu Asn Ile Ser Thr Ile Ala Thr Val Glu Glu Thr Asn Gln
690 695 700

Thr Asp Glu Asp His Lys Lys Tyr Ser Ser Gln Thr Ser Gln Asp Ser
705 710 715 720

Gly Asn Tyr Ser Asn Glu Asp Glu Ser Glu Ser Lys Thr Ser Glu Glu
725 730 735

Leu Gln Gln Asp Phe Val
740

<210> 84
<211> 701
<212> PRT
<213> Artificial Sequence

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

<400> 84
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser

```
            20                  25                  30

Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Lys Ile Ser Leu Phe
        35                  40                  45

Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe
    50                  55                  60

Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His Glu Met
65                  70                  75                  80

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

Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln
            100                 105                 110

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

Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe
    130                 135                 140

Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala
145                 150                 155                 160

Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr
                165                 170                 175

Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu Ser Gly Gly Gly Ser Gly
            180                 185                 190

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        195                 200                 205

Gly Ser Leu Gln Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu Ser
    210                 215                 220
```

```
Cys Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser Trp
225                 230                 235                 240

Glu Leu Lys Asn His Ser Ile Val Pro Thr His Tyr Thr Leu Leu Tyr
                245                 250                 255

Thr Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys Ala
            260                 265                 270

Asn Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser Thr
        275                 280                 285

His Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr Thr
    290                 295                 300

Leu Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser Phe
305                 310                 315                 320

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

Met Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp Leu
            340                 345                 350

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

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

Lys Leu Ile Pro Asn Thr Asn Tyr Cys Val Ser Val Tyr Leu Glu His
385                 390                 395                 400

Ser Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu Leu
                405                 410                 415

Pro Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys Ile Gly Gly
```

```
            420                 425                 430

Ile Ile Thr Val Phe Leu Ile Ala Leu Val Leu Thr Ser Thr Ile Val
        435                 440                 445

Thr Leu Lys Trp Ile Gly Tyr Ile Cys Leu Arg Asn Ser Leu Pro Lys
    450                 455                 460

Val Leu Asn Phe His Asn Phe Leu Ala Trp Pro Phe Pro Asn Leu Pro
465                 470                 475                 480

Pro Leu Glu Ala Met Asp Met Val Glu Val Ile Tyr Ile Asn Arg Lys
                485                 490                 495

Lys Lys Val Trp Asp Tyr Asn Tyr Asp Asp Glu Ser Asp Ser Asp Thr
            500                 505                 510

Glu Ala Ala Pro Arg Thr Ser Gly Gly Gly Tyr Thr Met His Gly Leu
        515                 520                 525

Thr Val Arg Pro Leu Gly Gln Ala Ser Ala Thr Ser Thr Glu Ser Gln
    530                 535                 540

Leu Ile Asp Pro Glu Ser Glu Glu Glu Pro Asp Leu Pro Glu Val Asp
545                 550                 555                 560

Val Glu Leu Pro Thr Met Pro Lys Asp Ser Pro Gln Gln Leu Glu Leu
                565                 570                 575

Leu Ser Gly Pro Cys Glu Arg Arg Lys Ser Pro Leu Gln Asp Pro Phe
            580                 585                 590

Pro Glu Glu Asp Tyr Ser Ser Thr Glu Gly Ser Gly Gly Arg Ile Thr
        595                 600                 605

Phe Asn Val Asp Leu Asn Ser Val Phe Leu Arg Val Leu Asp Asp Glu
    610                 615                 620
```

```
Asp Ser Asp Asp Leu Glu Ala Pro Leu Met Leu Ser Ser His Leu Glu
625                 630                 635                 640


Glu Met Val Asp Pro Glu Asp Pro Asp Asn Val Gln Ser Asn His Leu
                645                 650                 655


Leu Ala Ser Gly Glu Gly Thr Gln Pro Thr Phe Pro Ser Pro Ser Ser
            660                 665                 670


Glu Gly Leu Trp Ser Glu Asp Ala Pro Ser Asp Gln Ser Asp Thr Ser
        675                 680                 685


Glu Ser Asp Val Asp Leu Gly Asp Gly Tyr Ile Met Arg
    690                 695                 700


<210> 85
<211> 743
<212> PRT
<213> Artificial Sequence

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

<400> 85
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15


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


Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
        35                  40                  45


Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
    50                  55                  60


Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
65                  70                  75                  80
```

```
Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
                85                  90                  95

Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
            100                 105                 110

Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
        115                 120                 125

Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
    130                 135                 140

Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
145                 150                 155                 160

His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
                165                 170                 175

Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn Ser Gly Gly Gly Ser
            180                 185                 190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        195                 200                 205

Gly Gly Ser Leu Gln Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val
    210                 215                 220

Asp Ile Ile Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu
225                 230                 235                 240

Ser Val Gly Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met
                245                 250                 255

Asp Asn Trp Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys
            260                 265                 270

Cys Asn Phe Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu
```

```
        275                 280                 285

Arg Ile Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp
    290                 295                 300

Ser Phe Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His
305                 310                 315                 320

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

Lys Asp Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser
            340                 345                 350

Leu Val Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn
        355                 360                 365

Ile Tyr Ser Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr
    370                 375                 380

Cys Leu Lys Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val
385                 390                 395                 400

Tyr Ser Pro Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro
                405                 410                 415

Pro Pro Glu Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu
            420                 425                 430

Lys Trp Asp Tyr Thr Tyr Ala Asn Met Thr Phe Gln Val Gln Trp Leu
        435                 440                 445

His Ala Phe Leu Lys Arg Asn Pro Gly Asn His Leu Tyr Lys Trp Lys
    450                 455                 460

Gln Ile Pro Asp Cys Glu Asn Val Lys Thr Thr Gln Cys Val Phe Pro
465                 470                 475                 480
```

```
Gln Asn Val Phe Gln Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser
                485                 490                 495

Asp Gly Asn Asn Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr
            500                 505                 510

Glu Ile Gln Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu
        515                 520                 525

Ser Asp Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn
    530                 535                 540

Thr Pro Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp
545                 550                 555                 560

Glu Asn Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr Asp
                565                 570                 575

Val Thr Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val Lys Ala
            580                 585                 590

Arg Ala His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser
        595                 600                 605

Asp Ala Val Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Ile Trp
    610                 615                 620

Leu Ile Val Gly Ile Cys Ile Ala Leu Phe Ala Leu Pro Phe Val Ile
625                 630                 635                 640

Tyr Ala Ala Lys Val Phe Leu Arg Cys Ile Asn Tyr Val Phe Phe Pro
                645                 650                 655

Ser Leu Lys Pro Ser Ser Ser Ile Asp Glu Tyr Phe Ser Glu Gln Pro
            660                 665                 670

Leu Lys Asn Leu Leu Leu Ser Thr Ser Glu Glu Gln Ile Glu Lys Cys
```

675 680 685

Phe Ile Ile Glu Asn Ile Ser Thr Ile Ala Thr Val Glu Glu Thr Asn
690 695 700

Gln Thr Asp Glu Asp His Lys Lys Tyr Ser Ser Gln Thr Ser Gln Asp
705 710 715 720

Ser Gly Asn Tyr Ser Asn Glu Asp Glu Ser Glu Ser Lys Thr Ser Glu
725 730 735

Glu Leu Gln Gln Asp Phe Val
740

<210> 86
<211> 702
<212> PRT
<213> Artificial Sequence

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

<400> 86
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
35 40 45

Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
50 55 60

Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
65 70 75 80

Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser

```
                85                  90                  95

Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
            100                 105                 110

Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
        115                 120                 125

Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
    130                 135                 140

Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
145                 150                 155                 160

His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
                165                 170                 175

Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn Ser Gly Gly Gly Ser
            180                 185                 190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        195                 200                 205

Gly Gly Ser Leu Gln Ile Ser Tyr Asp Ser Pro Asp Tyr Thr Asp Glu
    210                 215                 220

Ser Cys Thr Phe Lys Ile Ser Leu Arg Asn Phe Arg Ser Ile Leu Ser
225                 230                 235                 240

Trp Glu Leu Lys Asn His Ser Ile Val Pro Thr His Tyr Thr Leu Leu
                245                 250                 255

Tyr Thr Ile Met Ser Lys Pro Glu Asp Leu Lys Val Val Lys Asn Cys
            260                 265                 270

Ala Asn Thr Thr Arg Ser Phe Cys Asp Leu Thr Asp Glu Trp Arg Ser
        275                 280                 285
```

```
Thr His Glu Ala Tyr Val Thr Val Leu Glu Gly Phe Ser Gly Asn Thr
    290                 295                 300

Thr Leu Phe Ser Cys Ser His Asn Phe Trp Leu Ala Ile Asp Met Ser
305                 310                 315                 320

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

Val Met Val Lys Phe Pro Ser Ile Val Glu Glu Glu Leu Gln Phe Asp
            340                 345                 350

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

Lys Pro Glu Ile Lys Gly Asn Met Ser Gly Asn Phe Thr Tyr Ile Ile
    370                 375                 380

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

His Ser Asp Glu Gln Ala Val Ile Lys Ser Pro Leu Lys Cys Thr Leu
                405                 410                 415

Leu Pro Pro Gly Gln Glu Ser Glu Ser Ala Glu Ser Ala Lys Ile Gly
            420                 425                 430

Gly Ile Ile Thr Val Phe Leu Ile Ala Leu Val Leu Thr Ser Thr Ile
        435                 440                 445

Val Thr Leu Lys Trp Ile Gly Tyr Ile Cys Leu Arg Asn Ser Leu Pro
    450                 455                 460

Lys Val Leu Asn Phe His Asn Phe Leu Ala Trp Pro Phe Pro Asn Leu
465                 470                 475                 480

Pro Pro Leu Glu Ala Met Asp Met Val Glu Val Ile Tyr Ile Asn Arg
```

```
                485                 490                 495

Lys Lys Lys Val Trp Asp Tyr Asn Tyr Asp Asp Glu Ser Asp Ser Asp
            500                 505                 510

Thr Glu Ala Ala Pro Arg Thr Ser Gly Gly Gly Tyr Thr Met His Gly
        515                 520                 525

Leu Thr Val Arg Pro Leu Gly Gln Ala Ser Ala Thr Ser Thr Glu Ser
    530                 535                 540

Gln Leu Ile Asp Pro Glu Ser Glu Glu Glu Pro Asp Leu Pro Glu Val
545                 550                 555                 560

Asp Val Glu Leu Pro Thr Met Pro Lys Asp Ser Pro Gln Gln Leu Glu
                565                 570                 575

Leu Leu Ser Gly Pro Cys Glu Arg Arg Lys Ser Pro Leu Gln Asp Pro
            580                 585                 590

Phe Pro Glu Glu Asp Tyr Ser Ser Thr Glu Gly Ser Gly Gly Arg Ile
        595                 600                 605

Thr Phe Asn Val Asp Leu Asn Ser Val Phe Leu Arg Val Leu Asp Asp
    610                 615                 620

Glu Asp Ser Asp Asp Leu Glu Ala Pro Leu Met Leu Ser Ser His Leu
625                 630                 635                 640

Glu Glu Met Val Asp Pro Glu Asp Pro Asp Asn Val Gln Ser Asn His
                645                 650                 655

Leu Leu Ala Ser Gly Glu Gly Thr Gln Pro Thr Phe Pro Ser Pro Ser
            660                 665                 670

Ser Glu Gly Leu Trp Ser Glu Asp Ala Pro Ser Asp Gln Ser Asp Thr
        675                 680                 685
```

Ser Glu Ser Asp Val Asp Leu Gly Asp Gly Tyr Ile Met Arg
690 695 700

<210> 87
<211> 657
<212> PRT
<213> Artificial Sequence

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

<400> 87
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu
20 25 30

Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr
35 40 45

Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys
50 55 60

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

Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu
85 90 95

Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp
100 105 110

Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg
115 120 125

Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala
130 135 140

```
Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Ser
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
                165                 170                 175

Gly Gly Ser Gly Gly Gly Ser Leu Gln Glu Met Gly Thr Ala Asp Leu
            180                 185                 190

Gly Pro Ser Ser Val Pro Thr Pro Thr Asn Val Thr Ile Glu Ser Tyr
        195                 200                 205

Asn Met Asn Pro Ile Val Tyr Trp Glu Tyr Gln Ile Met Pro Gln Val
    210                 215                 220

Pro Val Phe Thr Val Glu Val Lys Asn Tyr Gly Val Lys Asn Ser Glu
225                 230                 235                 240

Trp Ile Asp Ala Cys Ile Asn Ile Ser His His Tyr Cys Asn Ile Ser
                245                 250                 255

Asp His Val Gly Asp Pro Ser Asn Ser Leu Trp Val Arg Val Lys Ala
            260                 265                 270

Arg Val Gly Gln Lys Glu Ser Ala Tyr Ala Lys Ser Glu Glu Phe Ala
        275                 280                 285

Val Cys Arg Asp Gly Lys Ile Gly Pro Pro Lys Leu Asp Ile Arg Lys
    290                 295                 300

Glu Glu Lys Gln Ile Met Ile Asp Ile Phe His Pro Ser Val Phe Val
305                 310                 315                 320

Asn Gly Asp Glu Gln Glu Val Asp Tyr Asp Pro Glu Thr Thr Cys Tyr
                325                 330                 335

Ile Arg Val Tyr Asn Val Tyr Val Arg Met Asn Gly Ser Glu Ile Gln
```

```
            340                 345                 350

Tyr Lys Ile Leu Thr Gln Lys Glu Asp Asp Cys Asp Glu Ile Gln Cys
        355                 360                 365

Gln Leu Ala Ile Pro Val Ser Ser Leu Asn Ser Gln Tyr Cys Val Ser
    370                 375                 380

Ala Glu Gly Val Leu His Val Trp Gly Val Thr Thr Glu Lys Ser Lys
385                 390                 395                 400

Glu Val Cys Ile Thr Ile Phe Asn Ser Ser Ile Lys Gly Ser Leu Trp
                405                 410                 415

Ile Pro Val Val Ala Ala Leu Leu Leu Phe Leu Val Leu Ser Leu Val
            420                 425                 430

Phe Ile Cys Phe Tyr Ile Lys Lys Ile Asn Pro Leu Lys Glu Lys Ser
        435                 440                 445

Ile Ile Leu Pro Lys Ser Leu Ile Ser Val Val Arg Ser Ala Thr Leu
    450                 455                 460

Glu Thr Lys Pro Glu Ser Lys Tyr Val Ser Leu Ile Thr Ser Tyr Gln
465                 470                 475                 480

Pro Phe Ser Leu Glu Lys Glu Val Val Cys Glu Glu Pro Leu Ser Pro
                485                 490                 495

Ala Thr Val Pro Gly Met His Thr Glu Asp Asn Pro Gly Lys Val Glu
            500                 505                 510

His Thr Glu Glu Leu Ser Ser Ile Thr Glu Val Val Thr Thr Glu Glu
        515                 520                 525

Asn Ile Pro Asp Val Val Pro Gly Ser His Leu Thr Pro Ile Glu Arg
    530                 535                 540
```

```
Glu Ser Ser Ser Pro Leu Ser Ser Asn Gln Ser Glu Pro Gly Ser Ile
545                 550                 555                 560

Ala Leu Asn Ser Tyr His Ser Arg Asn Cys Ser Glu Ser Asp His Ser
                565                 570                 575

Arg Asn Gly Phe Asp Thr Asp Ser Ser Cys Leu Glu Ser His Ser Ser
            580                 585                 590

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

Glu Gly Gln Glu Leu Ile Thr Val Ile Lys Ala Pro Thr Ser Phe Gly
    610                 615                 620

Tyr Asp Lys Pro His Val Leu Val Asp Leu Leu Val Asp Asp Ser Gly
625                 630                 635                 640

Lys Glu Ser Leu Ile Gly Tyr Arg Pro Thr Glu Asp Ser Lys Glu Phe
                645                 650                 655

Ser
```

<210> 88
<211> 501
<212> PRT
<213> Artificial Sequence

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

<400> 88

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15

His Ala Ala Arg Pro Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu
            20                  25                  30
```

```
Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr
        35                  40                  45

Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys
    50                  55                  60

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

Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu
                85                  90                  95

Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp
            100                 105                 110

Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg
        115                 120                 125

Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala
    130                 135                 140

Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Ser
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
                165                 170                 175

Gly Gly Ser Gly Gly Gly Ser Leu Gln Ala Pro Pro Asp Pro Leu Ser
            180                 185                 190

Gln Leu Pro Ala Pro Gln His Pro Lys Ile Arg Leu Tyr Asn Ala Glu
        195                 200                 205

Gln Val Leu Ser Trp Glu Pro Val Ala Leu Ser Asn Ser Thr Arg Pro
    210                 215                 220

Val Val Tyr Gln Val Gln Phe Lys Tyr Thr Asp Ser Lys Trp Phe Thr
```

225 230 235 240

Ala Asp Ile Met Ser Ile Gly Val Asn Cys Thr Gln Ile Thr Ala Thr
245 250 255

Glu Cys Asp Phe Thr Ala Ala Ser Pro Ser Ala Gly Phe Pro Met Asp
260 265 270

Phe Asn Val Thr Leu Arg Leu Arg Ala Glu Leu Gly Ala Leu His Ser
275 280 285

Ala Trp Val Thr Met Pro Trp Phe Gln His Tyr Arg Asn Val Thr Val
290 295 300

Gly Pro Pro Glu Asn Ile Glu Val Thr Pro Gly Glu Gly Ser Leu Ile
305 310 315 320

Ile Arg Phe Ser Ser Pro Phe Asp Ile Ala Asp Thr Ser Thr Ala Phe
325 330 335

Phe Cys Tyr Tyr Val His Tyr Trp Glu Lys Gly Gly Ile Gln Gln Val
340 345 350

Lys Gly Pro Phe Arg Ser Asn Ser Ile Ser Leu Asp Asn Leu Lys Pro
355 360 365

Ser Arg Val Tyr Cys Leu Gln Val Gln Ala Gln Leu Leu Trp Asn Lys
370 375 380

Ser Asn Ile Phe Arg Val Gly His Leu Ser Asn Ile Ser Cys Tyr Glu
385 390 395 400

Thr Met Ala Asp Ala Ser Thr Glu Leu Gln Gln Val Ile Leu Ile Ser
405 410 415

Val Gly Thr Phe Ser Leu Leu Ser Val Leu Ala Gly Ala Cys Phe Phe
420 425 430

Leu Val Leu Lys Tyr Arg Gly Leu Ile Lys Tyr Trp Phe His Thr Pro
435 440 445

Pro Ser Ile Pro Leu Gln Ile Glu Glu Tyr Leu Lys Asp Pro Thr Gln
450 455 460

Pro Ile Leu Glu Ala Leu Asp Lys Asp Ser Ser Pro Lys Asp Asp Val
465 470 475 480

Trp Asp Ser Val Ser Ile Ile Ser Phe Pro Glu Lys Glu Gln Glu Asp
485 490 495

Val Leu Gln Thr Leu
500

<210> 89
<211> 781
<212> PRT
<213> Artificial Sequence

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

<400> 89
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu
20 25 30

Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr
35 40 45

Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys
50 55 60

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

```
Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu
                85                  90                  95

Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp
            100                 105                 110

Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg
        115                 120                 125

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

Val Ser Gly Glu Phe Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe
145                 150                 155                 160

Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly
                165                 170                 175

Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser
            180                 185                 190

Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp
        195                 200                 205

Gln Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val
    210                 215                 220

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

Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg Lys Ala Ile His
                245                 250                 255

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

Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Ser Gly Gly Gly Ser
```

```
        275                 280                 285

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    290                 295                 300

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

Val Pro Thr Pro Thr Asn Val Thr Ile Glu Ser Tyr Asn Met Asn Pro
                325                 330                 335

Ile Val Tyr Trp Glu Tyr Gln Ile Met Pro Gln Val Pro Val Phe Thr
            340                 345                 350

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

Cys Ile Asn Ile Ser His His Tyr Cys Asn Ile Ser Asp His Val Gly
    370                 375                 380

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

Lys Glu Ser Ala Tyr Ala Lys Ser Glu Glu Phe Ala Val Cys Arg Asp
                405                 410                 415

Gly Lys Ile Gly Pro Pro Lys Leu Asp Ile Arg Lys Glu Glu Lys Gln
            420                 425                 430

Ile Met Ile Asp Ile Phe His Pro Ser Val Phe Val Asn Gly Asp Glu
        435                 440                 445

Gln Glu Val Asp Tyr Asp Pro Glu Thr Thr Cys Tyr Ile Arg Val Tyr
    450                 455                 460

Asn Val Tyr Val Arg Met Asn Gly Ser Glu Ile Gln Tyr Lys Ile Leu
465                 470                 475                 480
```

```
Thr Gln Lys Glu Asp Asp Cys Asp Glu Ile Gln Cys Gln Leu Ala Ile
                485                 490                 495

Pro Val Ser Ser Leu Asn Ser Gln Tyr Cys Val Ser Ala Glu Gly Val
            500                 505                 510

Leu His Val Trp Gly Val Thr Thr Glu Lys Ser Lys Glu Val Cys Ile
        515                 520                 525

Thr Ile Phe Asn Ser Ser Ile Lys Gly Ser Leu Trp Ile Pro Val Val
    530                 535                 540

Ala Ala Leu Leu Leu Phe Leu Val Leu Ser Leu Val Phe Ile Cys Phe
545                 550                 555                 560

Tyr Ile Lys Lys Ile Asn Pro Leu Lys Glu Lys Ser Ile Ile Leu Pro
                565                 570                 575

Lys Ser Leu Ile Ser Val Val Arg Ser Ala Thr Leu Glu Thr Lys Pro
            580                 585                 590

Glu Ser Lys Tyr Val Ser Leu Ile Thr Ser Tyr Gln Pro Phe Ser Leu
        595                 600                 605

Glu Lys Glu Val Val Cys Glu Glu Pro Leu Ser Pro Ala Thr Val Pro
    610                 615                 620

Gly Met His Thr Glu Asp Asn Pro Gly Lys Val Glu His Thr Glu Glu
625                 630                 635                 640

Leu Ser Ser Ile Thr Glu Val Val Thr Thr Glu Glu Asn Ile Pro Asp
                645                 650                 655

Val Val Pro Gly Ser His Leu Thr Pro Ile Glu Arg Glu Ser Ser Ser
            660                 665                 670

Pro Leu Ser Ser Asn Gln Ser Glu Pro Gly Ser Ile Ala Leu Asn Ser
```

675 680 685

Tyr His Ser Arg Asn Cys Ser Glu Ser Asp His Ser Arg Asn Gly Phe
690 695 700

Asp Thr Asp Ser Ser Cys Leu Glu Ser His Ser Ser Leu Ser Asp Ser
705 710 715 720

Glu Phe Pro Pro Asn Asn Lys Gly Glu Ile Lys Thr Glu Gly Gln Glu
725 730 735

Leu Ile Thr Val Ile Lys Ala Pro Thr Ser Phe Gly Tyr Asp Lys Pro
740 745 750

His Val Leu Val Asp Leu Leu Val Asp Asp Ser Gly Lys Glu Ser Leu
755 760 765

Ile Gly Tyr Arg Pro Thr Glu Asp Ser Lys Glu Phe Ser
770 775 780

<210> 90
<211> 625
<212> PRT
<213> Artificial Sequence

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

<400> 90
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu
20 25 30

Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr
35 40 45

Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys

```
    50                  55                  60

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

Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu
                85                  90                  95

Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp
            100                 105                 110

Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg
        115                 120                 125

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

Val Ser Gly Glu Phe Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe
145                 150                 155                 160

Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly
                165                 170                 175

Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser
            180                 185                 190

Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp
        195                 200                 205

Gln Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val
    210                 215                 220

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

Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg Lys Ala Ile His
                245                 250                 255
```

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

Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Ser Gly Gly Gly Ser
        275                 280                 285

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    290                 295                 300

Gly Gly Ser Leu Gln Ala Pro Pro Asp Pro Leu Ser Gln Leu Pro Ala
305                 310                 315                 320

Pro Gln His Pro Lys Ile Arg Leu Tyr Asn Ala Glu Gln Val Leu Ser
                325                 330                 335

Trp Glu Pro Val Ala Leu Ser Asn Ser Thr Arg Pro Val Val Tyr Gln
            340                 345                 350

Val Gln Phe Lys Tyr Thr Asp Ser Lys Trp Phe Thr Ala Asp Ile Met
        355                 360                 365

Ser Ile Gly Val Asn Cys Thr Gln Ile Thr Ala Thr Glu Cys Asp Phe
    370                 375                 380

Thr Ala Ala Ser Pro Ser Ala Gly Phe Pro Met Asp Phe Asn Val Thr
385                 390                 395                 400

Leu Arg Leu Arg Ala Glu Leu Gly Ala Leu His Ser Ala Trp Val Thr
                405                 410                 415

Met Pro Trp Phe Gln His Tyr Arg Asn Val Thr Val Gly Pro Pro Glu
            420                 425                 430

Asn Ile Glu Val Thr Pro Gly Glu Gly Ser Leu Ile Ile Arg Phe Ser
        435                 440                 445

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

```
    450                 455                 460

Val His Tyr Trp Glu Lys Gly Gly Ile Gln Gln Val Lys Gly Pro Phe
465                 470                 475                 480

Arg Ser Asn Ser Ile Ser Leu Asp Asn Leu Lys Pro Ser Arg Val Tyr
                485                 490                 495

Cys Leu Gln Val Gln Ala Gln Leu Leu Trp Asn Lys Ser Asn Ile Phe
            500                 505                 510

Arg Val Gly His Leu Ser Asn Ile Ser Cys Tyr Glu Thr Met Ala Asp
        515                 520                 525

Ala Ser Thr Glu Leu Gln Gln Val Ile Leu Ile Ser Val Gly Thr Phe
    530                 535                 540

Ser Leu Leu Ser Val Leu Ala Gly Ala Cys Phe Phe Leu Val Leu Lys
545                 550                 555                 560

Tyr Arg Gly Leu Ile Lys Tyr Trp Phe His Thr Pro Pro Ser Ile Pro
                565                 570                 575

Leu Gln Ile Glu Glu Tyr Leu Lys Asp Pro Thr Gln Pro Ile Leu Glu
            580                 585                 590

Ala Leu Asp Lys Asp Ser Ser Pro Lys Asp Asp Val Trp Asp Ser Val
        595                 600                 605

Ser Ile Ile Ser Phe Pro Glu Lys Glu Gln Glu Asp Val Leu Gln Thr
    610                 615                 620

Leu
625
```

<210> 91
<211> 630
<212> PRT

<213> Artificial Sequence

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

<400> 91
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys
20 25 30

Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln
35 40 45

Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu
50 55 60

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

Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu
85 90 95

Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val
100 105 110

Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu
115 120 125

Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val
130 135 140

Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro
145 150 155 160

Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile
165 170 175

```
Ala Leu Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
            180                 185                 190

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Leu Val Pro His
        195                 200                 205

Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr
    210                 215                 220

Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly
225                 230                 235                 240

Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys
                245                 250                 255

Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg
            260                 265                 270

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

Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys
    290                 295                 300

Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn
305                 310                 315                 320

Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys
                325                 330                 335

Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn
            340                 345                 350

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

Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly
```

```
    370                 375                 380

Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu
385                 390                 395                 400

Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys Ser
                405                 410                 415

Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly
            420                 425                 430

Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe
        435                 440                 445

Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val Pro
    450                 455                 460

Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys Pro
465                 470                 475                 480

Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala
                485                 490                 495

Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro
            500                 505                 510

Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp Thr
        515                 520                 525

Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro Leu
    530                 535                 540

Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu Ile
545                 550                 555                 560

Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr
                565                 570                 575
```

Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr
580 585 590

Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys
595 600 605

Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro Pro
610 615 620

Ala Pro Ser Leu Leu Arg
625 630

<210> 92
<211> 643
<212> PRT
<213> Artificial Sequence

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

<400> 92
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys
20 25 30

Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln
35 40 45

Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu
50 55 60

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

Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu
85 90 95

```
Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val
            100                 105                 110

Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu
        115                 120                 125

Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val
    130                 135                 140

Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro
145                 150                 155                 160

Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile
                165                 170                 175

Ala Leu Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
            180                 185                 190

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Leu Pro Ala Gln
        195                 200                 205

Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu
    210                 215                 220

Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser
225                 230                 235                 240

Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val
                245                 250                 255

Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val
            260                 265                 270

Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu
        275                 280                 285

Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro
```

```
    290                 295                 300

Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala
305                 310                 315                 320

Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg Pro Gly Thr
                325                 330                 335

Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser
            340                 345                 350

Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn
        355                 360                 365

Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser
    370                 375                 380

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

Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr Pro Glu Pro Ser
                405                 410                 415

Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly Pro Ser Pro Pro
            420                 425                 430

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

Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val
    450                 455                 460

Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala
465                 470                 475                 480

Lys Val Pro His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro
                485                 490                 495
```

```
Glu Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser
            500                 505                 510

Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn
        515                 520                 525

Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu Ala Arg
    530                 535                 540

Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly Thr Gln
545                 550                 555                 560

Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp His Ser
                565                 570                 575

Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser
            580                 585                 590

Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val Pro Phe Ser Lys Glu
        595                 600                 605

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

Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala Gly Met
625                 630                 635                 640

Lys Pro Ser
```

<210> 93
<211> 752
<212> PRT
<213> Artificial Sequence

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

<400> 93
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg
20 25 30

Asp Ser Gln Gln Lys Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys
35 40 45

Ala Leu His Leu Gln Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser
50 55 60

Met Ser Phe Val Gln Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala
65 70 75 80

Leu Gly Leu Lys Glu Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp
85 90 95

Asp Lys Pro Thr Leu Gln Leu Glu Ser Val Asp Pro Lys Asn Tyr Pro
100 105 110

Lys Lys Lys Met Glu Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn
115 120 125

Asn Lys Leu Glu Phe Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser
130 135 140

Thr Ser Gln Ala Glu Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly
145 150 155 160

Gly Gln Asp Ile Thr Asp Phe Thr Met Gln Phe Val Ser Ser Ser Gly
165 170 175

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
180 185 190

Gly Ser Gly Gly Gly Ser Leu Gln Leu Glu Ala Asp Lys Cys Lys Glu

```
        195                 200                 205

Arg Glu Glu Lys Ile Ile Leu Val Ser Ser Ala Asn Glu Ile Asp Val
    210                 215                 220

Arg Pro Cys Pro Leu Asn Pro Asn Glu His Lys Gly Thr Ile Thr Trp
225                 230                 235                 240

Tyr Lys Asp Asp Ser Lys Thr Pro Val Ser Thr Glu Gln Ala Ser Arg
                245                 250                 255

Ile His Gln His Lys Glu Lys Leu Trp Phe Val Pro Ala Lys Val Glu
            260                 265                 270

Asp Ser Gly His Tyr Tyr Cys Val Val Arg Asn Ser Ser Tyr Cys Leu
        275                 280                 285

Arg Ile Lys Ile Ser Ala Lys Phe Val Glu Asn Glu Pro Asn Leu Cys
    290                 295                 300

Tyr Asn Ala Gln Ala Ile Phe Lys Gln Lys Leu Pro Val Ala Gly Asp
305                 310                 315                 320

Gly Gly Leu Val Cys Pro Tyr Met Glu Phe Phe Lys Asn Glu Asn Asn
                325                 330                 335

Glu Leu Pro Lys Leu Gln Trp Tyr Lys Asp Cys Lys Pro Leu Leu Leu
            340                 345                 350

Asp Asn Ile His Phe Ser Gly Val Lys Asp Arg Leu Ile Val Met Asn
        355                 360                 365

Val Ala Glu Lys His Arg Gly Asn Tyr Thr Cys His Ala Ser Tyr Thr
    370                 375                 380

Tyr Leu Gly Lys Gln Tyr Pro Ile Thr Arg Val Ile Glu Phe Ile Thr
385                 390                 395                 400
```

```
Leu Glu Glu Asn Lys Pro Thr Arg Pro Val Ile Val Ser Pro Ala Asn
                405                 410                 415

Glu Thr Met Glu Val Asp Leu Gly Ser Gln Ile Gln Leu Ile Cys Asn
            420                 425                 430

Val Thr Gly Gln Leu Ser Asp Ile Ala Tyr Trp Lys Trp Asn Gly Ser
        435                 440                 445

Val Ile Asp Glu Asp Asp Pro Val Leu Gly Glu Asp Tyr Tyr Ser Val
    450                 455                 460

Glu Asn Pro Ala Asn Lys Arg Arg Ser Thr Leu Ile Thr Val Leu Asn
465                 470                 475                 480

Ile Ser Glu Ile Glu Ser Arg Phe Tyr Lys His Pro Phe Thr Cys Phe
                485                 490                 495

Ala Lys Asn Thr His Gly Ile Asp Ala Ala Tyr Ile Gln Leu Ile Tyr
            500                 505                 510

Pro Val Thr Asn Phe Gln Lys His Met Ile Gly Ile Cys Val Thr Leu
        515                 520                 525

Thr Val Ile Ile Val Cys Ser Val Phe Ile Tyr Lys Ile Phe Lys Ile
    530                 535                 540

Asp Ile Val Leu Trp Tyr Arg Asp Ser Cys Tyr Asp Phe Leu Pro Ile
545                 550                 555                 560

Lys Ala Ser Asp Gly Lys Thr Tyr Asp Ala Tyr Ile Leu Tyr Pro Lys
                565                 570                 575

Thr Val Gly Glu Gly Ser Thr Ser Asp Cys Asp Ile Phe Val Phe Lys
            580                 585                 590

Val Leu Pro Glu Val Leu Glu Lys Gln Cys Gly Tyr Lys Leu Phe Ile
```

595 600 605

Tyr Gly Arg Asp Asp Tyr Val Gly Glu Asp Ile Val Glu Val Ile Asn
610 615 620

Glu Asn Val Lys Lys Ser Arg Arg Leu Ile Ile Ile Leu Val Arg Glu
625 630 635 640

Thr Ser Gly Phe Ser Trp Leu Gly Gly Ser Ser Glu Glu Gln Ile Ala
645 650 655

Met Tyr Asn Ala Leu Val Gln Asp Gly Ile Lys Val Val Leu Leu Glu
660 665 670

Leu Glu Lys Ile Gln Asp Tyr Glu Lys Met Pro Glu Ser Ile Lys Phe
675 680 685

Ile Lys Gln Lys His Gly Ala Ile Arg Trp Ser Gly Asp Phe Thr Gln
690 695 700

Gly Pro Gln Ser Ala Lys Thr Arg Phe Trp Lys Asn Val Arg Tyr His
705 710 715 720

Met Pro Val Gln Arg Arg Ser Pro Ser Ser Lys His Gln Leu Leu Ser
725 730 735

Pro Ala Thr Lys Glu Lys Leu Gln Arg Glu Ala His Val Pro Leu Gly
740 745 750

<210> 94
<211> 750
<212> PRT
<213> Artificial Sequence

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

<400> 94
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu

```
1               5                   10                  15

His Ala Ala Arg Pro Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg
            20                  25                  30

Asp Ser Gln Gln Lys Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys
        35                  40                  45

Ala Leu His Leu Gln Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser
    50                  55                  60

Met Ser Phe Val Gln Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala
65                  70                  75                  80

Leu Gly Leu Lys Glu Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp
                85                  90                  95

Asp Lys Pro Thr Leu Gln Leu Glu Ser Val Asp Pro Lys Asn Tyr Pro
            100                 105                 110

Lys Lys Lys Met Glu Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn
        115                 120                 125

Asn Lys Leu Glu Phe Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser
    130                 135                 140

Thr Ser Gln Ala Glu Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly
145                 150                 155                 160

Gly Gln Asp Ile Thr Asp Phe Thr Met Gln Phe Val Ser Ser Ser Gly
                165                 170                 175

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            180                 185                 190

Gly Ser Gly Gly Gly Ser Leu Gln Ser Glu Arg Cys Asp Asp Trp Gly
        195                 200                 205
```

```
Leu Asp Thr Met Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg
    210                 215                 220

Ile Lys Cys Pro Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr
225                 230                 235                 240

Ala His Ser Ala Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp
                245                 250                 255

Arg Asp Leu Glu Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile
            260                 265                 270

Ser Lys Glu Lys Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp
        275                 280                 285

Thr Gly Asn Tyr Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys
    290                 295                 300

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

Pro Met Lys Leu Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln
                325                 330                 335

Arg Ile Thr Cys Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys
            340                 345                 350

Pro Thr Ile Thr Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn
        355                 360                 365

Asn Val Ile Pro Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile
    370                 375                 380

Ser Asn Asn Gly Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly
385                 390                 395                 400

Arg Thr Phe His Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser
```

```
                405                 410                 415

Pro Lys Asn Ala Val Pro Pro Val Ile His Ser Pro Asn Asp His Val
            420                 425                 430

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

Tyr Phe Ser Phe Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile
    450                 455                 460

Asp Gly Lys Lys Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu
465                 470                 475                 480

Ser Ile Ser His Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu
                485                 490                 495

Ser Ile Lys Lys Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys
            500                 505                 510

His Ala Arg Ser Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys
        515                 520                 525

Gln Lys Val Pro Ala Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe
    530                 535                 540

Gly Ala Thr Val Leu Leu Val Val Ile Leu Ile Val Val Tyr His Val
545                 550                 555                 560

Tyr Trp Leu Glu Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp
                565                 570                 575

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

Arg Asn Ala Glu Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val
        595                 600                 605
```

```
Leu Glu Asn Glu Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser
    610                 615                 620

Leu Pro Gly Gly Ile Val Thr Asp Glu Thr Leu Ser Phe Ile Gln Lys
625                 630                 635                 640

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

Thr Gln Ala Leu Leu Glu Leu Lys Ala Gly Leu Glu Asn Met Ala Ser
            660                 665                 670

Arg Gly Asn Ile Asn Val Ile Leu Val Gln Tyr Lys Ala Val Lys Glu
        675                 680                 685

Thr Lys Val Lys Glu Leu Lys Arg Ala Lys Thr Val Leu Thr Val Ile
    690                 695                 700

Lys Trp Lys Gly Glu Lys Ser Lys Tyr Pro Gln Gly Arg Phe Trp Lys
705                 710                 715                 720

Gln Leu Gln Val Ala Met Pro Val Lys Lys Ser Pro Arg Arg Ser Ser
                725                 730                 735

Ser Asp Glu Gln Gly Leu Ser Tyr Ser Ser Leu Lys Asn Val
            740                 745                 750
```

<210> 95
<211> 767
<212> PRT
<213> Artificial Sequence

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

<400> 95

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15
```

```
His Ala Ala Arg Pro Asn Tyr Pro Lys Lys Lys Met Glu Lys Arg Phe
            20                  25                  30

Val Phe Asn Lys Ile Glu Ile Asn Asn Lys Leu Glu Phe Glu Ser Ala
        35                  40                  45

Gln Phe Pro Asn Trp Tyr Ile Ser Thr Ser Gln Ala Glu Asn Met Pro
    50                  55                  60

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

Met Gln Phe Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                85                  90                  95

Gly Gly Gly Gly Ser Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg
            100                 105                 110

Asp Ser Gln Gln Lys Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys
        115                 120                 125

Ala Leu His Leu Gln Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser
    130                 135                 140

Met Ser Phe Val Gln Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala
145                 150                 155                 160

Leu Gly Leu Lys Glu Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp
                165                 170                 175

Asp Lys Pro Thr Leu Gln Leu Glu Ser Val Asp Pro Lys Ser Gly Gly
            180                 185                 190

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        195                 200                 205

Ser Gly Gly Gly Ser Leu Gln Leu Glu Ala Asp Lys Cys Lys Glu Arg
```

```
    210                 215                 220

Glu Glu Lys Ile Ile Leu Val Ser Ser Ala Asn Glu Ile Asp Val Arg
225                 230                 235                 240

Pro Cys Pro Leu Asn Pro Asn Glu His Lys Gly Thr Ile Thr Trp Tyr
                245                 250                 255

Lys Asp Asp Ser Lys Thr Pro Val Ser Thr Glu Gln Ala Ser Arg Ile
            260                 265                 270

His Gln His Lys Glu Lys Leu Trp Phe Val Pro Ala Lys Val Glu Asp
        275                 280                 285

Ser Gly His Tyr Tyr Cys Val Val Arg Asn Ser Ser Tyr Cys Leu Arg
    290                 295                 300

Ile Lys Ile Ser Ala Lys Phe Val Glu Asn Glu Pro Asn Leu Cys Tyr
305                 310                 315                 320

Asn Ala Gln Ala Ile Phe Lys Gln Lys Leu Pro Val Ala Gly Asp Gly
                325                 330                 335

Gly Leu Val Cys Pro Tyr Met Glu Phe Phe Lys Asn Glu Asn Asn Glu
            340                 345                 350

Leu Pro Lys Leu Gln Trp Tyr Lys Asp Cys Lys Pro Leu Leu Leu Asp
        355                 360                 365

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

Ala Glu Lys His Arg Gly Asn Tyr Thr Cys His Ala Ser Tyr Thr Tyr
385                 390                 395                 400

Leu Gly Lys Gln Tyr Pro Ile Thr Arg Val Ile Glu Phe Ile Thr Leu
                405                 410                 415
```

```
Glu Glu Asn Lys Pro Thr Arg Pro Val Ile Val Ser Pro Ala Asn Glu
            420                 425                 430

Thr Met Glu Val Asp Leu Gly Ser Gln Ile Gln Leu Ile Cys Asn Val
        435                 440                 445

Thr Gly Gln Leu Ser Asp Ile Ala Tyr Trp Lys Trp Asn Gly Ser Val
    450                 455                 460

Ile Asp Glu Asp Asp Pro Val Leu Gly Glu Asp Tyr Tyr Ser Val Glu
465                 470                 475                 480

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

Ser Glu Ile Glu Ser Arg Phe Tyr Lys His Pro Phe Thr Cys Phe Ala
            500                 505                 510

Lys Asn Thr His Gly Ile Asp Ala Ala Tyr Ile Gln Leu Ile Tyr Pro
        515                 520                 525

Val Thr Asn Phe Gln Lys His Met Ile Gly Ile Cys Val Thr Leu Thr
    530                 535                 540

Val Ile Ile Val Cys Ser Val Phe Ile Tyr Lys Ile Phe Lys Ile Asp
545                 550                 555                 560

Ile Val Leu Trp Tyr Arg Asp Ser Cys Tyr Asp Phe Leu Pro Ile Lys
                565                 570                 575

Ala Ser Asp Gly Lys Thr Tyr Asp Ala Tyr Ile Leu Tyr Pro Lys Thr
            580                 585                 590

Val Gly Glu Gly Ser Thr Ser Asp Cys Asp Ile Phe Val Phe Lys Val
        595                 600                 605

Leu Pro Glu Val Leu Glu Lys Gln Cys Gly Tyr Lys Leu Phe Ile Tyr
```

610 615 620

Gly Arg Asp Asp Tyr Val Gly Glu Asp Ile Val Glu Val Ile Asn Glu
625 630 635 640

Asn Val Lys Lys Ser Arg Arg Leu Ile Ile Ile Leu Val Arg Glu Thr
645 650 655

Ser Gly Phe Ser Trp Leu Gly Gly Ser Ser Glu Glu Gln Ile Ala Met
660 665 670

Tyr Asn Ala Leu Val Gln Asp Gly Ile Lys Val Val Leu Leu Glu Leu
675 680 685

Glu Lys Ile Gln Asp Tyr Glu Lys Met Pro Glu Ser Ile Lys Phe Ile
690 695 700

Lys Gln Lys His Gly Ala Ile Arg Trp Ser Gly Asp Phe Thr Gln Gly
705 710 715 720

Pro Gln Ser Ala Lys Thr Arg Phe Trp Lys Asn Val Arg Tyr His Met
725 730 735

Pro Val Gln Arg Arg Ser Pro Ser Ser Lys His Gln Leu Leu Ser Pro
740 745 750

Ala Thr Lys Glu Lys Leu Gln Arg Glu Ala His Val Pro Leu Gly
755 760 765

<210> 96
<211> 765
<212> PRT
<213> Artificial Sequence

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

<400> 96
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu

```
1               5                   10                  15

His Ala Ala Arg Pro Asn Tyr Pro Lys Lys Lys Met Glu Lys Arg Phe
            20                  25                  30

Val Phe Asn Lys Ile Glu Ile Asn Asn Lys Leu Glu Phe Glu Ser Ala
        35                  40                  45

Gln Phe Pro Asn Trp Tyr Ile Ser Thr Ser Gln Ala Glu Asn Met Pro
    50                  55                  60

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

Met Gln Phe Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                85                  90                  95

Gly Gly Gly Gly Ser Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg
            100                 105                 110

Asp Ser Gln Gln Lys Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys
        115                 120                 125

Ala Leu His Leu Gln Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser
    130                 135                 140

Met Ser Phe Val Gln Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala
145                 150                 155                 160

Leu Gly Leu Lys Glu Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp
                165                 170                 175

Asp Lys Pro Thr Leu Gln Leu Glu Ser Val Asp Pro Lys Ser Gly Gly
            180                 185                 190

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        195                 200                 205
```

```
Ser Gly Gly Gly Ser Leu Gln Ser Glu Arg Cys Asp Asp Trp Gly Leu
    210                 215                 220

Asp Thr Met Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile
225                 230                 235                 240

Lys Cys Pro Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala
                245                 250                 255

His Ser Ala Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg
            260                 265                 270

Asp Leu Glu Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser
        275                 280                 285

Lys Glu Lys Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr
    290                 295                 300

Gly Asn Tyr Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val
305                 310                 315                 320

Ala Phe Pro Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Pro
                325                 330                 335

Met Lys Leu Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg
            340                 345                 350

Ile Thr Cys Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro
        355                 360                 365

Thr Ile Thr Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn
    370                 375                 380

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

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

```
                405                 410                 415

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

Lys Asn Ala Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val
        435                 440                 445

Tyr Glu Lys Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr
    450                 455                 460

Phe Ser Phe Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp
465                 470                 475                 480

Gly Lys Lys Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser
                485                 490                 495

Ile Ser His Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser
            500                 505                 510

Ile Lys Lys Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His
        515                 520                 525

Ala Arg Ser Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln
    530                 535                 540

Lys Val Pro Ala Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe Gly
545                 550                 555                 560

Ala Thr Val Leu Leu Val Val Ile Leu Ile Val Val Tyr His Val Tyr
                565                 570                 575

Trp Leu Glu Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp Glu
            580                 585                 590

Thr Ile Leu Asp Gly Lys Glu Tyr Asp Ile Tyr Val Ser Tyr Ala Arg
        595                 600                 605
```

```
Asn Ala Glu Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val Leu
    610                 615                 620

Glu Asn Glu Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser Leu
625                 630                 635                 640

Pro Gly Gly Ile Val Thr Asp Glu Thr Leu Ser Phe Ile Gln Lys Ser
                645                 650                 655

Arg Arg Leu Leu Val Val Leu Ser Pro Asn Tyr Val Leu Gln Gly Thr
            660                 665                 670

Gln Ala Leu Leu Glu Leu Lys Ala Gly Leu Glu Asn Met Ala Ser Arg
        675                 680                 685

Gly Asn Ile Asn Val Ile Leu Val Gln Tyr Lys Ala Val Lys Glu Thr
    690                 695                 700

Lys Val Lys Glu Leu Lys Arg Ala Lys Thr Val Leu Thr Val Ile Lys
705                 710                 715                 720

Trp Lys Gly Glu Lys Ser Lys Tyr Pro Gln Gly Arg Phe Trp Lys Gln
                725                 730                 735

Leu Gln Val Ala Met Pro Val Lys Lys Ser Pro Arg Arg Ser Ser Ser
            740                 745                 750

Asp Glu Gln Gly Leu Ser Tyr Ser Ser Leu Lys Asn Val
        755                 760                 765
```

<210> 97
<211> 679
<212> PRT
<213> Artificial Sequence

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

<400> 97
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Val Pro Pro Gly Glu Asp Ser Lys Asp Val Ala
20 25 30

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

Ile Arg Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys
50 55 60

Asn Lys Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn
65 70 75 80

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

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

Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser
115 120 125

Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile Gln
130 135 140

Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro Asp
145 150 155 160

Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn Gln
165 170 175

Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys Glu
180 185 190

Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met Ser Gly Gly Gly

```
        195                 200                 205

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    210                 215                 220

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

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

Thr Cys Pro Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val
            260                 265                 270

Leu Arg Lys Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met
        275                 280                 285

Gly Arg Arg Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn
    290                 295                 300

Tyr Ser Cys Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu
305                 310                 315                 320

Val Asp Val Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser
                325                 330                 335

Pro Leu Ser Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser
            340                 345                 350

Leu Thr Thr Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro
        355                 360                 365

Ala Glu Asp Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys
    370                 375                 380

Phe Ser Cys Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile
385                 390                 395                 400
```

```
Val Ser Met Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr
                405                 410                 415

Gln Thr Phe Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn
            420                 425                 430

Ile Thr Val Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr
        435                 440                 445

Trp Gln Asp Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe
    450                 455                 460

Glu Leu Arg Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met
465                 470                 475                 480

Val Lys Asp Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly
                485                 490                 495

Leu Arg His Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly
            500                 505                 510

Glu Trp Ser Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu
        515                 520                 525

Ser Arg Ser Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Gln Ala
    530                 535                 540

Leu Thr Thr Asn Lys Asp Asp Asp Asn Ile Leu Phe Arg Asp Ser Ala
545                 550                 555                 560

Asn Ala Thr Ser Leu Pro Val Gln Asp Ser Ser Ser Val Pro Leu Pro
                565                 570                 575

Thr Phe Leu Val Ala Gly Gly Ser Leu Ala Phe Gly Thr Leu Leu Cys
            580                 585                 590

Ile Ala Ile Val Leu Arg Phe Lys Lys Thr Trp Lys Leu Arg Ala Leu
```

595 600 605

Lys Glu Gly Lys Thr Ser Met His Pro Pro Tyr Ser Leu Gly Gln Leu
610 615 620

Val Pro Glu Arg Pro Arg Pro Thr Pro Val Leu Val Pro Leu Ile Ser
625 630 635 640

Pro Pro Val Ser Pro Ser Ser Leu Gly Ser Asp Asn Thr Ser Ser His
645 650 655

Asn Arg Pro Asp Ala Arg Asp Pro Arg Ser Pro Tyr Asp Ile Ser Asn
660 665 670

Thr Asp Tyr Phe Phe Pro Arg
675

<210> 98
<211> 1126
<212> PRT
<213> Artificial Sequence

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

<400> 98
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Val Pro Pro Gly Glu Asp Ser Lys Asp Val Ala
20 25 30

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

Ile Arg Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys
50 55 60

Asn Lys Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn

65 70 75 80

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

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

Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser
115 120 125

Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile Gln
130 135 140

Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro Asp
145 150 155 160

Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn Gln
165 170 175

Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys Glu
180 185 190

Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met Ser Gly Gly Gly
195 200 205

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
210 215 220

Gly Gly Gly Ser Leu Gln Glu Leu Leu Asp Pro Cys Gly Tyr Ile Ser
225 230 235 240

Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys
245 250 255

Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr
260 265 270

```
Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr
        275                 280                 285

Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ala Ser
    290                 295                 300

Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu
305                 310                 315                 320

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

Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys
            340                 345                 350

Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu
        355                 360                 365

Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg
    370                 375                 380

Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val
385                 390                 395                 400

Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr
                405                 410                 415

Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro
            420                 425                 430

Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu
        435                 440                 445

Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val Ile Ile Leu Lys
    450                 455                 460

Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile
```

```
465                 470                 475                 480

Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe Thr Val Gln Asp
                485                 490                 495

Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg Cys Met Lys Glu
            500                 505                 510

Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu Ala Ser Gly Ile
        515                 520                 525

Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Phe Trp Tyr Lys Ile
    530                 535                 540

Asp Pro Ser His Thr Gln Gly Tyr Arg Thr Val Gln Leu Val Trp Lys
545                 550                 555                 560

Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu Asp Tyr Glu Val
                565                 570                 575

Thr Leu Thr Arg Trp Lys Ser His Leu Gln Asn Tyr Thr Val Asn Ala
            580                 585                 590

Thr Lys Leu Thr Val Asn Leu Thr Asn Asp Arg Tyr Leu Ala Thr Leu
        595                 600                 605

Thr Val Arg Asn Leu Val Gly Lys Ser Asp Ala Ala Val Leu Thr Ile
    610                 615                 620

Pro Ala Cys Asp Phe Gln Ala Thr His Pro Val Met Asp Leu Lys Ala
625                 630                 635                 640

Phe Pro Lys Asp Asn Met Leu Trp Val Glu Trp Thr Thr Pro Arg Glu
                645                 650                 655

Ser Val Lys Lys Tyr Ile Leu Glu Trp Cys Val Leu Ser Asp Lys Ala
            660                 665                 670
```

```
Pro Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly Thr Val His Arg Thr
        675                 680                 685

Tyr Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys Tyr Leu Ile Thr Val
    690                 695                 700

Thr Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro Glu Ser Ile Lys Ala
705                 710                 715                 720

Tyr Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro Thr Val Arg Thr Lys
                725                 730                 735

Lys Val Gly Lys Asn Glu Ala Val Leu Glu Trp Asp Gln Leu Pro Val
            740                 745                 750

Asp Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr Ile Phe Tyr Arg Thr
        755                 760                 765

Ile Ile Gly Asn Glu Thr Ala Val Asn Val Asp Ser Ser His Thr Glu
    770                 775                 780

Tyr Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu Tyr Met Val Arg Met
785                 790                 795                 800

Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly Pro Glu Phe Thr Phe
                805                 810                 815

Thr Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu Ala Ile Val Val Pro
            820                 825                 830

Val Cys Leu Ala Phe Leu Leu Thr Thr Leu Leu Gly Val Leu Phe Cys
        835                 840                 845

Phe Asn Lys Arg Asp Leu Ile Lys Lys His Ile Trp Pro Asn Val Pro
    850                 855                 860

Asp Pro Ser Lys Ser His Ile Ala Gln Trp Ser Pro His Thr Pro Pro
```

865 870 875 880

Arg His Asn Phe Asn Ser Lys Asp Gln Met Tyr Ser Asp Gly Asn Phe
885 890 895

Thr Asp Val Ser Val Val Glu Ile Glu Ala Asn Asp Lys Lys Pro Phe
900 905 910

Pro Glu Asp Leu Lys Ser Leu Asp Leu Phe Lys Lys Glu Lys Ile Asn
915 920 925

Thr Glu Gly His Ser Ser Gly Ile Gly Gly Ser Ser Cys Met Ser Ser
930 935 940

Ser Arg Pro Ser Ile Ser Ser Ser Asp Glu Asn Glu Ser Ser Gln Asn
945 950 955 960

Thr Ser Ser Thr Val Gln Tyr Ser Thr Val Val His Ser Gly Tyr Arg
965 970 975

His Gln Val Pro Ser Val Gln Val Phe Ser Arg Ser Glu Ser Thr Gln
980 985 990

Pro Leu Leu Asp Ser Glu Glu Arg Pro Glu Asp Leu Gln Leu Val Asp
995 1000 1005

His Val Asp Gly Gly Asp Gly Ile Leu Pro Arg Gln Gln Tyr Phe
1010 1015 1020

Lys Gln Asn Cys Ser Gln His Glu Ser Ser Pro Asp Ile Ser His
1025 1030 1035

Phe Glu Arg Ser Lys Gln Val Ser Ser Val Asn Glu Glu Asp Phe
1040 1045 1050

Val Arg Leu Lys Gln Gln Ile Ser Asp His Ile Ser Gln Ser Cys
1055 1060 1065

Gly Ser Gly Gln Met Lys Met Phe Gln Glu Val Ser Ala Ala Asp
1070 1075 1080

Ala Phe Gly Pro Gly Thr Glu Gly Gln Val Glu Arg Phe Glu Thr
1085 1090 1095

Val Gly Met Glu Ala Ala Thr Asp Glu Gly Met Pro Lys Ser Tyr
1100 1105 1110

Leu Pro Gln Thr Val Arg Gln Gly Gly Tyr Met Pro Gln
1115 1120 1125

<210> 99
<211> 1207
<212> PRT
<213> Artificial Sequence

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

<400> 99
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val
20 25 30

Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr
35 40 45

Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser
50 55 60

Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu
65 70 75 80

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

```
Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser
            100                 105                 110

Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu
        115                 120                 125

Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu
    130                 135                 140

Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly
145                 150                 155                 160

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

Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys
            180                 185                 190

Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu
        195                 200                 205

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

Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu
225                 230                 235                 240

Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu
                245                 250                 255

Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe
            260                 265                 270

Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val
        275                 280                 285

Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser
```

```
    290                 295                 300

Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu
305                 310                 315                 320

Trp Ala Ser Val Pro Cys Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro
                325                 330                 335

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

Pro Asp Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu
        355                 360                 365

Arg Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe
    370                 375                 380

Tyr Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
385                 390                 395                 400

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn
                405                 410                 415

Glu Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser
            420                 425                 430

Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser
        435                 440                 445

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met
    450                 455                 460

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
465                 470                 475                 480

Asn Met Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn
                485                 490                 495
```

```
Ser Glu Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
            500                 505                 510

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
        515                 520                 525

Ala Val Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser Ser Gly
    530                 535                 540

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
545                 550                 555                 560

Gly Ser Gly Gly Gly Ser Leu Gln Cys Arg Thr Ser Glu Cys Cys Phe
                565                 570                 575

Gln Asp Pro Pro Tyr Pro Asp Ala Asp Ser Gly Ser Ala Ser Gly Pro
            580                 585                 590

Arg Asp Leu Arg Cys Tyr Arg Ile Ser Ser Asp Arg Tyr Glu Cys Ser
        595                 600                 605

Trp Gln Tyr Glu Gly Pro Thr Ala Gly Val Ser His Phe Leu Arg Cys
    610                 615                 620

Cys Leu Ser Ser Gly Arg Cys Cys Tyr Phe Ala Ala Gly Ser Ala Thr
625                 630                 635                 640

Arg Leu Gln Phe Ser Asp Gln Ala Gly Val Ser Val Leu Tyr Thr Val
                645                 650                 655

Thr Leu Trp Val Glu Ser Trp Ala Arg Asn Gln Thr Glu Lys Ser Pro
            660                 665                 670

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

Gly Asp Ile Lys Val Ser Lys Leu Ala Gly Gln Leu Arg Met Glu Trp
```

690 695 700

Glu Thr Pro Asp Asn Gln Val Gly Ala Glu Val Gln Phe Arg His Arg
705 710 715 720

Thr Pro Ser Ser Pro Trp Lys Leu Gly Asp Cys Gly Pro Gln Asp Asp
725 730 735

Asp Thr Glu Ser Cys Leu Cys Pro Leu Glu Met Asn Val Ala Gln Glu
740 745 750

Phe Gln Leu Arg Arg Arg Gln Leu Gly Ser Gln Gly Ser Ser Trp Ser
755 760 765

Lys Trp Ser Ser Pro Val Cys Val Pro Pro Glu Asn Pro Pro Gln Pro
770 775 780

Gln Val Arg Phe Ser Val Glu Gln Leu Gly Gln Asp Gly Arg Arg Arg
785 790 795 800

Leu Thr Leu Lys Glu Gln Pro Thr Gln Leu Glu Leu Pro Glu Gly Cys
805 810 815

Gln Gly Leu Ala Pro Gly Thr Glu Val Thr Tyr Arg Leu Gln Leu His
820 825 830

Met Leu Ser Cys Pro Cys Lys Ala Lys Ala Thr Arg Thr Leu His Leu
835 840 845

Gly Lys Met Pro Tyr Leu Ser Gly Ala Ala Tyr Asn Val Ala Val Ile
850 855 860

Ser Ser Asn Gln Phe Gly Pro Gly Leu Asn Gln Thr Trp His Ile Pro
865 870 875 880

Ala Asp Thr His Thr Glu Pro Val Ala Leu Asn Ile Ser Val Gly Thr
885 890 895

```
Asn Gly Thr Thr Met Tyr Trp Pro Ala Arg Ala Gln Ser Met Thr Tyr
            900                 905                 910

Cys Ile Glu Trp Gln Pro Val Gly Gln Asp Gly Gly Leu Ala Thr Cys
        915                 920                 925

Ser Leu Thr Ala Pro Gln Asp Pro Asp Pro Ala Gly Met Ala Thr Tyr
    930                 935                 940

Ser Trp Ser Arg Glu Ser Gly Ala Met Gly Gln Glu Lys Cys Tyr Tyr
945                 950                 955                 960

Ile Thr Ile Phe Ala Ser Ala His Pro Glu Lys Leu Thr Leu Trp Ser
                965                 970                 975

Thr Val Leu Ser Thr Tyr His Phe Gly Gly Asn Ala Ser Ala Ala Gly
            980                 985                 990

Thr Pro His His Val Ser Val Lys  Asn His Ser Leu Asp  Ser Val Ser
        995                 1000                1005

Val Asp  Trp Ala Pro Ser Leu  Leu Ser Thr Cys Pro  Gly Val Leu
    1010                1015                1020

Lys Glu  Tyr Val Val Arg Cys  Arg Asp Glu Asp Ser  Lys Gln Val
    1025                1030                1035

Ser Glu  His Pro Val Gln Pro  Thr Glu Thr Gln Val  Thr Leu Ser
    1040                1045                1050

Gly Leu  Arg Ala Gly Val Ala  Tyr Thr Val Gln Val  Arg Ala Asp
    1055                1060                1065

Thr Ala  Trp Leu Arg Gly Val  Trp Ser Gln Pro Gln  Arg Phe Ser
    1070                1075                1080

Ile Glu  Val Gln Val Ser Asp  Trp Leu Ile Phe Phe  Ala Ser Leu
```

```
    1085                1090                1095


Gly Ser  Phe Leu Ser Ile Leu  Leu Val Gly Val Leu  Gly Tyr Leu
    1100                1105                1110


Gly Leu  Asn Arg Ala Ala Arg  His Leu Cys Pro Pro  Leu Pro Thr
    1115                1120                1125


Pro Cys  Ala Ser Ser Ala Ile  Glu Phe Pro Gly Gly  Lys Glu Thr
    1130                1135                1140


Trp Gln  Trp Ile Asn Pro Val  Asp Phe Gln Glu Glu  Ala Ser Leu
    1145                1150                1155


Gln Glu  Ala Leu Val Val Glu  Met Ser Trp Asp Lys  Gly Glu Arg
    1160                1165                1170


Thr Glu  Pro Leu Glu Lys Thr  Glu Leu Pro Glu Gly  Ala Pro Glu
    1175                1180                1185


Leu Ala  Leu Asp Thr Glu Leu  Ser Leu Glu Asp Gly  Asp Arg Cys
    1190                1195                1200


Lys Ala  Lys Met
    1205


<210> 100
<211> 1407
<212> PRT
<213> Artificial Sequence

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

<400> 100
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15


His Ala Ala Arg Pro Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val
```

```
            20                  25                  30

Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr
        35                  40                  45

Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser
    50                  55                  60

Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu
65                  70                  75                  80

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

Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser
            100                 105                 110

Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu
        115                 120                 125

Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu
    130                 135                 140

Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly
145                 150                 155                 160

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

Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys
            180                 185                 190

Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu
        195                 200                 205

Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser
    210                 215                 220
```

```
Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu
225                 230                 235                 240

Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu
                245                 250                 255

Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe
            260                 265                 270

Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val
        275                 280                 285

Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser
    290                 295                 300

Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu
305                 310                 315                 320

Trp Ala Ser Val Pro Cys Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro
                325                 330                 335

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

Pro Asp Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu
        355                 360                 365

Arg Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe
    370                 375                 380

Tyr Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
385                 390                 395                 400

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn
                405                 410                 415

Glu Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser
```

```
            420                 425                 430

Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser
        435                 440                 445

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met
    450                 455                 460

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
465                 470                 475                 480

Asn Met Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn
                485                 490                 495

Ser Glu Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
            500                 505                 510

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
        515                 520                 525

Ala Val Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser Ser Gly
    530                 535                 540

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
545                 550                 555                 560

Gly Ser Gly Gly Gly Ser Leu Gln Lys Ile Asp Ala Cys Lys Arg Gly
                565                 570                 575

Asp Val Thr Val Lys Pro Ser His Val Ile Leu Leu Gly Ser Thr Val
            580                 585                 590

Asn Ile Thr Cys Ser Leu Lys Pro Arg Gln Gly Cys Phe His Tyr Ser
        595                 600                 605

Arg Arg Asn Lys Leu Ile Leu Tyr Lys Phe Asp Arg Arg Ile Asn Phe
    610                 615                 620
```

```
His His Gly His Ser Leu Asn Ser Gln Val Thr Gly Leu Pro Leu Gly
625                 630                 635                 640

Thr Thr Leu Phe Val Cys Lys Leu Ala Cys Ile Asn Ser Asp Glu Ile
                645                 650                 655

Gln Ile Cys Gly Ala Glu Ile Phe Val Gly Val Ala Pro Glu Gln Pro
            660                 665                 670

Gln Asn Leu Ser Cys Ile Gln Lys Gly Glu Gln Gly Thr Val Ala Cys
        675                 680                 685

Thr Trp Glu Arg Gly Arg Asp Thr His Leu Tyr Thr Glu Tyr Thr Leu
    690                 695                 700

Gln Leu Ser Gly Pro Lys Asn Leu Thr Trp Gln Lys Gln Cys Lys Asp
705                 710                 715                 720

Ile Tyr Cys Asp Tyr Leu Asp Phe Gly Ile Asn Leu Thr Pro Glu Ser
                725                 730                 735

Pro Glu Ser Asn Phe Thr Ala Lys Val Thr Ala Val Asn Ser Leu Gly
            740                 745                 750

Ser Ser Ser Ser Leu Pro Ser Thr Phe Thr Phe Leu Asp Ile Val Arg
        755                 760                 765

Pro Leu Pro Pro Trp Asp Ile Arg Ile Lys Phe Gln Lys Ala Ser Val
    770                 775                 780

Ser Arg Cys Thr Leu Tyr Trp Arg Asp Glu Gly Leu Val Leu Leu Asn
785                 790                 795                 800

Arg Leu Arg Tyr Arg Pro Ser Asn Ser Arg Leu Trp Asn Met Val Asn
                805                 810                 815

Val Thr Lys Ala Lys Gly Arg His Asp Leu Leu Asp Leu Lys Pro Phe
```

```
            820                 825                 830

Thr Glu Tyr Glu Phe Gln Ile Ser Ser Lys Leu His Leu Tyr Lys Gly
        835                 840                 845

Ser Trp Ser Asp Trp Ser Glu Ser Leu Arg Ala Gln Thr Pro Glu Glu
    850                 855                 860

Glu Pro Thr Gly Met Leu Asp Val Trp Tyr Met Lys Arg His Ile Asp
865                 870                 875                 880

Tyr Ser Arg Gln Gln Ile Ser Leu Phe Trp Lys Asn Leu Ser Val Ser
                885                 890                 895

Glu Ala Arg Gly Lys Ile Leu His Tyr Gln Val Thr Leu Gln Glu Leu
            900                 905                 910

Thr Gly Gly Lys Ala Met Thr Gln Asn Ile Thr Gly His Thr Ser Trp
        915                 920                 925

Thr Thr Val Ile Pro Arg Thr Gly Asn Trp Ala Val Ala Val Ser Ala
    930                 935                 940

Ala Asn Ser Lys Gly Ser Ser Leu Pro Thr Arg Ile Asn Ile Met Asn
945                 950                 955                 960

Leu Cys Glu Ala Gly Leu Leu Ala Pro Arg Gln Val Ser Ala Asn Ser
                965                 970                 975

Glu Gly Met Asp Asn Ile Leu Val Thr Trp Gln Pro Pro Arg Lys Asp
            980                 985                 990

Pro Ser Ala Val Gln Glu Tyr Val  Val Glu Trp Arg Glu  Leu His Pro
        995                 1000                1005

Gly Gly  Asp Thr Gln Val Pro  Leu Asn Trp Leu Arg  Ser Arg Pro
    1010                1015                1020
```

```
Tyr Asn  Val Ser Ala Leu Ile  Ser Glu Asn Ile Lys  Ser Tyr Ile
    1025                1030                1035

Cys Tyr  Glu Ile Arg Val Tyr  Ala Leu Ser Gly Asp  Gln Gly Gly
    1040                1045                1050

Cys Ser  Ser Ile Leu Gly Asn  Ser Lys His Lys Ala  Pro Leu Ser
    1055                1060                1065

Gly Pro  His Ile Asn Ala Ile  Thr Glu Glu Lys Gly  Ser Ile Leu
    1070                1075                1080

Ile Ser  Trp Asn Ser Ile Pro  Val Gln Glu Gln Met  Gly Cys Leu
    1085                1090                1095

Leu His  Tyr Arg Ile Tyr Trp  Lys Glu Arg Asp Ser  Asn Ser Gln
    1100                1105                1110

Pro Gln  Leu Cys Glu Ile Pro  Tyr Arg Val Ser Gln  Asn Ser His
    1115                1120                1125

Pro Ile  Asn Ser Leu Gln Pro  Arg Val Thr Tyr Val  Leu Trp Met
    1130                1135                1140

Thr Ala  Leu Thr Ala Ala Gly  Glu Ser Ser His Gly  Asn Glu Arg
    1145                1150                1155

Glu Phe  Cys Leu Gln Gly Lys  Ala Asn Trp Met Ala  Phe Val Ala
    1160                1165                1170

Pro Ser  Ile Cys Ile Ala Ile  Ile Met Val Gly Ile  Phe Ser Thr
    1175                1180                1185

His Tyr  Phe Gln Gln Lys Val  Phe Val Leu Leu Ala  Ala Leu Arg
    1190                1195                1200

Pro Gln  Trp Cys Ser Arg Glu  Ile Pro Asp Pro Ala  Asn Ser Thr
```

```
    1205                1210                1215

Cys Ala  Lys Lys Tyr Pro Ile  Ala Glu Glu Lys Thr  Gln Leu Pro
    1220                1225                1230

Leu Asp  Arg Leu Leu Ile Asp  Trp Pro Thr Pro Glu  Asp Pro Glu
    1235                1240                1245

Pro Leu  Val Ile Ser Glu Val  Leu His Gln Val Thr  Pro Val Phe
    1250                1255                1260

Arg His  Pro Pro Cys Ser Asn  Trp Pro Gln Arg Glu  Lys Gly Ile
    1265                1270                1275

Gln Gly  His Gln Ala Ser Glu  Lys Asp Met Met His  Ser Ala Ser
    1280                1285                1290

Ser Pro  Pro Pro Pro Arg Ala  Leu Gln Ala Glu Ser  Arg Gln Leu
    1295                1300                1305

Val Asp  Leu Tyr Lys Val Leu  Glu Ser Arg Gly Ser  Asp Pro Lys
    1310                1315                1320

Pro Glu  Asn Pro Ala Cys Pro  Trp Thr Val Leu Pro  Ala Gly Asp
    1325                1330                1335

Leu Pro  Thr His Asp Gly Tyr  Leu Pro Ser Asn Ile  Asp Asp Leu
    1340                1345                1350

Pro Ser  His Glu Ala Pro Leu  Ala Asp Ser Leu Glu  Glu Leu Glu
    1355                1360                1365

Pro Gln  His Ile Ser Leu Ser  Val Phe Pro Ser Ser  Ser Leu His
    1370                1375                1380

Pro Leu  Thr Phe Ser Cys Gly  Asp Lys Leu Thr Leu  Asp Gln Leu
    1385                1390                1395
```

Lys Met Arg Cys Asp Ser Leu Met Leu
    1400   1405

<210> 101
<211> 976
<212> PRT
<213> Artificial Sequence

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

<400> 101
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

His Ala Ala Arg Pro His Lys Cys Asp Ile Thr Leu Gln Glu Ile Ile
            20   25   30

Lys Thr Leu Asn Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu
        35   40   45

Thr Val Thr Asp Ile Phe Ala Ala Ser Lys Asn Thr Thr Glu Lys Glu
    50   55   60

Thr Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Phe Tyr Ser His His
65   70   75   80

Glu Lys Asp Thr Arg Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg
                85   90   95

His Lys Gln Leu Ile Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp
            100   105   110

Gly Leu Ala Gly Leu Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser
        115   120   125

Thr Leu Glu Asn Phe Leu Glu Arg Leu Lys Thr Ile Met Arg Glu Lys
    130   135   140

```
Tyr Ser Lys Cys Ser Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln
                165                 170                 175

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

Ser Thr Cys Glu Trp Lys Met Asn Gly Pro Thr Asn Cys Ser Thr Glu
        195                 200                 205

Leu Arg Leu Leu Tyr Gln Leu Val Phe Leu Leu Ser Glu Ala His Thr
    210                 215                 220

Cys Ile Pro Glu Asn Asn Gly Gly Ala Gly Cys Val Cys His Leu Leu
225                 230                 235                 240

Met Asp Asp Val Val Ser Ala Asp Asn Tyr Thr Leu Asp Leu Trp Ala
                245                 250                 255

Gly Gln Gln Leu Leu Trp Lys Gly Ser Phe Lys Pro Ser Glu His Val
            260                 265                 270

Lys Pro Arg Ala Pro Gly Asn Leu Thr Val His Thr Asn Val Ser Asp
        275                 280                 285

Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp Asn Tyr Leu
    290                 295                 300

Tyr Asn His Leu Thr Tyr Ala Val Asn Ile Trp Ser Glu Asn Asp Pro
305                 310                 315                 320

Ala Asp Phe Arg Ile Tyr Asn Val Thr Tyr Leu Glu Pro Ser Leu Arg
                325                 330                 335

Ile Ala Ala Ser Thr Leu Lys Ser Gly Ile Ser Tyr Arg Ala Arg Val
```

```
            340                 345                 350

Arg Ala Trp Ala Gln Cys Tyr Asn Thr Thr Trp Ser Glu Trp Ser Pro
        355                 360                 365

Ser Thr Lys Trp His Asn Ser Tyr Arg Glu Pro Phe Glu Gln His Leu
    370                 375                 380

Leu Leu Gly Val Ser Val Ser Cys Ile Val Ile Leu Ala Val Cys Leu
385                 390                 395                 400

Leu Cys Tyr Val Ser Ile Thr Lys Ile Lys Lys Glu Trp Trp Asp Gln
                405                 410                 415

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

Ala Gln Gly Ser Gln Trp Glu Lys Arg Ser Arg Gly Gln Glu Pro Ala
        435                 440                 445

Lys Cys Pro His Trp Lys Asn Cys Leu Thr Lys Leu Leu Pro Cys Phe
    450                 455                 460

Leu Glu His Asn Met Lys Arg Asp Glu Asp Pro His Lys Ala Ala Lys
465                 470                 475                 480

Glu Met Pro Phe Gln Gly Ser Gly Lys Ser Ala Trp Cys Pro Val Glu
                485                 490                 495

Ile Ser Lys Thr Val Leu Trp Pro Glu Ser Ile Ser Val Val Arg Cys
            500                 505                 510

Val Glu Leu Phe Glu Ala Pro Val Glu Cys Glu Glu Glu Glu Glu Val
        515                 520                 525

Glu Glu Glu Lys Gly Ser Phe Cys Ala Ser Pro Glu Ser Ser Arg Asp
    530                 535                 540
```

```
Asp Phe Gln Glu Gly Arg Glu Gly Ile Val Ala Arg Leu Thr Glu Ser
545                 550                 555                 560

Leu Phe Leu Asp Leu Leu Gly Glu Glu Asn Gly Gly Phe Cys Gln Gln
                565                 570                 575

Asp Met Gly Glu Ser Cys Leu Leu Pro Pro Ser Gly Ser Thr Ser Ala
            580                 585                 590

His Met Pro Trp Asp Glu Phe Pro Ser Ala Gly Pro Lys Glu Ala Pro
        595                 600                 605

Pro Trp Gly Lys Glu Gln Pro Leu His Leu Glu Pro Ser Pro Pro Ala
    610                 615                 620

Ser Pro Thr Gln Ser Pro Asp Asn Leu Thr Cys Thr Glu Thr Pro Leu
625                 630                 635                 640

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

Gln Ser Pro Cys Pro Arg Glu Leu Gly Pro Asp Pro Leu Leu Ala Arg
            660                 665                 670

His Leu Glu Glu Val Glu Pro Glu Met Pro Cys Val Pro Gln Leu Ser
        675                 680                 685

Glu Pro Thr Thr Val Pro Gln Pro Glu Pro Glu Thr Trp Glu Gln Ile
    690                 695                 700

Leu Arg Arg Asn Val Leu Gln His Gly Ala Ala Ala Ala Pro Val Ser
705                 710                 715                 720

Ala Pro Thr Ser Gly Tyr Gln Glu Phe Val His Ala Val Glu Gln Gly
                725                 730                 735

Gly Thr Gln Ala Ser Ala Val Val Gly Leu Gly Pro Pro Gly Glu Ala
```

```
            740                 745                 750

Gly Tyr Lys Ala Phe Ser Ser Leu Leu Ala Ser Ser Ala Val Ser Pro
        755                 760                 765

Glu Lys Cys Gly Phe Gly Ala Ser Ser Gly Glu Glu Gly Tyr Lys Pro
    770                 775                 780

Phe Gln Asp Leu Ile Pro Gly Cys Pro Gly Asp Pro Ala Pro Val Pro
785                 790                 795                 800

Val Pro Leu Phe Thr Phe Gly Leu Asp Arg Glu Pro Pro Arg Ser Pro
                805                 810                 815

Gln Ser Ser His Leu Pro Ser Ser Ser Pro Glu His Leu Gly Leu Glu
            820                 825                 830

Pro Gly Glu Lys Val Glu Asp Met Pro Lys Pro Pro Leu Pro Gln Glu
        835                 840                 845

Gln Ala Thr Asp Pro Leu Val Asp Ser Leu Gly Ser Gly Ile Val Tyr
    850                 855                 860

Ser Ala Leu Thr Cys His Leu Cys Gly His Leu Lys Gln Cys His Gly
865                 870                 875                 880

Gln Glu Asp Gly Gly Gln Thr Pro Val Met Ala Ser Pro Cys Cys Gly
                885                 890                 895

Cys Cys Cys Gly Asp Arg Ser Ser Pro Pro Thr Thr Pro Leu Arg Ala
            900                 905                 910

Pro Asp Pro Ser Pro Gly Gly Val Pro Leu Glu Ala Ser Leu Cys Pro
        915                 920                 925

Ala Ser Leu Ala Pro Ser Gly Ile Ser Glu Lys Ser Lys Ser Ser Ser
    930                 935                 940
```

Ser Phe His Pro Ala Pro Gly Asn Ala Gln Ser Ser Ser Gln Thr Pro
945 950 955 960

Lys Ile Val Asn Phe Val Ser Val Gly Pro Thr Tyr Met Arg Val Ser
965 970 975

<210> 102
<211> 523
<212> PRT
<213> Artificial Sequence

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

<400> 102
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro His Lys Cys Asp Ile Thr Leu Gln Glu Ile Ile
20 25 30

Lys Thr Leu Asn Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu
35 40 45

Thr Val Thr Asp Ile Phe Ala Ala Ser Lys Asn Thr Thr Glu Lys Glu
50 55 60

Thr Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Phe Tyr Ser His His
65 70 75 80

Glu Lys Asp Thr Arg Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg
85 90 95

His Lys Gln Leu Ile Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp
100 105 110

Gly Leu Ala Gly Leu Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser
115 120 125

```
Thr Leu Glu Asn Phe Leu Glu Arg Leu Lys Thr Ile Met Arg Glu Lys
    130                 135                 140

Tyr Ser Lys Cys Ser Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln
                165                 170                 175

Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly Asn Glu Asp Thr Thr Ala
            180                 185                 190

Asp Phe Phe Leu Thr Thr Met Pro Thr Asp Ser Leu Ser Val Ser Thr
        195                 200                 205

Leu Pro Leu Pro Glu Val Gln Cys Phe Val Phe Asn Val Glu Tyr Met
    210                 215                 220

Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro Gln Pro Thr Asn Leu Thr
225                 230                 235                 240

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

Ser His Tyr Leu Phe Ser Glu Glu Ile Thr Ser Gly Cys Gln Leu Gln
            260                 265                 270

Lys Lys Glu Ile His Leu Tyr Gln Thr Phe Val Val Gln Leu Gln Asp
        275                 280                 285

Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln Met Leu Lys Leu Gln Asn
    290                 295                 300

Leu Val Ile Pro Trp Ala Pro Glu Asn Leu Thr Leu His Lys Leu Ser
305                 310                 315                 320

Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn Arg Phe Leu Asn His Cys
```

```
                325                 330                 335

Leu Glu His Leu Val Gln Tyr Arg Thr Asp Trp Asp His Ser Trp Thr
            340                 345                 350

Glu Gln Ser Val Asp Tyr Arg His Lys Phe Ser Leu Pro Ser Val Asp
        355                 360                 365

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

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

Gly Ser Asn Thr Ser Lys Glu Asn Pro Phe Leu Phe Ala Leu Glu Ala
                405                 410                 415

Val Val Ile Ser Val Gly Ser Met Gly Leu Ile Ile Ser Leu Leu Cys
            420                 425                 430

Val Tyr Phe Trp Leu Glu Arg Thr Met Pro Arg Ile Pro Thr Leu Lys
        435                 440                 445

Asn Leu Glu Asp Leu Val Thr Glu Tyr His Gly Asn Phe Ser Ala Trp
    450                 455                 460

Ser Gly Val Ser Lys Gly Leu Ala Glu Ser Leu Gln Pro Asp Tyr Ser
465                 470                 475                 480

Glu Arg Leu Cys Leu Val Ser Glu Ile Pro Pro Lys Gly Gly Ala Leu
                485                 490                 495

Gly Glu Gly Pro Gly Ala Ser Pro Cys Asn Gln His Ser Pro Tyr Trp
            500                 505                 510

Ala Pro Pro Cys Tyr Thr Leu Lys Pro Glu Thr
        515                 520
```

<210> 103
<211> 582
<212> PRT
<213> Artificial Sequence

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

<400> 103
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro His Lys Cys Asp Ile Thr Leu Gln Glu Ile Ile
20 25 30

Lys Thr Leu Asn Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu
35 40 45

Thr Val Thr Asp Ile Phe Ala Ala Ser Lys Asn Thr Thr Glu Lys Glu
50 55 60

Thr Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Phe Tyr Ser His His
65 70 75 80

Glu Lys Asp Thr Arg Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg
85 90 95

His Lys Gln Leu Ile Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp
100 105 110

Gly Leu Ala Gly Leu Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser
115 120 125

Thr Leu Glu Asn Phe Leu Glu Arg Leu Lys Thr Ile Met Arg Glu Lys
130 135 140

Tyr Ser Lys Cys Ser Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
145 150 155 160

```
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln
                165                 170                 175

Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn
            180                 185                 190

Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn
        195                 200                 205

Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp Tyr Phe Ser His
    210                 215                 220

Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr Arg Arg Ser
225                 230                 235                 240

Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln
                245                 250                 255

Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu Val Glu Lys Cys
            260                 265                 270

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

Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp Leu Pro Gly
    290                 295                 300

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

Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe Arg Glu Gly Gln
                325                 330                 335

Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys Asp Ser Ser Phe
            340                 345                 350

Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn Ala Gly Lys Ile
```

```
        355                 360                 365

Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg Val Lys Pro Asp
    370                 375                 380

Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp Asp Leu Tyr Val
385                 390                 395                 400

Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys Leu Phe Tyr Glu
                405                 410                 415

Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn Val Phe Tyr Val
            420                 425                 430

Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg Asn Val Glu Asn
        435                 440                 445

Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr
    450                 455                 460

Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys
465                 470                 475                 480

Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly Lys Lys Arg Asn
                485                 490                 495

Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro Val Ile Val Ala
            500                 505                 510

Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg Leu Lys Ile Ile
        515                 520                 525

Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu Met Phe
    530                 535                 540

Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys Tyr Asp Ile Tyr
545                 550                 555                 560
```

Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val Leu Ile Glu Asn
565 570 575

Leu Lys Lys Ala Ser Gln
580

<210> 104
<211> 981
<212> PRT
<213> Artificial Sequence

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

<400> 104
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asn Thr Thr Glu Lys Glu Thr Phe Cys Arg Ala
20 25 30

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

Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His Lys Gln Leu Ile
50 55 60

Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly Leu
65 70 75 80

Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser Thr Leu Glu Asn Phe
85 90 95

Leu Glu Arg Leu Lys Thr Ile Met Arg Glu Lys Tyr Ser Lys Cys Ser
100 105 110

Ser Gly Gly Asn Gly Gly His Lys Cys Asp Ile Thr Leu Gln Glu Ile
115 120 125

```
Ile Lys Thr Leu Asn Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu
    130                 135                 140

Leu Thr Val Thr Asp Ile Phe Ala Ala Ser Lys Ser Gly Gly Gly Ser
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
                165                 170                 175

Gly Gly Ser Leu Gln Met Lys Val Leu Gln Glu Pro Thr Cys Val Ser
            180                 185                 190

Asp Tyr Met Ser Ile Ser Thr Cys Glu Trp Lys Met Asn Gly Pro Thr
        195                 200                 205

Asn Cys Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu Val Phe Leu Leu
    210                 215                 220

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

Val Cys His Leu Leu Met Asp Asp Val Val Ser Ala Asp Asn Tyr Thr
                245                 250                 255

Leu Asp Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys Gly Ser Phe Lys
            260                 265                 270

Pro Ser Glu His Val Lys Pro Arg Ala Pro Gly Asn Leu Thr Val His
        275                 280                 285

Thr Asn Val Ser Asp Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr Pro
    290                 295                 300

Pro Asp Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala Val Asn Ile Trp
305                 310                 315                 320

Ser Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn Val Thr Tyr Leu
```

```
                325                 330                 335

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

Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Cys Tyr Asn Thr Thr Trp
        355                 360                 365

Ser Glu Trp Ser Pro Ser Thr Lys Trp His Asn Ser Tyr Arg Glu Pro
    370                 375                 380

Phe Glu Gln His Leu Leu Leu Gly Val Ser Val Ser Cys Ile Val Ile
385                 390                 395                 400

Leu Ala Val Cys Leu Leu Cys Tyr Val Ser Ile Thr Lys Ile Lys Lys
                405                 410                 415

Glu Trp Trp Asp Gln Ile Pro Asn Pro Ala Arg Ser Arg Leu Val Ala
            420                 425                 430

Ile Ile Ile Gln Asp Ala Gln Gly Ser Gln Trp Glu Lys Arg Ser Arg
        435                 440                 445

Gly Gln Glu Pro Ala Lys Cys Pro His Trp Lys Asn Cys Leu Thr Lys
    450                 455                 460

Leu Leu Pro Cys Phe Leu Glu His Asn Met Lys Arg Asp Glu Asp Pro
465                 470                 475                 480

His Lys Ala Ala Lys Glu Met Pro Phe Gln Gly Ser Gly Lys Ser Ala
                485                 490                 495

Trp Cys Pro Val Glu Ile Ser Lys Thr Val Leu Trp Pro Glu Ser Ile
            500                 505                 510

Ser Val Val Arg Cys Val Glu Leu Phe Glu Ala Pro Val Glu Cys Glu
        515                 520                 525
```

```
Glu Glu Glu Glu Val Glu Glu Glu Lys Gly Ser Phe Cys Ala Ser Pro
    530                 535                 540

Glu Ser Ser Arg Asp Asp Phe Gln Glu Gly Arg Glu Gly Ile Val Ala
545                 550                 555                 560

Arg Leu Thr Glu Ser Leu Phe Leu Asp Leu Leu Gly Glu Glu Asn Gly
                565                 570                 575

Gly Phe Cys Gln Gln Asp Met Gly Glu Ser Cys Leu Leu Pro Pro Ser
            580                 585                 590

Gly Ser Thr Ser Ala His Met Pro Trp Asp Glu Phe Pro Ser Ala Gly
        595                 600                 605

Pro Lys Glu Ala Pro Pro Trp Gly Lys Glu Gln Pro Leu His Leu Glu
    610                 615                 620

Pro Ser Pro Pro Ala Ser Pro Thr Gln Ser Pro Asp Asn Leu Thr Cys
625                 630                 635                 640

Thr Glu Thr Pro Leu Val Ile Ala Gly Asn Pro Ala Tyr Arg Ser Phe
                645                 650                 655

Ser Asn Ser Leu Ser Gln Ser Pro Cys Pro Arg Glu Leu Gly Pro Asp
            660                 665                 670

Pro Leu Leu Ala Arg His Leu Glu Glu Val Glu Pro Glu Met Pro Cys
        675                 680                 685

Val Pro Gln Leu Ser Glu Pro Thr Thr Val Pro Gln Pro Glu Pro Glu
    690                 695                 700

Thr Trp Glu Gln Ile Leu Arg Arg Asn Val Leu Gln His Gly Ala Ala
705                 710                 715                 720

Ala Ala Pro Val Ser Ala Pro Thr Ser Gly Tyr Gln Glu Phe Val His
```

```
                725                 730                 735

Ala Val Glu Gln Gly Gly Thr Gln Ala Ser Ala Val Val Gly Leu Gly
            740                 745                 750

Pro Pro Gly Glu Ala Gly Tyr Lys Ala Phe Ser Ser Leu Leu Ala Ser
        755                 760                 765

Ser Ala Val Ser Pro Glu Lys Cys Gly Phe Gly Ala Ser Ser Gly Glu
    770                 775                 780

Glu Gly Tyr Lys Pro Phe Gln Asp Leu Ile Pro Gly Cys Pro Gly Asp
785                 790                 795                 800

Pro Ala Pro Val Pro Val Pro Leu Phe Thr Phe Gly Leu Asp Arg Glu
                805                 810                 815

Pro Pro Arg Ser Pro Gln Ser Ser His Leu Pro Ser Ser Ser Pro Glu
            820                 825                 830

His Leu Gly Leu Glu Pro Gly Glu Lys Val Glu Asp Met Pro Lys Pro
        835                 840                 845

Pro Leu Pro Gln Glu Gln Ala Thr Asp Pro Leu Val Asp Ser Leu Gly
    850                 855                 860

Ser Gly Ile Val Tyr Ser Ala Leu Thr Cys His Leu Cys Gly His Leu
865                 870                 875                 880

Lys Gln Cys His Gly Gln Glu Asp Gly Gly Gln Thr Pro Val Met Ala
                885                 890                 895

Ser Pro Cys Cys Gly Cys Cys Cys Gly Asp Arg Ser Ser Pro Pro Thr
            900                 905                 910

Thr Pro Leu Arg Ala Pro Asp Pro Ser Pro Gly Gly Val Pro Leu Glu
        915                 920                 925
```

Ala Ser Leu Cys Pro Ala Ser Leu Ala Pro Ser Gly Ile Ser Glu Lys
930 935 940

Ser Lys Ser Ser Ser Ser Phe His Pro Ala Pro Gly Asn Ala Gln Ser
945 950 955 960

Ser Ser Gln Thr Pro Lys Ile Val Asn Phe Val Ser Val Gly Pro Thr
965 970 975

Tyr Met Arg Val Ser
980

<210> 105
<211> 528
<212> PRT
<213> Artificial Sequence

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

<400> 105
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asn Thr Thr Glu Lys Glu Thr Phe Cys Arg Ala
20 25 30

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

Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His Lys Gln Leu Ile
50 55 60

Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly Leu
65 70 75 80

Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser Thr Leu Glu Asn Phe
85 90 95

```
Leu Glu Arg Leu Lys Thr Ile Met Arg Glu Lys Tyr Ser Lys Cys Ser
            100                 105                 110

Ser Gly Gly Asn Gly Gly His Lys Cys Asp Ile Thr Leu Gln Glu Ile
        115                 120                 125

Ile Lys Thr Leu Asn Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu
    130                 135                 140

Leu Thr Val Thr Asp Ile Phe Ala Ala Ser Lys Ser Gly Gly Gly Ser
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
                165                 170                 175

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

Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp Ser
        195                 200                 205

Leu Ser Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val Phe
    210                 215                 220

Asn Val Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro Gln
225                 230                 235                 240

Pro Thr Asn Leu Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn Asp
                245                 250                 255

Lys Val Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr Ser
            260                 265                 270

Gly Cys Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe Val
        275                 280                 285

Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln Met
```

290 295 300

Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu Thr
305 310 315 320

Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn Arg
325 330 335

Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp Trp
340 345 350

Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe Ser
355 360 365

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

Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp Ser
385 390 395 400

His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Pro Phe Leu
405 410 415

Phe Ala Leu Glu Ala Val Val Ile Ser Val Gly Ser Met Gly Leu Ile
420 425 430

Ile Ser Leu Leu Cys Val Tyr Phe Trp Leu Glu Arg Thr Met Pro Arg
435 440 445

Ile Pro Thr Leu Lys Asn Leu Glu Asp Leu Val Thr Glu Tyr His Gly
450 455 460

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

Gln Pro Asp Tyr Ser Glu Arg Leu Cys Leu Val Ser Glu Ile Pro Pro
485 490 495

Lys Gly Gly Ala Leu Gly Glu Gly Pro Gly Ala Ser Pro Cys Asn Gln
500 505 510

His Ser Pro Tyr Trp Ala Pro Pro Cys Tyr Thr Leu Lys Pro Glu Thr
515 520 525

<210> 106
<211> 587
<212> PRT
<213> Artificial Sequence

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

<400> 106
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asn Thr Thr Glu Lys Glu Thr Phe Cys Arg Ala
20 25 30

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

Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His Lys Gln Leu Ile
50 55 60

Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly Leu
65 70 75 80

Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser Thr Leu Glu Asn Phe
85 90 95

Leu Glu Arg Leu Lys Thr Ile Met Arg Glu Lys Tyr Ser Lys Cys Ser
100 105 110

Ser Gly Gly Asn Gly Gly His Lys Cys Asp Ile Thr Leu Gln Glu Ile
115 120 125

```
Ile Lys Thr Leu Asn Ser Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu
    130                 135                 140

Leu Thr Val Thr Asp Ile Phe Ala Ala Ser Lys Ser Gly Gly Gly Ser
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
                165                 170                 175

Gly Gly Ser Leu Gln Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln
            180                 185                 190

Pro Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val
        195                 200                 205

Ile Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu
    210                 215                 220

Trp Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro
225                 230                 235                 240

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

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

Leu Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala
        275                 280                 285

Val Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys
    290                 295                 300

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

Tyr Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile
```

```
                325                 330                 335

Phe Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val
            340                 345                 350

Lys Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp
        355                 360                 365

Asn Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser
    370                 375                 380

Arg Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn
385                 390                 395                 400

Asp Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg
                405                 410                 415

Cys Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His
            420                 425                 430

Asn Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu
        435                 440                 445

Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro
    450                 455                 460

Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys
465                 470                 475                 480

Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile
                485                 490                 495

Gly Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val
            500                 505                 510

Pro Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys
        515                 520                 525
```

Arg Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile
530 535 540

Phe Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys
545 550 555 560

Lys Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val
565 570 575

Val Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln
580 585

<210> 107
<211> 764
<212> PRT
<213> Artificial Sequence

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

<400> 107
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser
20 25 30

Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg
35 40 45

Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu
50 55 60

Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr
65 70 75 80

Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu
85 90 95

```
Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val
            100                 105                 110

Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg
        115                 120                 125

Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln
    130                 135                 140

Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala
145                 150                 155                 160

Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr
                165                 170                 175

Met Lys Ile Arg Asn Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
            180                 185                 190

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln His
        195                 200                 205

Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe Glu Ala Glu Phe
    210                 215                 220

Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn Gln Ser Glu Ser
225                 230                 235                 240

Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile Glu Ser Trp Asn
                245                 250                 255

Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp Leu Thr Ala Val
            260                 265                 270

Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala Arg Val Arg Ala
        275                 280                 285

Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr Asn Thr Arg Phe
```

```
    290                 295                 300

Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val Asn Leu Glu Ile
305                 310                 315                 320

His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro Arg Pro Lys Met
                325                 330                 335

Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser His Phe Arg Glu
            340                 345                 350

Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe Thr Phe Thr His
        355                 360                 365

Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr Ser Gly Glu Val
    370                 375                 380

Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala Ser Arg Ser Asn
385                 390                 395                 400

Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu Thr Arg Gln Tyr
                405                 410                 415

Phe Thr Val Thr Asn Val Ile Ile Phe Phe Ala Phe Val Leu Leu Leu
            420                 425                 430

Ser Gly Ala Leu Ala Tyr Cys Leu Ala Leu Gln Leu Tyr Val Arg Arg
        435                 440                 445

Arg Lys Lys Leu Pro Ser Val Leu Leu Phe Lys Lys Pro Ser Pro Phe
    450                 455                 460

Ile Phe Ile Ser Gln Arg Pro Ser Pro Glu Thr Gln Asp Thr Ile His
465                 470                 475                 480

Pro Leu Asp Glu Glu Ala Phe Leu Lys Val Ser Pro Glu Leu Lys Asn
                485                 490                 495
```

```
Leu Asp Leu His Gly Ser Thr Asp Ser Gly Phe Gly Ser Thr Lys Pro
            500                 505                 510

Ser Leu Gln Thr Glu Glu Pro Gln Phe Leu Leu Pro Asp Pro His Pro
        515                 520                 525

Gln Ala Asp Arg Thr Leu Gly Asn Arg Glu Pro Pro Val Leu Gly Asp
    530                 535                 540

Ser Cys Ser Ser Gly Ser Ser Asn Ser Thr Asp Ser Gly Ile Cys Leu
545                 550                 555                 560

Gln Glu Pro Ser Leu Ser Pro Ser Thr Gly Pro Thr Trp Glu Gln Gln
                565                 570                 575

Val Gly Ser Asn Ser Arg Gly Gln Asp Asp Ser Gly Ile Asp Leu Val
            580                 585                 590

Gln Asn Ser Glu Gly Arg Ala Gly Asp Thr Gln Gly Gly Ser Ala Leu
        595                 600                 605

Gly His His Ser Pro Pro Glu Pro Glu Val Pro Gly Glu Glu Asp Pro
    610                 615                 620

Ala Ala Val Ala Phe Gln Gly Tyr Leu Arg Gln Thr Arg Cys Ala Glu
625                 630                 635                 640

Glu Lys Ala Thr Lys Thr Gly Cys Leu Glu Glu Glu Ser Pro Leu Thr
                645                 650                 655

Asp Gly Leu Gly Pro Lys Phe Gly Arg Cys Leu Val Asp Glu Ala Gly
            660                 665                 670

Leu His Pro Pro Ala Leu Ala Lys Gly Tyr Leu Lys Gln Asp Pro Leu
        675                 680                 685

Glu Met Thr Leu Ala Ser Ser Gly Ala Pro Thr Gly Gln Trp Asn Gln
```

690 695 700

Pro Thr Glu Glu Trp Ser Leu Leu Ala Leu Ser Ser Cys Ser Asp Leu
705 710 715 720

Gly Ile Ser Asp Trp Ser Phe Ala His Asp Leu Ala Pro Leu Gly Cys
725 730 735

Val Ala Ala Pro Gly Gly Leu Leu Gly Ser Phe Asn Ser Asp Leu Val
740 745 750

Thr Leu Pro Leu Ile Ser Ser Leu Gln Ser Ser Glu
755 760

<210> 108
<211> 513
<212> PRT
<213> Artificial Sequence

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

<400> 108
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser
20 25 30

Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg
35 40 45

Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu
50 55 60

Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr
65 70 75 80

Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu

```
                85                  90                  95

Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val
            100                 105                 110

Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg
        115                 120                 125

Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln
    130                 135                 140

Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala
145                 150                 155                 160

Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr
                165                 170                 175

Met Lys Ile Arg Asn Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
            180                 185                 190

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Met
        195                 200                 205

Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val Asn Phe Lys Asn
    210                 215                 220

Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly Asn Leu Thr Phe
225                 230                 235                 240

Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp Lys Cys Met Asn
                245                 250                 255

Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly Asp
            260                 265                 270

His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp Trp
        275                 280                 285
```

```
Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro Pro
    290                 295                 300

Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe Leu
305                 310                 315                 320

Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn Val
                325                 330                 335

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

Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg Asn
        355                 360                 365

Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu Pro
    370                 375                 380

Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln Thr
385                 390                 395                 400

Thr His Asp Glu Thr Val Pro Ser Trp Met Val Ala Val Ile Leu Met
                405                 410                 415

Ala Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly Cys Phe Ala Leu
            420                 425                 430

Leu Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala Phe Ser Pro Arg Asn
        435                 440                 445

Ser Leu Pro Gln His Leu Lys Glu Phe Leu Gly His Pro His His Asn
    450                 455                 460

Thr Leu Leu Phe Phe Ser Phe Pro Leu Ser Asp Glu Asn Asp Val Phe
465                 470                 475                 480

Asp Lys Leu Ser Val Ile Ala Glu Asp Ser Glu Ser Gly Lys Gln Asn
```

485 490 495

Pro Gly Asp Ser Cys Ser Leu Gly Thr Pro Pro Gly Gln Gly Pro Gln
500 505 510

Ser

<210> 109
<211> 770
<212> PRT
<213> Artificial Sequence

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

<400> 109
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser
20 25 30

Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg
35 40 45

Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu
50 55 60

Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr
65 70 75 80

Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu
85 90 95

Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val
100 105 110

Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg

```
        115                 120                 125

Cys His Arg Phe Leu Pro Cys Glu Asn Gly Gly Gly Ser Gly Gly Lys
    130                 135                 140

Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu
145                 150                 155                 160

Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr
                165                 170                 175

Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn Ser Gly Gly Gly Ser
            180                 185                 190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        195                 200                 205

Gly Gly Ser Leu Gln His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val
    210                 215                 220

Trp Phe Glu Ala Glu Phe Phe His His Ile Leu His Trp Thr Pro Ile
225                 230                 235                 240

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

Gly Ile Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser
            260                 265                 270

Tyr Asp Leu Thr Ala Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr
        275                 280                 285

Arg Ala Arg Val Arg Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr
    290                 295                 300

Val Thr Asn Thr Arg Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly
305                 310                 315                 320
```

```
Ser Val Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln
                325                 330                 335

Leu Pro Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile
            340                 345                 350

Phe Ser His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly
        355                 360                 365

Asn Phe Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu
    370                 375                 380

Leu Thr Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser
385                 390                 395                 400

Val Ala Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile
                405                 410                 415

Ser Leu Thr Arg Gln Tyr Phe Thr Val Thr Asn Val Ile Ile Phe Phe
            420                 425                 430

Ala Phe Val Leu Leu Leu Ser Gly Ala Leu Ala Tyr Cys Leu Ala Leu
        435                 440                 445

Gln Leu Tyr Val Arg Arg Arg Lys Lys Leu Pro Ser Val Leu Leu Phe
    450                 455                 460

Lys Lys Pro Ser Pro Phe Ile Phe Ile Ser Gln Arg Pro Ser Pro Glu
465                 470                 475                 480

Thr Gln Asp Thr Ile His Pro Leu Asp Glu Glu Ala Phe Leu Lys Val
                485                 490                 495

Ser Pro Glu Leu Lys Asn Leu Asp Leu His Gly Ser Thr Asp Ser Gly
            500                 505                 510

Phe Gly Ser Thr Lys Pro Ser Leu Gln Thr Glu Glu Pro Gln Phe Leu
```

```
        515                 520                 525

Leu Pro Asp Pro His Pro Gln Ala Asp Arg Thr Leu Gly Asn Arg Glu
    530                 535                 540

Pro Pro Val Leu Gly Asp Ser Cys Ser Ser Gly Ser Ser Asn Ser Thr
545                 550                 555                 560

Asp Ser Gly Ile Cys Leu Gln Glu Pro Ser Leu Ser Pro Ser Thr Gly
                565                 570                 575

Pro Thr Trp Glu Gln Gln Val Gly Ser Asn Ser Arg Gly Gln Asp Asp
            580                 585                 590

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

Gln Gly Gly Ser Ala Leu Gly His His Ser Pro Pro Glu Pro Glu Val
    610                 615                 620

Pro Gly Glu Glu Asp Pro Ala Ala Val Ala Phe Gln Gly Tyr Leu Arg
625                 630                 635                 640

Gln Thr Arg Cys Ala Glu Glu Lys Ala Thr Lys Thr Gly Cys Leu Glu
                645                 650                 655

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

Leu Val Asp Glu Ala Gly Leu His Pro Pro Ala Leu Ala Lys Gly Tyr
        675                 680                 685

Leu Lys Gln Asp Pro Leu Glu Met Thr Leu Ala Ser Ser Gly Ala Pro
    690                 695                 700

Thr Gly Gln Trp Asn Gln Pro Thr Glu Glu Trp Ser Leu Leu Ala Leu
705                 710                 715                 720
```

Ser Ser Cys Ser Asp Leu Gly Ile Ser Asp Trp Ser Phe Ala His Asp
725 730 735

Leu Ala Pro Leu Gly Cys Val Ala Ala Pro Gly Gly Leu Leu Gly Ser
740 745 750

Phe Asn Ser Asp Leu Val Thr Leu Pro Leu Ile Ser Ser Leu Gln Ser
755 760 765

Ser Glu
770

<210> 110
<211> 519
<212> PRT
<213> Artificial Sequence

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

<400> 110
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser
20 25 30

Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg
35 40 45

Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu
50 55 60

Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr
65 70 75 80

Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu
85 90 95

```
Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val
            100                 105                 110

Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg
        115                 120                 125

Cys His Arg Phe Leu Pro Cys Glu Asn Gly Gly Gly Ser Gly Gly Lys
    130                 135                 140

Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu
145                 150                 155                 160

Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr
                165                 170                 175

Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn Ser Gly Gly Gly Ser
            180                 185                 190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        195                 200                 205

Gly Gly Ser Leu Gln Met Val Pro Pro Pro Glu Asn Val Arg Met Asn
    210                 215                 220

Ser Val Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala
225                 230                 235                 240

Lys Gly Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe
                245                 250                 255

Gln Asp Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser
            260                 265                 270

Leu Ser Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala
        275                 280                 285

Asp Glu His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp
```

```
    290                 295                 300

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

Leu His Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr
                325                 330                 335

Trp Thr Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr
            340                 345                 350

Trp Lys Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp
        355                 360                 365

Phe Glu Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln
    370                 375                 380

Val Arg Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu
385                 390                 395                 400

Pro Val Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Trp Met
                405                 410                 415

Val Ala Val Ile Leu Met Ala Ser Val Phe Met Val Cys Leu Ala Leu
            420                 425                 430

Leu Gly Cys Phe Ala Leu Leu Trp Cys Val Tyr Lys Lys Thr Lys Tyr
        435                 440                 445

Ala Phe Ser Pro Arg Asn Ser Leu Pro Gln His Leu Lys Glu Phe Leu
    450                 455                 460

Gly His Pro His His Asn Thr Leu Leu Phe Phe Ser Phe Pro Leu Ser
465                 470                 475                 480

Asp Glu Asn Asp Val Phe Asp Lys Leu Ser Val Ile Ala Glu Asp Ser
                485                 490                 495
```

Glu Ser Gly Lys Gln Asn Pro Gly Asp Ser Cys Ser Leu Gly Thr Pro
500 505 510

Pro Gly Gln Gly Pro Gln Ser
515

<210> 111
<211> 779
<212> PRT
<213> Artificial Sequence

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

<400> 111
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met
20 25 30

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

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

Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn
65 70 75 80

Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln
85 90 95

Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn
100 105 110

Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn Gly Gly Gly Gly
115 120 125

```
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Pro Gly Gln Gly
    130                 135                 140

Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro Asn
145                 150                 155                 160

Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe Phe
                165                 170                 175

Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu
            180                 185                 190

Glu Asp Phe Lys Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        195                 200                 205

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln His Gly
    210                 215                 220

Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe Glu Ala Glu Phe Phe
225                 230                 235                 240

His His Ile Leu His Trp Thr Pro Ile Pro Asn Gln Ser Glu Ser Thr
                245                 250                 255

Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile Glu Ser Trp Asn Ser
            260                 265                 270

Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp Leu Thr Ala Val Thr
        275                 280                 285

Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala Arg Val Arg Ala Val
    290                 295                 300

Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr Asn Thr Arg Phe Ser
305                 310                 315                 320

Val Asp Glu Val Thr Leu Thr Val Gly Ser Val Asn Leu Glu Ile His
```

```
                325                 330                 335

Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro Arg Pro Lys Met Ala
            340                 345                 350

Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser His Phe Arg Glu Tyr
        355                 360                 365

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

Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr Ser Gly Glu Val Gly
385                 390                 395                 400

Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala Ser Arg Ser Asn Lys
                405                 410                 415

Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu Thr Arg Gln Tyr Phe
            420                 425                 430

Thr Val Thr Asn Val Ile Ile Phe Phe Ala Phe Val Leu Leu Leu Ser
        435                 440                 445

Gly Ala Leu Ala Tyr Cys Leu Ala Leu Gln Leu Tyr Val Arg Arg Arg
    450                 455                 460

Lys Lys Leu Pro Ser Val Leu Leu Phe Lys Lys Pro Ser Pro Phe Ile
465                 470                 475                 480

Phe Ile Ser Gln Arg Pro Ser Pro Glu Thr Gln Asp Thr Ile His Pro
                485                 490                 495

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

Asp Leu His Gly Ser Thr Asp Ser Gly Phe Gly Ser Thr Lys Pro Ser
        515                 520                 525
```

```
Leu Gln Thr Glu Glu Pro Gln Phe Leu Leu Pro Asp Pro His Pro Gln
    530                 535                 540

Ala Asp Arg Thr Leu Gly Asn Arg Glu Pro Pro Val Leu Gly Asp Ser
545                 550                 555                 560

Cys Ser Ser Gly Ser Ser Asn Ser Thr Asp Ser Gly Ile Cys Leu Gln
                565                 570                 575

Glu Pro Ser Leu Ser Pro Ser Thr Gly Pro Thr Trp Glu Gln Gln Val
            580                 585                 590

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

Asn Ser Glu Gly Arg Ala Gly Asp Thr Gln Gly Gly Ser Ala Leu Gly
    610                 615                 620

His His Ser Pro Pro Glu Pro Glu Val Pro Gly Glu Glu Asp Pro Ala
625                 630                 635                 640

Ala Val Ala Phe Gln Gly Tyr Leu Arg Gln Thr Arg Cys Ala Glu Glu
                645                 650                 655

Lys Ala Thr Lys Thr Gly Cys Leu Glu Glu Glu Ser Pro Leu Thr Asp
            660                 665                 670

Gly Leu Gly Pro Lys Phe Gly Arg Cys Leu Val Asp Glu Ala Gly Leu
        675                 680                 685

His Pro Pro Ala Leu Ala Lys Gly Tyr Leu Lys Gln Asp Pro Leu Glu
    690                 695                 700

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

Thr Glu Glu Trp Ser Leu Leu Ala Leu Ser Ser Cys Ser Asp Leu Gly
```

725 730 735

Ile Ser Asp Trp Ser Phe Ala His Asp Leu Ala Pro Leu Gly Cys Val
740 745 750

Ala Ala Pro Gly Gly Leu Leu Gly Ser Phe Asn Ser Asp Leu Val Thr
755 760 765

Leu Pro Leu Ile Ser Ser Leu Gln Ser Ser Glu
770 775

<210> 112
<211> 528
<212> PRT
<213> Artificial Sequence

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

<400> 112
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met
20 25 30

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

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

Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn
65 70 75 80

Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln
85 90 95

Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn

```
            100                 105                 110

Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Pro Gly Gln Gly
    130                 135                 140

Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro Asn
145                 150                 155                 160

Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe Phe
                165                 170                 175

Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu
            180                 185                 190

Glu Asp Phe Lys Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        195                 200                 205

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Met Val
    210                 215                 220

Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val Asn Phe Lys Asn Ile
225                 230                 235                 240

Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly Asn Leu Thr Phe Thr
                245                 250                 255

Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp Lys Cys Met Asn Thr
            260                 265                 270

Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly Asp His
        275                 280                 285

Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp Trp Val
    290                 295                 300
```

```
Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro Pro Gly
305                 310                 315                 320

Met Gln Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe Leu Ala
                325                 330                 335

Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn Val Tyr
            340                 345                 350

Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr Asp Glu
        355                 360                 365

Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg Asn Leu
    370                 375                 380

Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu Pro Asp
385                 390                 395                 400

Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln Thr Thr
                405                 410                 415

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

Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly Cys Phe Ala Leu Leu
        435                 440                 445

Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala Phe Ser Pro Arg Asn Ser
    450                 455                 460

Leu Pro Gln His Leu Lys Glu Phe Leu Gly His Pro His His Asn Thr
465                 470                 475                 480

Leu Leu Phe Phe Ser Phe Pro Leu Ser Asp Glu Asn Asp Val Phe Asp
                485                 490                 495

Lys Leu Ser Val Ile Ala Glu Asp Ser Glu Ser Gly Lys Gln Asn Pro
```

500 505 510

Gly Asp Ser Cys Ser Leu Gly Thr Pro Pro Gly Gln Gly Pro Gln Ser
515 520 525

<210> 113
<211> 939
<212> PRT
<213> Artificial Sequence

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

<400> 113
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser
20 25 30

Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg
35 40 45

Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu
50 55 60

Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr
65 70 75 80

Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu
85 90 95

Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val
100 105 110

Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg
115 120 125

Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln

```
    130                 135                 140

Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala
145                 150                 155                 160

Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr
                165                 170                 175

Met Lys Ile Arg Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
            180                 185                 190

Gly Gly Gly Ser Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys
        195                 200                 205

Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp
    210                 215                 220

Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp
225                 230                 235                 240

Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu
                245                 250                 255

Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val
            260                 265                 270

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

Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys
    290                 295                 300

His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val
305                 310                 315                 320

Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met
                325                 330                 335
```

```
Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met
            340                 345                 350

Lys Ile Arg Asn Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        355                 360                 365

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln His Gly
    370                 375                 380

Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe Glu Ala Glu Phe Phe
385                 390                 395                 400

His His Ile Leu His Trp Thr Pro Ile Pro Asn Gln Ser Glu Ser Thr
                405                 410                 415

Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile Glu Ser Trp Asn Ser
            420                 425                 430

Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp Leu Thr Ala Val Thr
        435                 440                 445

Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala Arg Val Arg Ala Val
    450                 455                 460

Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr Asn Thr Arg Phe Ser
465                 470                 475                 480

Val Asp Glu Val Thr Leu Thr Val Gly Ser Val Asn Leu Glu Ile His
                485                 490                 495

Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro Arg Pro Lys Met Ala
            500                 505                 510

Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser His Phe Arg Glu Tyr
        515                 520                 525

Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe Thr Phe Thr His Lys
```

```
    530                 535                 540

Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr Ser Gly Glu Val Gly
545                 550                 555                 560

Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala Ser Arg Ser Asn Lys
                565                 570                 575

Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu Thr Arg Gln Tyr Phe
            580                 585                 590

Thr Val Thr Asn Val Ile Ile Phe Phe Ala Phe Val Leu Leu Leu Ser
        595                 600                 605

Gly Ala Leu Ala Tyr Cys Leu Ala Leu Gln Leu Tyr Val Arg Arg Arg
    610                 615                 620

Lys Lys Leu Pro Ser Val Leu Leu Phe Lys Lys Pro Ser Pro Phe Ile
625                 630                 635                 640

Phe Ile Ser Gln Arg Pro Ser Pro Glu Thr Gln Asp Thr Ile His Pro
                645                 650                 655

Leu Asp Glu Glu Ala Phe Leu Lys Val Ser Pro Glu Leu Lys Asn Leu
            660                 665                 670

Asp Leu His Gly Ser Thr Asp Ser Gly Phe Gly Ser Thr Lys Pro Ser
        675                 680                 685

Leu Gln Thr Glu Glu Pro Gln Phe Leu Leu Pro Asp Pro His Pro Gln
    690                 695                 700

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

Cys Ser Ser Gly Ser Ser Asn Ser Thr Asp Ser Gly Ile Cys Leu Gln
                725                 730                 735
```

```
Glu Pro Ser Leu Ser Pro Ser Thr Gly Pro Thr Trp Glu Gln Gln Val
            740                 745                 750

Gly Ser Asn Ser Arg Gly Gln Asp Asp Ser Gly Ile Asp Leu Val Gln
        755                 760                 765

Asn Ser Glu Gly Arg Ala Gly Asp Thr Gln Gly Gly Ser Ala Leu Gly
    770                 775                 780

His His Ser Pro Pro Glu Pro Glu Val Pro Gly Glu Glu Asp Pro Ala
785                 790                 795                 800

Ala Val Ala Phe Gln Gly Tyr Leu Arg Gln Thr Arg Cys Ala Glu Glu
                805                 810                 815

Lys Ala Thr Lys Thr Gly Cys Leu Glu Glu Glu Ser Pro Leu Thr Asp
            820                 825                 830

Gly Leu Gly Pro Lys Phe Gly Arg Cys Leu Val Asp Glu Ala Gly Leu
        835                 840                 845

His Pro Pro Ala Leu Ala Lys Gly Tyr Leu Lys Gln Asp Pro Leu Glu
    850                 855                 860

Met Thr Leu Ala Ser Ser Gly Ala Pro Thr Gly Gln Trp Asn Gln Pro
865                 870                 875                 880

Thr Glu Glu Trp Ser Leu Leu Ala Leu Ser Ser Cys Ser Asp Leu Gly
                885                 890                 895

Ile Ser Asp Trp Ser Phe Ala His Asp Leu Ala Pro Leu Gly Cys Val
            900                 905                 910

Ala Ala Pro Gly Gly Leu Leu Gly Ser Phe Asn Ser Asp Leu Val Thr
        915                 920                 925

Leu Pro Leu Ile Ser Ser Leu Gln Ser Ser Glu
```

930 935

<210> 114
<211> 688
<212> PRT
<213> Artificial Sequence

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

<400> 114
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser
20 25 30

Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg
35 40 45

Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu
50 55 60

Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr
65 70 75 80

Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu
85 90 95

Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val
100 105 110

Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg
115 120 125

Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln
130 135 140

Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala

```
145                 150                 155                 160

Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr
                165                 170                 175

Met Lys Ile Arg Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
            180                 185                 190

Gly Gly Gly Ser Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys
        195                 200                 205

Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp
    210                 215                 220

Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp
225                 230                 235                 240

Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu
                245                 250                 255

Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val
            260                 265                 270

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

Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys
    290                 295                 300

His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val
305                 310                 315                 320

Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met
                325                 330                 335

Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met
            340                 345                 350
```

```
Lys Ile Arg Asn Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        355                 360                 365

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Met Val
    370                 375                 380

Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val Asn Phe Lys Asn Ile
385                 390                 395                 400

Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly Asn Leu Thr Phe Thr
                405                 410                 415

Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp Lys Cys Met Asn Thr
            420                 425                 430

Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly Asp His
        435                 440                 445

Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp Trp Val
    450                 455                 460

Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro Pro Gly
465                 470                 475                 480

Met Gln Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe Leu Ala
                485                 490                 495

Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn Val Tyr
            500                 505                 510

Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr Asp Glu
        515                 520                 525

Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg Asn Leu
    530                 535                 540

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

545 550 555 560

Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln Thr Thr
565 570 575

His Asp Glu Thr Val Pro Ser Trp Met Val Ala Val Ile Leu Met Ala
580 585 590

Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly Cys Phe Ala Leu Leu
595 600 605

Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala Phe Ser Pro Arg Asn Ser
610 615 620

Leu Pro Gln His Leu Lys Glu Phe Leu Gly His Pro His His Asn Thr
625 630 635 640

Leu Leu Phe Phe Ser Phe Pro Leu Ser Asp Glu Asn Asp Val Phe Asp
645 650 655

Lys Leu Ser Val Ile Ala Glu Asp Ser Glu Ser Gly Lys Gln Asn Pro
660 665 670

Gly Asp Ser Cys Ser Leu Gly Thr Pro Pro Gly Gln Gly Pro Gln Ser
675 680 685

<210> 115
<211> 575
<212> PRT
<213> Artificial Sequence

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

<400> 115
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Leu Thr Cys Leu Gly Gly Phe Ala Ser Pro Gly

```
            20                  25                  30

Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu Glu Leu Val
        35                  40                  45

Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly Ser Met Val
    50                  55                  60

Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser
65                  70                  75                  80

Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr Gln Arg Met
                85                  90                  95

Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln Phe Ser Ser
            100                 105                 110

Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe Val Lys Asp
        115                 120                 125

Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg Phe Asn Ser
    130                 135                 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Ser Leu Gln Gly Gly Gly Gly Ala Ala Pro
                165                 170                 175

Thr Glu Thr Gln Pro Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn
            180                 185                 190

Leu Cys Thr Val Ile Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser
        195                 200                 205

Asn Cys Ser Leu Trp Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys
    210                 215                 220
```

```
Lys Ile Ala Pro Glu Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu
225                 230                 235                 240


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


Lys Pro Ser Ile Leu Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp
            260                 265                 270


Pro Glu Ser Ala Val Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser
        275                 280                 285


Tyr Met Lys Cys Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr
    290                 295                 300


Asn Tyr Thr Leu Tyr Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln
305                 310                 315                 320


Cys Glu Asn Ile Phe Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp
                325                 330                 335


Leu Thr Lys Val Lys Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile
            340                 345                 350


Met Val Lys Asp Asn Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val
        355                 360                 365


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


Ser Phe His Asn Asp Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn
385                 390                 395                 400


Phe Ile Ser Arg Cys Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln
                405                 410                 415


Thr Glu Thr His Asn Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn
```

```
            420                 425                 430

Pro Glu Phe Glu Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro
        435                 440                 445

Gly Val Leu Pro Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr
    450                 455                 460

Asn Lys Leu Cys Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln
465                 470                 475                 480

Glu Met Ser Ile Gly Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met
                485                 490                 495

Leu Leu Ile Val Pro Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu
            500                 505                 510

Leu Tyr Leu Lys Arg Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp
        515                 520                 525

Pro Gly Lys Ile Phe Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr
    530                 535                 540

Leu His Trp Lys Lys Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu
545                 550                 555                 560

Thr Asp Ser Val Val Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln
                565                 570                 575


<210> 116
<211> 969
<212> PRT
<213> Artificial Sequence

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

<400> 116
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
```

```
1               5                   10                  15

His Ala Ala Arg Pro Leu Thr Cys Leu Gly Gly Phe Ala Ser Pro Gly
            20                  25                  30

Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu Glu Leu Val
        35                  40                  45

Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly Ser Met Val
    50                  55                  60

Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser
65                  70                  75                  80

Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr Gln Arg Met
                85                  90                  95

Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln Phe Ser Ser
            100                 105                 110

Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe Val Lys Asp
        115                 120                 125

Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg Phe Asn Ser
    130                 135                 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Ser Leu Gln Met Lys Val Leu Gln Glu Pro
                165                 170                 175

Thr Cys Val Ser Asp Tyr Met Ser Ile Ser Thr Cys Glu Trp Lys Met
            180                 185                 190

Asn Gly Pro Thr Asn Cys Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu
        195                 200                 205
```

```
Val Phe Leu Leu Ser Glu Ala His Thr Cys Ile Pro Glu Asn Asn Gly
    210                 215                 220

Gly Ala Gly Cys Val Cys His Leu Leu Met Asp Asp Val Val Ser Ala
225                 230                 235                 240

Asp Asn Tyr Thr Leu Asp Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys
                245                 250                 255

Gly Ser Phe Lys Pro Ser Glu His Val Lys Pro Arg Ala Pro Gly Asn
            260                 265                 270

Leu Thr Val His Thr Asn Val Ser Asp Thr Leu Leu Leu Thr Trp Ser
        275                 280                 285

Asn Pro Tyr Pro Pro Asp Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala
    290                 295                 300

Val Asn Ile Trp Ser Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn
305                 310                 315                 320

Val Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys
                325                 330                 335

Ser Gly Ile Ser Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Cys Tyr
            340                 345                 350

Asn Thr Thr Trp Ser Glu Trp Ser Pro Ser Thr Lys Trp His Asn Ser
        355                 360                 365

Tyr Arg Glu Pro Phe Glu Gln His Leu Leu Leu Gly Val Ser Val Ser
    370                 375                 380

Cys Ile Val Ile Leu Ala Val Cys Leu Leu Cys Tyr Val Ser Ile Thr
385                 390                 395                 400

Lys Ile Lys Lys Glu Trp Trp Asp Gln Ile Pro Asn Pro Ala Arg Ser
```

```
                405                 410                 415

Arg Leu Val Ala Ile Ile Ile Gln Asp Ala Gln Gly Ser Gln Trp Glu
            420                 425                 430

Lys Arg Ser Arg Gly Gln Glu Pro Ala Lys Cys Pro His Trp Lys Asn
        435                 440                 445

Cys Leu Thr Lys Leu Leu Pro Cys Phe Leu Glu His Asn Met Lys Arg
    450                 455                 460

Asp Glu Asp Pro His Lys Ala Ala Lys Glu Met Pro Phe Gln Gly Ser
465                 470                 475                 480

Gly Lys Ser Ala Trp Cys Pro Val Glu Ile Ser Lys Thr Val Leu Trp
                485                 490                 495

Pro Glu Ser Ile Ser Val Val Arg Cys Val Glu Leu Phe Glu Ala Pro
            500                 505                 510

Val Glu Cys Glu Glu Glu Glu Glu Val Glu Glu Glu Lys Gly Ser Phe
        515                 520                 525

Cys Ala Ser Pro Glu Ser Ser Arg Asp Asp Phe Gln Glu Gly Arg Glu
    530                 535                 540

Gly Ile Val Ala Arg Leu Thr Glu Ser Leu Phe Leu Asp Leu Leu Gly
545                 550                 555                 560

Glu Glu Asn Gly Gly Phe Cys Gln Gln Asp Met Gly Glu Ser Cys Leu
                565                 570                 575

Leu Pro Pro Ser Gly Ser Thr Ser Ala His Met Pro Trp Asp Glu Phe
            580                 585                 590

Pro Ser Ala Gly Pro Lys Glu Ala Pro Pro Trp Gly Lys Glu Gln Pro
        595                 600                 605
```

```
Leu His Leu Glu Pro Ser Pro Pro Ala Ser Pro Thr Gln Ser Pro Asp
    610                 615                 620

Asn Leu Thr Cys Thr Glu Thr Pro Leu Val Ile Ala Gly Asn Pro Ala
625                 630                 635                 640

Tyr Arg Ser Phe Ser Asn Ser Leu Ser Gln Ser Pro Cys Pro Arg Glu
                645                 650                 655

Leu Gly Pro Asp Pro Leu Leu Ala Arg His Leu Glu Glu Val Glu Pro
            660                 665                 670

Glu Met Pro Cys Val Pro Gln Leu Ser Glu Pro Thr Thr Val Pro Gln
        675                 680                 685

Pro Glu Pro Glu Thr Trp Glu Gln Ile Leu Arg Arg Asn Val Leu Gln
    690                 695                 700

His Gly Ala Ala Ala Ala Pro Val Ser Ala Pro Thr Ser Gly Tyr Gln
705                 710                 715                 720

Glu Phe Val His Ala Val Glu Gln Gly Gly Thr Gln Ala Ser Ala Val
                725                 730                 735

Val Gly Leu Gly Pro Pro Gly Glu Ala Gly Tyr Lys Ala Phe Ser Ser
            740                 745                 750

Leu Leu Ala Ser Ser Ala Val Ser Pro Glu Lys Cys Gly Phe Gly Ala
        755                 760                 765

Ser Ser Gly Glu Glu Gly Tyr Lys Pro Phe Gln Asp Leu Ile Pro Gly
    770                 775                 780

Cys Pro Gly Asp Pro Ala Pro Val Pro Val Pro Leu Phe Thr Phe Gly
785                 790                 795                 800

Leu Asp Arg Glu Pro Pro Arg Ser Pro Gln Ser Ser His Leu Pro Ser
```

805 810 815

Ser Ser Pro Glu His Leu Gly Leu Glu Pro Gly Glu Lys Val Glu Asp
820 825 830

Met Pro Lys Pro Pro Leu Pro Gln Glu Gln Ala Thr Asp Pro Leu Val
835 840 845

Asp Ser Leu Gly Ser Gly Ile Val Tyr Ser Ala Leu Thr Cys His Leu
850 855 860

Cys Gly His Leu Lys Gln Cys His Gly Gln Glu Asp Gly Gly Gln Thr
865 870 875 880

Pro Val Met Ala Ser Pro Cys Cys Gly Cys Cys Cys Gly Asp Arg Ser
885 890 895

Ser Pro Pro Thr Thr Pro Leu Arg Ala Pro Asp Pro Ser Pro Gly Gly
900 905 910

Val Pro Leu Glu Ala Ser Leu Cys Pro Ala Ser Leu Ala Pro Ser Gly
915 920 925

Ile Ser Glu Lys Ser Lys Ser Ser Ser Ser Phe His Pro Ala Pro Gly
930 935 940

Asn Ala Gln Ser Ser Ser Gln Thr Pro Lys Ile Val Asn Phe Val Ser
945 950 955 960

Val Gly Pro Thr Tyr Met Arg Val Ser
965

<210> 117
<211> 580
<212> PRT
<213> Artificial Sequence

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

polypeptide

<400> 117

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

His Ala Ala Arg Pro Val Ser Ala Gly Gln Phe Ser Ser Leu His Val
            20                  25                  30

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

His Leu Lys Lys Leu Phe Arg Glu Gly Arg Phe Asn Gly Gly Gly Gly
    50                  55                  60

Ser Leu Thr Cys Leu Gly Gly Phe Ala Ser Pro Gly Pro Val Pro Pro
65                  70                  75                  80

Ser Thr Ala Leu Arg Glu Leu Ile Glu Glu Leu Val Asn Ile Thr Gln
                85                  90                  95

Asn Gln Lys Ala Pro Leu Cys Asn Gly Ser Met Val Trp Ser Ile Asn
            100                 105                 110

Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser Leu Ile Asn Val
        115                 120                 125

Ser Gly Cys Ser Ala Ile Glu Lys Thr Gln Arg Met Leu Ser Gly Phe
    130                 135                 140

Cys Pro His Lys Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Gly Gly
                165                 170                 175

Gly Gly Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn Leu Ser
            180                 185                 190
```

```
Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn Pro Pro
        195                 200                 205

Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp Tyr Phe Ser His Phe Gly
    210                 215                 220

Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr Arg Arg Ser Ile Glu
225                 230                 235                 240

Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln Cys Ser
                245                 250                 255

Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu Val Glu Lys Cys Ile Ser
            260                 265                 270

Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln Cys Ile
        275                 280                 285

Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp Leu Pro Gly Arg Asn
    290                 295                 300

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

Glu Lys Ile His Gln Cys Glu Asn Ile Phe Arg Glu Gly Gln Tyr Phe
                325                 330                 335

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

His Ser Val Gln Ile Met Val Lys Asp Asn Ala Gly Lys Ile Lys Pro
        355                 360                 365

Ser Phe Asn Ile Val Pro Leu Thr Ser Arg Val Lys Pro Asp Pro Pro
    370                 375                 380

His Ile Lys Asn Leu Ser Phe His Asn Asp Asp Leu Tyr Val Gln Trp
```

385 390 395 400

Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys Leu Phe Tyr Glu Val Glu
405 410 415

Val Asn Asn Ser Gln Thr Glu Thr His Asn Val Phe Tyr Val Gln Glu
420 425 430

Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg Asn Val Glu Asn Thr Ser
435 440 445

Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr Val Arg
450 455 460

Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys Leu Trp
465 470 475 480

Ser Asn Trp Ser Gln Glu Met Ser Ile Gly Lys Lys Arg Asn Ser Thr
485 490 495

Leu Tyr Ile Thr Met Leu Leu Ile Val Pro Val Ile Val Ala Gly Ala
500 505 510

Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg Leu Lys Ile Ile Ile Phe
515 520 525

Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu Met Phe Gly Asp
530 535 540

Gln Asn Asp Asp Thr Leu His Trp Lys Lys Tyr Asp Ile Tyr Glu Lys
545 550 555 560

Gln Thr Lys Glu Glu Thr Asp Ser Val Val Leu Ile Glu Asn Leu Lys
565 570 575

Lys Ala Ser Gln
580

<210> 118
<211> 974
<212> PRT
<213> Artificial Sequence

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

<400> 118
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Val Ser Ala Gly Gln Phe Ser Ser Leu His Val
20 25 30

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

His Leu Lys Lys Leu Phe Arg Glu Gly Arg Phe Asn Gly Gly Gly Gly
50 55 60

Ser Leu Thr Cys Leu Gly Gly Phe Ala Ser Pro Gly Pro Val Pro Pro
65 70 75 80

Ser Thr Ala Leu Arg Glu Leu Ile Glu Glu Leu Val Asn Ile Thr Gln
85 90 95

Asn Gln Lys Ala Pro Leu Cys Asn Gly Ser Met Val Trp Ser Ile Asn
100 105 110

Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser Leu Ile Asn Val
115 120 125

Ser Gly Cys Ser Ala Ile Glu Lys Thr Gln Arg Met Leu Ser Gly Phe
130 135 140

Cys Pro His Lys Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

```
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Met Lys
                165                 170                 175

Val Leu Gln Glu Pro Thr Cys Val Ser Asp Tyr Met Ser Ile Ser Thr
            180                 185                 190

Cys Glu Trp Lys Met Asn Gly Pro Thr Asn Cys Ser Thr Glu Leu Arg
        195                 200                 205

Leu Leu Tyr Gln Leu Val Phe Leu Leu Ser Glu Ala His Thr Cys Ile
    210                 215                 220

Pro Glu Asn Asn Gly Gly Ala Gly Cys Val Cys His Leu Leu Met Asp
225                 230                 235                 240

Asp Val Val Ser Ala Asp Asn Tyr Thr Leu Asp Leu Trp Ala Gly Gln
                245                 250                 255

Gln Leu Leu Trp Lys Gly Ser Phe Lys Pro Ser Glu His Val Lys Pro
            260                 265                 270

Arg Ala Pro Gly Asn Leu Thr Val His Thr Asn Val Ser Asp Thr Leu
        275                 280                 285

Leu Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp Asn Tyr Leu Tyr Asn
    290                 295                 300

His Leu Thr Tyr Ala Val Asn Ile Trp Ser Glu Asn Asp Pro Ala Asp
305                 310                 315                 320

Phe Arg Ile Tyr Asn Val Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala
                325                 330                 335

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

Trp Ala Gln Cys Tyr Asn Thr Thr Trp Ser Glu Trp Ser Pro Ser Thr
```

```
        355                 360                 365

Lys Trp His Asn Ser Tyr Arg Glu Pro Phe Glu Gln His Leu Leu Leu
    370                 375                 380

Gly Val Ser Val Ser Cys Ile Val Ile Leu Ala Val Cys Leu Leu Cys
385                 390                 395                 400

Tyr Val Ser Ile Thr Lys Ile Lys Lys Glu Trp Trp Asp Gln Ile Pro
                405                 410                 415

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

Gly Ser Gln Trp Glu Lys Arg Ser Arg Gly Gln Glu Pro Ala Lys Cys
        435                 440                 445

Pro His Trp Lys Asn Cys Leu Thr Lys Leu Leu Pro Cys Phe Leu Glu
    450                 455                 460

His Asn Met Lys Arg Asp Glu Asp Pro His Lys Ala Ala Lys Glu Met
465                 470                 475                 480

Pro Phe Gln Gly Ser Gly Lys Ser Ala Trp Cys Pro Val Glu Ile Ser
                485                 490                 495

Lys Thr Val Leu Trp Pro Glu Ser Ile Ser Val Val Arg Cys Val Glu
            500                 505                 510

Leu Phe Glu Ala Pro Val Glu Cys Glu Glu Glu Glu Glu Val Glu Glu
        515                 520                 525

Glu Lys Gly Ser Phe Cys Ala Ser Pro Glu Ser Ser Arg Asp Asp Phe
    530                 535                 540

Gln Glu Gly Arg Glu Gly Ile Val Ala Arg Leu Thr Glu Ser Leu Phe
545                 550                 555                 560
```

```
Leu Asp Leu Leu Gly Glu Glu Asn Gly Gly Phe Cys Gln Gln Asp Met
                565                 570                 575

Gly Glu Ser Cys Leu Leu Pro Pro Ser Gly Ser Thr Ser Ala His Met
            580                 585                 590

Pro Trp Asp Glu Phe Pro Ser Ala Gly Pro Lys Glu Ala Pro Pro Trp
        595                 600                 605

Gly Lys Glu Gln Pro Leu His Leu Glu Pro Ser Pro Pro Ala Ser Pro
    610                 615                 620

Thr Gln Ser Pro Asp Asn Leu Thr Cys Thr Glu Thr Pro Leu Val Ile
625                 630                 635                 640

Ala Gly Asn Pro Ala Tyr Arg Ser Phe Ser Asn Ser Leu Ser Gln Ser
                645                 650                 655

Pro Cys Pro Arg Glu Leu Gly Pro Asp Pro Leu Leu Ala Arg His Leu
            660                 665                 670

Glu Glu Val Glu Pro Glu Met Pro Cys Val Pro Gln Leu Ser Glu Pro
        675                 680                 685

Thr Thr Val Pro Gln Pro Glu Pro Glu Thr Trp Glu Gln Ile Leu Arg
    690                 695                 700

Arg Asn Val Leu Gln His Gly Ala Ala Ala Ala Pro Val Ser Ala Pro
705                 710                 715                 720

Thr Ser Gly Tyr Gln Glu Phe Val His Ala Val Glu Gln Gly Gly Thr
                725                 730                 735

Gln Ala Ser Ala Val Val Gly Leu Gly Pro Pro Gly Glu Ala Gly Tyr
            740                 745                 750

Lys Ala Phe Ser Ser Leu Leu Ala Ser Ser Ala Val Ser Pro Glu Lys
```

```
        755                 760                 765

Cys Gly Phe Gly Ala Ser Ser Gly Glu Glu Gly Tyr Lys Pro Phe Gln
    770                 775                 780

Asp Leu Ile Pro Gly Cys Pro Gly Asp Pro Ala Pro Val Pro Val Pro
785                 790                 795                 800

Leu Phe Thr Phe Gly Leu Asp Arg Glu Pro Pro Arg Ser Pro Gln Ser
                805                 810                 815

Ser His Leu Pro Ser Ser Ser Pro Glu His Leu Gly Leu Glu Pro Gly
            820                 825                 830

Glu Lys Val Glu Asp Met Pro Lys Pro Pro Leu Pro Gln Glu Gln Ala
        835                 840                 845

Thr Asp Pro Leu Val Asp Ser Leu Gly Ser Gly Ile Val Tyr Ser Ala
    850                 855                 860

Leu Thr Cys His Leu Cys Gly His Leu Lys Gln Cys His Gly Gln Glu
865                 870                 875                 880

Asp Gly Gly Gln Thr Pro Val Met Ala Ser Pro Cys Cys Gly Cys Cys
                885                 890                 895

Cys Gly Asp Arg Ser Ser Pro Pro Thr Thr Pro Leu Arg Ala Pro Asp
            900                 905                 910

Pro Ser Pro Gly Gly Val Pro Leu Glu Ala Ser Leu Cys Pro Ala Ser
        915                 920                 925

Leu Ala Pro Ser Gly Ile Ser Glu Lys Ser Lys Ser Ser Ser Ser Phe
    930                 935                 940

His Pro Ala Pro Gly Asn Ala Gln Ser Ser Ser Gln Thr Pro Lys Ile
945                 950                 955                 960
```

Val Asn Phe Val Ser Val Gly Pro Thr Tyr Met Arg Val Ser
965 970

<210> 119
<211> 727
<212> PRT
<213> Artificial Sequence

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

<400> 119
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

Ile Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg
35 40 45

Pro Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro
50 55 60

Arg Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly
65 70 75 80

Met Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser
85 90 95

Cys Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn
100 105 110

Ile Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro
115 120 125

Gly His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr
130 135 140

```
Phe Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys
145                 150                 155                 160

Lys Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn
                165                 170                 175

Glu Asp Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
            180                 185                 190

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Ala Glu Ser Cys
        195                 200                 205

Thr Ser Arg Pro His Ile Thr Val Val Glu Gly Glu Pro Phe Tyr Leu
    210                 215                 220

Lys His Cys Ser Cys Ser Leu Ala His Glu Ile Glu Thr Thr Thr Lys
225                 230                 235                 240

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

Arg Ser Ser Ser Arg Ile Ala Leu His Asp Cys Val Leu Glu Phe Trp
            260                 265                 270

Pro Val Glu Leu Asn Asp Thr Gly Ser Tyr Phe Phe Gln Met Lys Asn
        275                 280                 285

Tyr Thr Gln Lys Trp Lys Leu Asn Val Ile Arg Arg Asn Lys His Ser
    290                 295                 300

Cys Phe Thr Glu Arg Gln Val Thr Ser Lys Ile Val Glu Val Lys Lys
305                 310                 315                 320

Phe Phe Gln Ile Thr Cys Glu Asn Ser Tyr Tyr Gln Thr Leu Val Asn
                325                 330                 335

Ser Thr Ser Leu Tyr Lys Asn Cys Lys Lys Leu Leu Leu Glu Asn Asn
```

```
            340                 345                 350

Lys Asn Pro Thr Ile Lys Lys Asn Ala Glu Phe Glu Asp Gln Gly Tyr
        355                 360                 365

Tyr Ser Cys Val His Phe Leu His His Asn Gly Lys Leu Phe Asn Ile
    370                 375                 380

Thr Lys Thr Phe Asn Ile Thr Ile Val Glu Asp Arg Ser Asn Ile Val
385                 390                 395                 400

Pro Val Leu Leu Gly Pro Lys Leu Asn His Val Ala Val Glu Leu Gly
                405                 410                 415

Lys Asn Val Arg Leu Asn Cys Ser Ala Leu Leu Asn Glu Glu Asp Val
            420                 425                 430

Ile Tyr Trp Met Phe Gly Glu Glu Asn Gly Ser Asp Pro Asn Ile His
        435                 440                 445

Glu Glu Lys Glu Met Arg Ile Met Thr Pro Glu Gly Lys Trp His Ala
    450                 455                 460

Ser Lys Val Leu Arg Ile Glu Asn Ile Gly Glu Ser Asn Leu Asn Val
465                 470                 475                 480

Leu Tyr Asn Cys Thr Val Ala Ser Thr Gly Gly Thr Asp Thr Lys Ser
                485                 490                 495

Phe Ile Leu Val Arg Lys Ala Asp Met Ala Asp Ile Pro Gly His Val
            500                 505                 510

Phe Thr Arg Gly Met Ile Ile Ala Val Leu Ile Leu Val Ala Val Val
        515                 520                 525

Cys Leu Val Thr Val Cys Val Ile Tyr Arg Val Asp Leu Val Leu Phe
    530                 535                 540
```

```
Tyr Arg His Leu Thr Arg Arg Asp Glu Thr Leu Thr Asp Gly Lys Thr
545                 550                 555                 560

Tyr Asp Ala Phe Val Ser Tyr Leu Lys Glu Cys Arg Pro Glu Asn Gly
                565                 570                 575

Glu Glu His Thr Phe Ala Val Glu Ile Leu Pro Arg Val Leu Glu Lys
            580                 585                 590

His Phe Gly Tyr Lys Leu Cys Ile Phe Glu Arg Asp Val Val Pro Gly
        595                 600                 605

Gly Ala Val Val Asp Glu Ile His Ser Leu Ile Glu Lys Ser Arg Arg
    610                 615                 620

Leu Ile Ile Val Leu Ser Lys Ser Tyr Met Ser Asn Glu Val Arg Tyr
625                 630                 635                 640

Glu Leu Glu Ser Gly Leu His Glu Ala Leu Val Glu Arg Lys Ile Lys
                645                 650                 655

Ile Ile Leu Ile Glu Phe Thr Pro Val Thr Asp Phe Thr Phe Leu Pro
            660                 665                 670

Gln Ser Leu Lys Leu Leu Lys Ser His Arg Val Leu Lys Trp Lys Ala
        675                 680                 685

Asp Lys Ser Leu Ser Tyr Asn Ser Arg Phe Trp Lys Asn Leu Leu Tyr
    690                 695                 700

Leu Met Pro Ala Lys Thr Val Lys Pro Gly Arg Asp Glu Pro Glu Val
705                 710                 715                 720

Leu Pro Val Leu Ser Glu Ser
                725
```

<210> 120

<211> 784
<212> PRT
<213> Artificial Sequence

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

<400> 120
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

Ile Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg
35 40 45

Pro Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro
50 55 60

Arg Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly
65 70 75 80

Met Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser
85 90 95

Cys Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn
100 105 110

Ile Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro
115 120 125

Gly His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr
130 135 140

Phe Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys
145 150 155 160

Lys Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn

```
                165                 170                 175

Glu Asp Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
            180                 185                 190

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Phe Asn Ile Ser
        195                 200                 205

Gly Cys Ser Thr Lys Lys Leu Leu Trp Thr Tyr Ser Thr Arg Ser Glu
    210                 215                 220

Glu Glu Phe Val Leu Phe Cys Asp Leu Pro Glu Pro Gln Lys Ser His
225                 230                 235                 240

Phe Cys His Arg Asn Arg Leu Ser Pro Lys Gln Val Pro Glu His Leu
                245                 250                 255

Pro Phe Met Gly Ser Asn Asp Leu Ser Asp Val Gln Trp Tyr Gln Gln
            260                 265                 270

Pro Ser Asn Gly Asp Pro Leu Glu Asp Ile Arg Lys Ser Tyr Pro His
        275                 280                 285

Ile Ile Gln Asp Lys Cys Thr Leu His Phe Leu Thr Pro Gly Val Asn
    290                 295                 300

Asn Ser Gly Ser Tyr Ile Cys Arg Pro Lys Met Ile Lys Ser Pro Tyr
305                 310                 315                 320

Asp Val Ala Cys Cys Val Lys Met Ile Leu Glu Val Lys Pro Gln Thr
                325                 330                 335

Asn Ala Ser Cys Glu Tyr Ser Ala Ser His Lys Gln Asp Leu Leu Leu
            340                 345                 350

Gly Ser Thr Gly Ser Ile Ser Cys Pro Ser Leu Ser Cys Gln Ser Asp
        355                 360                 365
```

```
Ala Gln Ser Pro Ala Val Thr Trp Tyr Lys Asn Gly Lys Leu Leu Ser
    370                 375                 380

Val Glu Arg Ser Asn Arg Ile Val Val Asp Glu Val Tyr Asp Tyr His
385                 390                 395                 400

Gln Gly Thr Tyr Val Cys Asp Tyr Thr Gln Ser Asp Thr Val Ser Ser
                405                 410                 415

Trp Thr Val Arg Ala Val Val Gln Val Arg Thr Ile Val Gly Asp Thr
            420                 425                 430

Lys Leu Lys Pro Asp Ile Leu Asp Pro Val Glu Asp Thr Leu Glu Val
        435                 440                 445

Glu Leu Gly Lys Pro Leu Thr Ile Ser Cys Lys Ala Arg Phe Gly Phe
    450                 455                 460

Glu Arg Val Phe Asn Pro Val Ile Lys Trp Tyr Ile Lys Asp Ser Asp
465                 470                 475                 480

Leu Glu Trp Glu Val Ser Val Pro Glu Ala Lys Ser Ile Lys Ser Thr
                485                 490                 495

Leu Lys Asp Glu Ile Ile Glu Arg Asn Ile Ile Leu Glu Lys Val Thr
            500                 505                 510

Gln Arg Asp Leu Arg Arg Lys Phe Val Cys Phe Val Gln Asn Ser Ile
        515                 520                 525

Gly Asn Thr Thr Gln Ser Val Gln Leu Lys Glu Lys Arg Gly Val Val
    530                 535                 540

Leu Leu Tyr Ile Leu Leu Gly Thr Ile Gly Thr Leu Val Ala Val Leu
545                 550                 555                 560

Ala Ala Ser Ala Leu Leu Tyr Arg His Trp Ile Glu Ile Val Leu Leu
```

```
                565                 570                 575

Tyr Arg Thr Tyr Gln Ser Lys Asp Gln Thr Leu Gly Asp Lys Lys Asp
            580                 585                 590

Phe Asp Ala Phe Val Ser Tyr Ala Lys Trp Ser Ser Phe Pro Ser Glu
        595                 600                 605

Ala Thr Ser Ser Leu Ser Glu Glu His Leu Ala Leu Ser Leu Phe Pro
    610                 615                 620

Asp Val Leu Glu Asn Lys Tyr Gly Tyr Ser Leu Cys Leu Leu Glu Arg
625                 630                 635                 640

Asp Val Ala Pro Gly Gly Val Tyr Ala Glu Asp Ile Val Ser Ile Ile
                645                 650                 655

Lys Arg Ser Arg Arg Gly Ile Phe Ile Leu Ser Pro Asn Tyr Val Asn
            660                 665                 670

Gly Pro Ser Ile Phe Glu Leu Gln Ala Ala Val Asn Leu Ala Leu Asp
        675                 680                 685

Asp Gln Thr Leu Lys Leu Ile Leu Ile Lys Phe Cys Tyr Phe Gln Glu
    690                 695                 700

Pro Glu Ser Leu Pro His Leu Val Lys Lys Ala Leu Arg Val Leu Pro
705                 710                 715                 720

Thr Val Thr Trp Arg Gly Leu Lys Ser Val Pro Pro Asn Ser Arg Phe
                725                 730                 735

Trp Ala Lys Met Arg Tyr His Met Pro Val Lys Asn Ser Gln Gly Phe
            740                 745                 750

Thr Trp Asn Gln Leu Arg Ile Thr Ser Arg Ile Phe Gln Trp Lys Gly
        755                 760                 765
```

Leu Ser Arg Thr Glu Thr Thr Gly Arg Ser Ser Gln Pro Lys Glu Trp
770 775 780

<210> 121
<211> 2226
<212> DNA
<213> Artificial Sequence

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

<400> 121
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgtgcgacc ttccacagac ccattccctc ggctctcgaa gaactctgat gttgctggcc 120

cagatgcgga agatttctct tttctcatgt ctgaaagaca ggcacgactt tggttttccc 180

caggaggagt tcggaaacca gttccagaaa gcggaaacca ttcctgtgct gcacgaaatg 240

atccaacaaa ttttcaacct gttttcaact aaagatagct ccgctgcatg ggacgagaca 300

ctcctcgata agttttatac agagctttac cagcagttaa atgatctgga agcttgtgtc 360

atccaagggg tcggcgtaac cgagacgccc ctgatgaagg aggatagcat actggcagtg 420

cggaagtact tccagaggat caccctctat ctaaaggaaa aaaagtacag tccgtgcgcc 480

tgggaagtgg ttagagccga aatcatgcgt agcttttcct tatctacaaa tttgcaggag 540

tcgttgcgca gtaaagagtc tggaggcgga agcgggggtg gcggcagcgg cggtggagga 600

tcaggtggcg gggggtccgg gggcggaagt ctgcagaaga acctgaaatc cccacagaaa 660

gtcgaggtgg acatcatcga tgacaatttc atcttaagat ggaaccgtag cgatgagtcc 720

gtcggaaatg tcacattttc ttttgattat cagaagaccg ggatggacaa ctggattaag 780

ctgtccggtt gccagaacat aaccagtacc aagtgtaact tcagcagcct caaactcaat 840

gtatatgagg aaatcaagct gaggatccgg gccgagaagg aaaacacaag ctcctggtat 900

gaagttgatt catttactcc atttcgaaaa gcgcaaatag gacccccgga agttcacctc 960

gaggctgaag ataaagcaat tgtaatacac atatcgcctg gcaccaagga ctctgtgatg 1020

tgggctttag atgggctgtc attcacgtac agcctggtga tctggaagaa cagttctggg 1080

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acaacctatt gcctgaaggt caaggcggca ctattgacgt cctggaagat cggcgtgtac 1200

tcaccagtgc attgtataaa gacaacagtg gaaaacgagc ttcccccgcc ggagaatatt 1260

gaggtttccg tgcagaatca gaattatgtg ttgaagtggg actacacata tgccaatatg 1320

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aaatggaagc agattcctga ctgcgagaat gtcaagacca cacagtgcgt gtttcctcaa 1440

aacgttttcc agaaaggcat ctatctgcta cgggtccagg cttccgatgg caataatacc 1500

tcattttgga gcgaggaaat taaattcgac actgaaatcc aagccttcct actccctccc 1560

gtatttaaca tcaggagtct gtctgatagc ttccatattt acatcggtgc tcccaagcag 1620

tctggaaaca ctcccgtgat ccaggattac cccctcatct acgagatcat tttctgggaa 1680

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aacaagtcta gcgtgttcag cgacgcagtt tgtgagaaaa cgaagccagg aaatacttct 1860

aagatttggc ttatcgtggg catttgtatc gctctgttcg cactgccctt tgtaatctac 1920

gccgccaagg tttttctccg ctgtattaat tatgtgtttt tcccatccct gaagccatca 1980

tcgtcgattg acgagtactt ctctgagcaa cctcttaaaa acctgttgtt gtccaccagt 2040

gaagagcaga ttgagaaatg cttcattatc gaaaatattt caacaatcgc cacagtggag 2100

gagacgaatc agaccgacga ggaccataag aagtacagca gtcagacatc tcaggattcc 2160

gggaattaca gcaatgaaga tgaaagtgaa tccaaaacta gcgaggagct ccaacaggac 2220

tttgtg 2226

<210> 122
<211> 2103
<212> DNA
<213> Artificial Sequence

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

<400> 122
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgtgcgacc ttccacagac ccattccctc ggctctcgaa gaactctgat gttgctggcc 120

cagatgcgga agatttctct tttctcatgt ctgaaagaca ggcacgactt tggttttccc 180

caggaggagt tcggaaacca gttccagaaa gcggaaacca ttcctgtgct gcacgaaatg 240

atccaacaaa ttttcaacct gttttcaact aaagatagct ccgctgcatg ggacgagaca 300

ctcctcgata agttttatac agagctttac cagcagttaa atgatctgga agcttgtgtc 360

atccaagggg tcggcgtaac cgagacgccc ctgatgaagg aggatagcat actggcagtg 420

cggaagtact tccagaggat caccctctat ctaaaggaaa aaaagtacag tccgtgcgcc 480

tgggaagtgg ttagagccga aatcatgcgt agcttttcct tatctacaaa tttgcaggag 540

tcgttgcgca gtaaagagtc tggaggcgga agcgggggtg gcggcagcgg cggtggagga 600

tcaggtggcg gggggtccgg gggcggaagt ctgcagatca gctacgactc ccccgattac 660

accgacgagt cctgtacctt taaaatctcc ctacgtaact tcaggtccat tctctcctgg 720

gaactgaaaa accatagcat tgtgccgact cactatacac tgctgtatac cataatgtct 780

aaacccgagg atctgaaggt ggtgaagaac tgtgcgaaca ccacaagatc cttctgcgac 840

ctgacagatg agtggcgatc tacccatgaa gcctacgtca cggtcctcga gggcttcagc 900

ggtaatacca cacttttcag ctgctcacat aacttttggt tggccatcga tatgtccttt 960

gaaccacccg agttcgagat tgtcggtttc acaaaccaca tcaatgtcat ggtgaaattt 1020

ccttctattg tcgaggaaga actccagttt gatttgagcc tcgtgattga ggagcagtca 1080

gagggaatcg tgaagaagca taagcccgaa ataaagggaa atatgagtgg gaacttcact 1140

tacataatcg acaagctcat ccccaacacg aattattgtg tgtcagtgta tctcgagcac 1200

tcggatgagc aagccgtgat caagtctcca cttaagtgca ctctcctgcc gccaggccag 1260

gagtcagaga gcgctgaatc ggctaagata ggcgggatca ttaccgtctt cctcatcgca 1320

ctggtgttga cttctactat tgttaccctg aagtggatcg gatacatctg cttgcgcaac 1380

tctctgccaa aagttctaaa ctttcacaat tttctggcct ggcccttccc caatcttcct 1440

cctctggagg ccatggacat ggttgaggtt atctatataa atcggaaaaa aaaagtctgg 1500

gactacaatt acgatgacga aagtgactca gacacggagg ccgcaccaag gacctctgga 1560

gggggctata ctatgcacgg ccttaccgtg agacctttag gacaggcatc tgctacaagc 1620

actgaaagcc agctgattga cccagagagc gaggaagagc ctgatctacc agaagtggat 1680

gtagagctgc cgacaatgcc taaggactcc ccccaacagc tcgaactgtt gagcggccct 1740

tgtgaaaggc gcaaaagtcc cttgcaagat ccgttccctg aagaagacta tagcagtacc 1800

gaaggatccg gcggtcggat tacattcaac gtggatttaa atagtgtatt tttacgggtt 1860

ctggacgatg aggacagtga tgatctggag gcgcccctta tgctgtcctc ccatctggag 1920

gagatggtag accccgaaga tccagataac gtgcagtcta atcaccttct ggcttccggg 1980

gaaggtactc agccaacctt tcctagtcct tcttcagagg gcttatggtc agaagacgca 2040

ccaagcgatc agtcagacac aagtgagagc gacgtagacc tcggggacgg gtacattatg 2100

aga 2103

<210> 123
<211> 2229
<212> DNA
<213> Artificial Sequence

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

<400> 123
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ccgatgagtt ataatttact cggatttcta cagcggtcta gcaacttcca atgtcagaag 120

ctgctgtggc aactcaacgg caggctggag tactgcctca aagatagaat gaactttgat 180

attcccgaag aaatcaagca gcttcagcag ttccagaaag aggacgccgc actaaccata 240

tacgagatgc tgcagaacat tttcgctata ttcagacagg actcgtcctc tactggatgg 300

aatgagacca tcgtcgagaa tttgctggcc aatgtgtatc atcaaattaa ccacctcaag 360

acggtgcttg aagaaaagtt ggaaaaagag gacttcacta gaggcaaact gatgtcatcc 420

cttcacctca aacgctacta tgggaggatc ctgcactact taaaggcgaa ggagtatagc 480

cattgcgctt ggacaatcgt tcgcgtagag attctgcgga atttttactt tatcaatcgt 540

ttgacaggtt acctgcgaaa ctctggaggc ggaagcgggg gtggcggcag cggcggtgga 600

ggatcaggtg gcgggggtc cgggggcgga agtctgcaga agaacctgaa atccccacag 660

aaagtcgagg tggacatcat cgatgacaat ttcatcttaa gatggaaccg tagcgatgag 720

tccgtcggaa atgtcacatt ttcttttgat tatcagaaga ccgggatgga caactggatt 780

aagctgtccg gttgccagaa cataaccagt accaagtgta acttcagcag cctcaaactc 840

aatgtatatg aggaaatcaa gctgaggatc cgggccgaga aggaaaacac aagctcctgg 900

tatgaagttg attcatttac tccatttcga aaagcgcaaa taggaccccc ggaagttcac 960

ctcgaggctg aagataaagc aattgtaata cacatatcgc ctggcaccaa ggactctgtg 1020

atgtgggctt tagatgggct gtcattcacg tacagcctgg tgatctggaa gaacagttct 1080

ggggtggagg agagaataga aaacatttat agtcgccaca aaatctacaa attgtcaccc 1140

gaaacaacct attgcctgaa ggtcaaggcg gcactattga cgtcctggaa gatcggcgtg 1200

tactcaccag tgcattgtat aaagacaaca gtggaaaacg agcttccccc gccggagaat 1260

attgaggttt ccgtgcagaa tcagaattat gtgttgaagt gggactacac atatgccaat 1320

atgaccttcc aggttcaatg gcttcatgca tttctgaaaa gaaaccctgg taaccacctt 1380

tacaaatgga agcagattcc tgactgcgag aatgtcaaga ccacacagtg cgtgtttcct 1440

caaaacgttt tccagaaagg catctatctg ctacgggtcc aggcttccga tggcaataat 1500

acctcatttt ggagcgagga aattaaattc gacactgaaa tccaagcctt cctactccct 1560

cccgtattta acatcaggag tctgtctgat agcttccata tttacatcgg tgctcccaag 1620

cagtctggaa acactcccgt gatccaggat taccccctca tctacgagat cattttctgg 1680

gaaaacacct ctaacgccga acggaagatt atagagaaga aaactgacgt cactgtgcct 1740

aacctgaaac cattaactgt ctattgcgtc aaagctaggg cccacaccat ggatgaaaaa 1800

ctgaacaagt ctagcgtgtt cagcgacgca gtttgtgaga aaacgaagcc aggaaatact 1860

tctaagattt ggcttatcgt gggcatttgt atcgctctgt tcgcactgcc ctttgtaatc 1920

tacgccgcca aggtttttct ccgctgtatt aattatgtgt ttttcccatc cctgaagcca 1980

tcatcgtcga ttgacgagta cttctctgag caacctctta aaaacctgtt gttgtccacc 2040

agtgaagagc agattgagaa atgcttcatt atcgaaaata tttcaacaat cgccacagtg 2100

gaggagacga atcagaccga cgaggaccat aagaagtaca gcagtcagac atctcaggat 2160

tccgggaatt acagcaatga agatgaaagt gaatccaaaa ctagcgagga gctccaacag 2220

gactttgtg 2229

<210> 124
<211> 2106
<212> DNA
<213> Artificial Sequence

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

<400> 124
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgatgagtt ataatttact cggatttcta cagcggtcta gcaacttcca atgtcagaag 120

ctgctgtggc aactcaacgg caggctggag tactgcctca aagatagaat gaactttgat 180

attcccgaag aaatcaagca gcttcagcag ttccagaaag aggacgccgc actaaccata 240

tacgagatgc tgcagaacat tttcgctata ttcagacagg actcgtcctc tactggatgg 300

aatgagacca tcgtcgagaa tttgctggcc aatgtgtatc atcaaattaa ccacctcaag 360

acggtgcttg aagaaaagtt ggaaaaagag gacttcacta gaggcaaact gatgtcatcc 420

cttcacctca aacgctacta tgggaggatc ctgcactact taaaggcgaa ggagtatagc 480

cattgcgctt ggacaatcgt tcgcgtagag attctgcgga atttttactt tatcaatcgt 540

ttgacaggtt acctgcgaaa ctctggaggc ggaagcgggg gtggcggcag cggcggtgga 600

ggatcaggtg gcgggggggtc cgggggcgga agtctgcaga tcagctacga ctcccccgat 660

tacaccgacg agtcctgtac ctttaaaatc tccctacgta acttcaggtc cattctctcc 720

tgggaactga aaaaccatag cattgtgccg actcactata cactgctgta taccataatg 780

tctaaacccg aggatctgaa ggtggtgaag aactgtgcga acaccacaag atccttctgc 840

gacctgacag atgagtggcg atctacccat gaagcctacg tcacggtcct cgagggcttc 900

agcggtaata ccacactttt cagctgctca cataactttt ggttggccat cgatatgtcc 960

tttgaaccac ccgagttcga gattgtcggt ttcacaaacc acatcaatgt catggtgaaa 1020

tttccttcta ttgtcgagga agaactccag tttgatttga gcctcgtgat tgaggagcag 1080

tcagagggaa tcgtgaagaa gcataagccc gaaataaagg gaaatatgag tgggaacttc 1140

acttacataa tcgacaagct catccccaac acgaattatt gtgtgtcagt gtatctcgag 1200

cactcggatg agcaagccgt gatcaagtct ccacttaagt gcactctcct gccgccaggc 1260

caggagtcag agagcgctga atcggctaag ataggcggga tcattaccgt cttcctcatc 1320

gcactggtgt tgacttctac tattgttacc ctgaagtgga tcggatacat ctgcttgcgc 1380

aactctctgc caaaagttct aaactttcac aattttctgg cctggccctt ccccaatctt 1440

cctcctctgg aggccatgga catggttgag gttatctata taaatcggaa aaaaaaagtc 1500

tgggactaca attacgatga cgaaagtgac tcagacacgg aggccgcacc aaggacctct 1560

ggaggggggct atactatgca cggccttacc gtgagacctt taggacaggc atctgctaca 1620

agcactgaaa gccagctgat tgacccagag agcgaggaag agcctgatct accagaagtg 1680

gatgtagagc tgccgacaat gcctaaggac tccccccaac agctcgaact gttgagcggc 1740

ccttgtgaaa ggcgcaaaag tcccttgcaa gatccgttcc ctgaagaaga ctatagcagt 1800

accgaaggat ccggcggtcg gattacattc aacgtggatt taaatagtgt atttttacgg 1860

gttctggacg atgaggacag tgatgatctg gaggcgcccc ttatgctgtc ctcccatctg 1920

gaggagatgg tagaccccga agatccagat aacgtgcagt ctaatcacct tctggcttcc 1980

ggggaaggta ctcagccaac ctttcctagt ccttcttcag agggcttatg gtcagaagac 2040

gcaccaagcg atcagtcaga cacaagtgag agcgacgtag acctcgggga cgggtacatt 2100

atgaga 2106

<210> 125
<211> 1971
<212> DNA
<213> Artificial Sequence

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

<400> 125
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgcaggatc cctacgtgaa ggaagcagaa aatctcaaaa agtatttcaa tgcgggccat 120

agcgatgtgg ccgataacgg caccctgttt ctggggattc ttaagaattg gaaagaggag 180

tctgatagga agattatgca gtcccagatc gtgagcttct atttcaagct gttcaaaaac 240

ttcaaagacg accagtcgat ccaaaaatct gttgagacaa taaaagagga catgaatgtg 300

aagtttttta attcaaacaa aaagaagcgc gacgattttg agaaattaac gaactactcc 360

gtcaccgact tgaacgtaca acgaaaggct attcacgaac taatccaggt catggctgaa 420

ctgagtcctg ccgccaagac tggtaagcgt aaacggagtc agatgctctt tagaggatct 480

ggaggcggaa gcgggggtgg cggcagcggc ggtggaggat caggtggcgg ggggtccggg 540

ggcggaagtc tgcaggaaat ggggactgcc gacttgggac ctagcagtgt ccccactccc 600

accaacgtga ccatcgagtc ttataatatg aatcctattg tttattggga atatcagatc 660

atgcctcagg ttccagtgtt cactgttgaa gtgaaaaatt acggagtgaa gaactcagag 720

tggatagacg cttgcataaa catatctcac cattactgca atatttccga ccacgtgggc 780

gaccccagca acagtttgtg ggtcagagtg aaagctcgcg tgggccagaa ggagagtgct 840

tatgccaaaa gcgaagaatt cgccgtttgt agagatggca agatcgggcc ccccaaatta 900

gacattcgca aagaagaaaa acaaattatg atcgatatct tccatccctc tgtcttcgtc 960

aacggcgacg aacaggaggt agattatgat ccagagacaa cgtgttacat cagggtatac 1020

aacgtttacg tgaggatgaa tgggtcagag atccagtata agatcctcac tcaaaaggag 1080

gacgactgtg acgaaattca gtgtcaactc gccatcccag tgtcttcgct gaatagccag 1140

tactgcgtgt ctgccgaggg tgtgcttcac gtttggggag tcacaactga aaagtccaaa 1200

gaagtttgta ttaccatttt taacagctct atcaagggct ccctgtggat accagtggtg 1260

gcggcactgc tgctgttcct tgtactcagc ctggtcttca tctgcttcta tattaagaag 1320

atcaaccctc tgaaggagaa gagcatcata ctacccaagt cgcttatctc agtcgtgcgg 1380

tccgccaccc tagaaactaa gcccgaatca aaatatgtat ccctgatcac aagctaccag 1440

ccattttcat tagagaaaga agtcgtgtgc gaggagcctc tgtccccagc aactgtgcca 1500

ggtatgcata cggaggacaa tccgggtaaa gtagagcaca ccgaggagct gtccagcatt 1560

acagaggtcg tcaccacaga ggagaacata cccgatgtgg tgcctggaag tcatctcaca 1620

cctattgagc gtgaatctag cagtcccttg tcttctaatc agagtgaacc ggggagtatt 1680

gcattaaact cctaccactc ccggaattgc agcgaaagcg accactcgag aaatgggttt 1740

gataccgata gttcttgtct ggaatcccac tcatcactga gcgattctga gtttccgcca 1800

aacaacaagg gcgaaattaa aacggaggga caagagctca tcaccgtcat caaggctcca 1860

accagttttg gttacgacaa gcctcatgtt ttggtggatc tgcttgtgga tgactcaggc 1920

aaggagtccc tcattggata ccgacctaca gaggattcca aagagtttag c 1971

<210> 126
<211> 1503
<212> DNA
<213> Artificial Sequence

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

<400> 126
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgcaggatc cctacgtgaa ggaagcagaa aatctcaaaa agtatttcaa tgcgggccat 120

agcgatgtgg ccgataacgg caccctgttt ctggggattc ttaagaattg gaaagaggag 180

tctgatagga agattatgca gtcccagatc gtgagcttct atttcaagct gttcaaaaac 240

ttcaaagacg accagtcgat ccaaaaatct gttgagacaa taaaagagga catgaatgtg 300

aagtttttta attcaaacaa aaagaagcgc gacgattttg agaaattaac gaactactcc 360

gtcaccgact tgaacgtaca acgaaaggct attcacgaac taatccaggt catggctgaa 420

ctgagtcctg ccgccaagac tggtaagcgt aaacggagtc agatgctctt tagaggatct 480

ggaggcggaa gcgggggtgg cggcagcggc ggtggaggat caggtggcgg ggggtccggg 540

ggcggaagtc tgcaggcccc ccctgatcct ctctcacagc tacccgcccc acagcatccc 600

aagataagac tgtacaatgc cgagcaggtg cttagctggg agcccgtggc actatcaaac 660

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gctgacatta tgagcattgg agtcaattgc actcagatca ccgcaaccga gtgtgacttt 780

acagcagctt caccctccgc cggattccct atggacttca acgtcactct gcggcttcgt 840

gcagaactgg gcgctcttca ttccgcctgg gtgacaatgc cttggttcca gcactatcgg 900

aacgtcaccg tagggccccc tgaaaatatc gaagtaaccc ctggagaagg ttcgctgata 960

ataaggttca gctctccgtt tgacattgct gatacatcca ctgcgttctt ctgctactat 1020

gtgcactact gggagaaggg cgggattcaa caagtgaaag ggccattcag gagcaacagt 1080

atcagtctcg acaacctgaa accttctcgc gtctattgcc tccaagtgca ggctcaactg 1140

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gatccaactc agccaatttt agaggcgctc gataaggact ctagcccgaa ggacgatgtg 1440

tgggattccg tgtccatcat cagctttccc gaaaaggagc aggaagatgt tctgcaaact 1500

ttg 1503

<210> 127
<211> 2343
<212> DNA
<213> Artificial Sequence

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

<400> 127
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgcaggatc cctacgtgaa agaagccgag aacttaaaga aatatttcaa cgcaggccat 120

tcagacgtcg ctgataatgg aacacttttt ttgggcattc tgaaaaattg gaaggaagaa 180

tcggaccgaa aaattatgca gagccagata gtatcctttt atttcaagtt atttaaaaac 240

ttcaaagacg atcagtctat ccaaaaaagt gtggagacta tcaaggagga catgaatgtg 300

aagttcttca acagcaataa aaagaaacgg gatgactttg aaaagctcac caattactca 360

gtcactgatc tgaacgtgca gagaaaggcg attcatgagc taatccaagt gatggctgag 420

ctcggagcca acgtgagcgg agagtttgtg aaggaagccg agaatctgaa gaagtatttc 480

aacgctggtc actctgacgt ggcagataac ggcacgctgt tcctggggat cctgaagaat 540

tggaaagaag agtccgacag gaagattatg caatcccaga tcgtcagttt ctactttaag 600

cttttcaaga atttcaaaga cgatcagagt atccagaagt ctgtcgagac cataaaagaa 660

gacatgaatg taaagttttt taattcaaac aaaaagaagc gtgacgattt cgaaaaactc 720

accaactact ccgttacaga tctgaacgtt cagagaaaag ccattcacga gttgatccaa 780

gttatggccg agctctctcc tgcagctaag acaggtaaga ggaaacggag ccagatgctg 840

tttcgcgggt ctggaggcgg aagcgggggt ggcggcagcg gcggtggagg atcaggtggc 900

ggggggtccg ggggcggaag tctgcaggaa atggggactg ccgacttggg acctagcagt 960

gtccccactc ccaccaacgt gaccatcgag tcttataata tgaatcctat tgtttattgg 1020

gaatatcaga tcatgcctca ggttccagtg ttcactgttg aagtgaaaaa ttacggagtg 1080

aagaactcag agtggataga cgcttgcata aacatatctc accattactg caatatttcc 1140

gaccacgtgg gcgaccccag caacagtttg tgggtcagag tgaaagctcg cgtgggccag 1200

aaggagagtg cttatgccaa aagcgaagaa ttcgccgttt gtagagatgg caagatcggg 1260

ccccccaaat tagacattcg caaagaagaa aaacaaatta tgatcgatat cttccatccc 1320

tctgtcttcg tcaacggcga cgaacaggag gtagattatg atccagagac aacgtgttac 1380

atcagggtat acaacgttta cgtgaggatg aatgggtcag agatccagta taagatcctc 1440

actcaaaagg aggacgactg tgacgaaatt cagtgtcaac tcgccatccc agtgtcttcg 1500

ctgaatagcc agtactgcgt gtctgccgag ggtgtgcttc acgtttgggg agtcacaact 1560

gaaaagtcca aagaagtttg tattaccatt tttaacagct ctatcaaggg ctccctgtgg 1620

ataccagtgg tggcggcact gctgctgttc cttgtactca gcctggtctt catctgcttc 1680

tatattaaga agatcaaccc tctgaaggag aagagcatca tactacccaa gtcgcttatc 1740

tcagtcgtgc ggtccgccac cctagaaact aagcccgaat caaaatatgt atccctgatc 1800

acaagctacc agccattttc attagagaaa gaagtcgtgt gcgaggagcc tctgtcccca 1860

gcaactgtgc caggtatgca tacggaggac aatccgggta aagtagagca caccgaggag 1920

ctgtccagca ttacagaggt cgtcaccaca gaggagaaca tacccgatgt ggtgcctgga 1980

agtcatctca cacctattga gcgtgaatct agcagtccct tgtcttctaa tcagagtgaa 2040

ccggggagta ttgcattaaa ctcctaccac tcccggaatt gcagcgaaag cgaccactcg 2100

agaaatgggt ttgataccga tagttcttgt ctggaatccc actcatcact gagcgattct 2160

gagtttccgc caaacaacaa gggcgaaatt aaaacggagg gacaagagct catcaccgtc 2220

atcaaggctc caaccagttt tggttacgac aagcctcatg ttttggtgga tctgcttgtg 2280

gatgactcag gcaaggagtc cctcattgga taccgaccta cagaggattc caaagagttt 2340

agc 2343

<210> 128
<211> 1875
<212> DNA
<213> Artificial Sequence

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

<400> 128
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgcaggatc cctacgtgaa agaagccgag aacttaaaga aatatttcaa cgcaggccat 120

tcagacgtcg ctgataatgg aacacttttt ttgggcattc tgaaaaattg gaaggaagaa 180

tcggaccgaa aaattatgca gagccagata gtatcctttt atttcaagtt atttaaaaac 240

ttcaaagacg atcagtctat ccaaaaaagt gtggagacta tcaaggagga catgaatgtg 300

aagttcttca acagcaataa aaagaaacgg gatgactttg aaaagctcac caattactca 360

gtcactgatc tgaacgtgca gagaaaggcg attcatgagc taatccaagt gatggctgag 420

ctcggagcca acgtgagcgg agagtttgtg aaggaagccg agaatctgaa gaagtatttc 480

aacgctggtc actctgacgt ggcagataac ggcacgctgt tcctggggat cctgaagaat 540

tggaaagaag agtccgacag gaagattatg caatcccaga tcgtcagttt ctactttaag 600

cttttcaaga atttcaaaga cgatcagagt atccagaagt ctgtcgagac cataaaagaa 660

gacatgaatg taaagttttt taattcaaac aaaaagaagc gtgacgattt cgaaaaactc 720

accaactact ccgttacaga tctgaacgtt cagagaaaag ccattcacga gttgatccaa 780

gttatggccg agctctctcc tgcagctaag acaggtaaga ggaaacggag ccagatgctg 840

tttcgcgggt ctggaggcgg aagcgggggt ggcggcagcg gcggtggagg atcaggtggc 900

gggggtccg ggggcggaag tctgcaggcc ccccctgatc ctctctcaca gctacccgcc 960

ccacagcatc ccaagataag actgtacaat gccgagcagg tgcttagctg ggagcccgtg 1020

gcactatcaa acagtacgag acccgtggtg taccaggtac agttcaagta cacagacagc 1080

aagtggttta ccgctgacat tatgagcatt ggagtcaatt gcactcagat caccgcaacc 1140

gagtgtgact ttacagcagc ttcaccctcc gccggattcc ctatggactt caacgtcact 1200

ctgcggcttc gtgcagaact gggcgctctt cattccgcct gggtgacaat gccttggttc 1260

cagcactatc ggaacgtcac cgtagggccc cctgaaaata tcgaagtaac ccctggagaa 1320

ggttcgctga taataaggtt cagctctccg tttgacattg ctgatacatc cactgcgttc 1380

ttctgctact atgtgcacta ctgggagaag ggcgggattc aacaagtgaa agggccattc 1440

aggagcaaca gtatcagtct cgacaacctg aaaccttctc gcgtctattg cctccaagtg 1500

caggctcaac tgctgtggaa caaaagtaat attttccgag ttggccacct gtctaatatc 1560

tcctgttatg agaccatggc cgacgcatct acggagttgc agcaggtcat cctcatttct 1620

gtgggcacat tttccctgct gtcggttctg gccggtgcct gttttttttct cgttttgaaa 1680

taccgcggct tgatcaaata ctggtttcat accccaccat caataccatt acagatcgaa 1740

gagtatctta aagatccaac tcagccaatt ttagaggcgc tcgataagga ctctagcccg 1800

aaggacgatg tgtgggattc cgtgtccatc atcagctttc ccgaaaagga gcaggaagat 1860

gttctgcaaa ctttg 1875

<210> 129
<211> 1890
<212> DNA
<213> Artificial Sequence

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

<400> 129
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggtgcgat cttcaagccg gacaccctca gacaagccag tggcacacgt ggtagcgaac 120

ccacaagctg aggggcagct ccagtggctc aatcggcgtg ccaacgccct gttagccaat 180

ggggtcgagc ttagggacaa ccaacttgtg gtaccctcgg aaggattata cttgatttac 240

agtcaggtgc tgttcaaagg acagggctgc ccttccacac atgttctgct cactcacacg 300

atctcccgca ttgcagtgtc ttatcagacc aaggtcaact tgctaagcgc tatcaaaagt 360

ccatgtcaga gagagacccc ggagggtgct gaggctaagc cttggtacga acctatttat 420

ctgggcggag tctttcaact ggaaaaaggt gatagactga gcgcagagat caataggccc 480

gattacctgg acttcgccga atccggccag gtttattttg ggataatcgc cctctctgga 540

ggcggaagcg ggggtggcgg cagcggcggt ggaggatcag gtggcggggg gtccgggggc 600

ggaagtctgc agttggtacc ccatcttggc gaccgagaga aacgggatag tgtctgtccc 660

caagggaaat atatacaccc acagaataac tctatctgct gcactaagtg ccataaagga 720

acgtaccttt ataacgactg cccaggcccc ggccaagata ctgactgcag agagtgcgag 780

tctgggagct tcaccgcctc cgagaatcac ttgagacatt gcctgagttg tagcaagtgc 840

aggaaggaga tggggcaggt tgagatctca tcatgtaccg ttgatcggga caccgtctgt 900

ggatgccgca aaaatcagta tcggcattat tggtccgaaa acctatttca gtgttttaac 960

tgttctttgt gcctgaacgg aacagtccac ctgagttgcc aggaaaaaca gaatacagtt 1020

tgcacttgcc acgctggctt ttttctccgc gagaacgaat gtgtgtcctg ttccaattgt 1080

aagaagtctc tagaatgtac aaagctgtgt ctgccccaaa tcgagaacgt gaaaggaact 1140

gaggacagtg gtacaaccgt gttgctgcct ctggtgatct tcttcgggct ctgcctcctc 1200

agtctgcttt tcattgggct aatgtaccgg taccagcgtt ggaaatctaa gttatactca 1260

attgtctgtg ggaagtccac ccctgagaag gaaggagaac tggaaggtac taccaccaaa 1320

ccactggctc caaacccctc cttctctcct acacccggct ttactcctac cctgggcttc 1380

tcaccggtgc ccagctcaac gttcaccagc tcgagcacat acacccctgg cgattgtccc 1440

aacttcgcag caccaaggcg tgaagtggcc ccaccctacc agggtgctga tccaatactt 1500

gccaccgcat tagccagcga tccgattcct aatcctttac agaagtggga ggattcggcc 1560

cacaaacccc agagcctgga cactgacgac cccgccacgc tgtatgctgt ggtcgagaat 1620

gtaccgcctc tcagatggaa ggaatttgtg aggcgactgg gcctgtccga tcacgagatc 1680

gacagactgg agttgcaaaa tggtcgatgc ctccgggagg cccagtacag catgctggct 1740

acatggagga ggcgcacacc tcgcagggag gcgactcttg aattgctggg acgcgtgctc 1800

agagatatgg acttactcgg atgtcttgaa gacattgaag aggcgctctg cggcccagca 1860

gccctgcctc cggcaccatc cctgctcaga 1890

<210> 130
<211> 1929
<212> DNA
<213> Artificial Sequence

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

<400> 130
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggtgcgat cttcaagccg gacaccctca gacaagccag tggcacacgt ggtagcgaac 120

ccacaagctg aggggcagct ccagtggctc aatcggcgtg ccaacgccct gttagccaat 180

ggggtcgagc ttagggacaa ccaacttgtg gtaccctcgg aaggattata cttgatttac 240

agtcaggtgc tgttcaaagg acagggctgc ccttccacac atgttctgct cactcacacg 300

atctcccgca ttgcagtgtc ttatcagacc aaggtcaact tgctaagcgc tatcaaaagt 360

ccatgtcaga gagagacccc ggagggtgct gaggctaagc cttggtacga acctatttat 420

ctgggcggag tctttcaact ggaaaaaggt gatagactga gcgcagagat caataggccc 480

gattacctgg acttcgccga atccggccag gtttattttg ggataatcgc cctctctgga 540

ggcggaagcg ggggtggcgg cagcggcggt ggaggatcag gtggcggggg gtccgggggc 600

ggaagtctgc agctgcctgc ccaggtcgct tttacaccat atgcacctga gcctggttcc 660

acgtgtaggc ttagggagta ctacgatcaa accgctcaga tgtgttgctc caagtgtagt 720

ccaggccagc acgcaaaagt cttttgtaca aagacgtcag ataccgtgtg cgacagctgc 780

gaagatagca cctataccca gctgtggaat tgggttcccg aatgtttgtc ttgtggctcc 840

cgctgctcta gtgaccaggt ggaaacacag gcctgcactc gggaacagaa ccgtatttgt 900

acctgcaggc ccggttggta ctgcgcactg tccaaacaag aggggtgtag actgtgtgcc 960

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cccgtgagca ctcggagcca acacacacag ccaacacccg agccaagtac cgccccgagt 1260

accagcttcc tactccccat gggcccatct ccaccggctg agggatctac cggggatttt 1320

gctctgcctg tcgggctaat cgtcggggtg acggcgctcg gattgctcat tatcggagtg 1380

gtaaactgcg tgattatgac tcaggtgaaa aagaagcctt tatgcctcca gagagaagcg 1440

aaagttcccc acctgcctgc agacaaggcc aggggtacac agggcccgga acagcaacat 1500

ctgctgatca ccgccccctc ttcaagctcc agcagcctgg aatccagtgc cagtgcactt 1560

gatcggcgcg caccaacgcg aaaccagccc caggcccctg gggtagaggc atcaggcgct 1620

ggagaagcgc gcgctagcac aggcagttcc gattccagcc ctggagggca tggaacacag 1680

gtaaatgtca cctgcatcgt taatgtgtgc tcgtcctcgg accacagctc tcaatgttca 1740

agccaggcct caagcactat gggcgacact gatagctctc cctccgagtc accgaaggac 1800

gagcaggtcc catttagtaa agaggagtgt gccttccgaa gtcagctgga gacaccagaa 1860

accctgcttg ggtctactga agagaaacca ctccctcttg gcgtgccaga tgcgggaatg 1920

aagccgtcg 1929

<210> 131
<211> 2256
<212> DNA
<213> Artificial Sequence

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

<400> 131
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggcgcctg tcagaagcct caactgcacg ctgagggact cacagcaaaa gagcctggtc 120

atgagtggcc cctacgagct gaaagcactc caccttcagg ggcaggacat ggaacaacag 180

gtggttttct ccatgtcttt cgtacaggga gaggagtcta acgataagat ccccgtggct 240

ttgggcttaa aagagaaaaa cctgtatctg agctgtgtgc taaaggacga taagcccaca 300

cttcagctcg agtccgttga tccaaaaaat tatccaaaga agaaaatgga aaagcggttt 360

gtgtttaaca agattgagat taataacaaa ttggaattcg aatcagccca gttccctaat 420

tggtacatca gtacctctca agccgaaaat atgccggtgt ttctgggagg gaccaagggt 480

ggccaggata taacagactt cactatgcag tttgtctcgt cctctggagg cggaagcggg 540

ggtggcggca gcggcggtgg aggatcaggt ggcggggggt ccgggggcgg aagtctgcag 600

ctcgaggccg ataagtgcaa agaaagagag gaaaaaatca ttctggtttc tagcgccaac 660

gaaatcgatg tccgcccctg tccactgaat cctaacgagc ataaggggac tataacatgg 720

tataaggacg acagcaagac ccctgtgtct acagaacaag caagcaggat acaccagcac 780

aaagaaaagc tttggtttgt accagcaaag gtcgaggaca gcgggcatta ttattgcgtg 840

gtacgaaaca gttcttactg cctcagaatc aagatttccg ctaagtttgt cgagaacgaa 900

cctaacttat gttacaacgc acaggctatt tttaaacaga agctcccagt tgctggggat 960

ggcggcctgg tgtgtcccta catggagttt tttaaaaatg agaataatga gctacctaaa 1020

ctgcaatggt acaaggactg caaacccctt ttgctcgaca atattcactt cagcggagtg 1080

aaagatcggc tgattgtgat gaacgtggct gagaaacacc gcgggaacta tacatgccac 1140

gcctcttata cgtacctggg caagcagtac ccgatcacta gagtgattga atttataaca 1200

ctggaagaga acaagccaac tcgtcctgtc atagtatccc ccgcaaacga aaccatggag 1260

gtggacttgg gttctcagat ccagctgatt tgcaatgtta ccgggcaatt gagtgatatc 1320

gcctattgga agtggaatgg ttctgtcatt gacgaagacg atccagtgtt aggagaggac 1380

tattatagcg tagaaaatcc tgcgaacaag aggcggtcga ctctgataac tgtcctgaac 1440

atcagtgaga tcgagagccg attttataaa catccattca catgtttcgc caaaaataca 1500

cacgggatcg acgccgccta cattcagctg atctaccccg taaccaattt ccagaagcac 1560

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gaagtcataa atgaaaatgt taagaaatca cggaggctga tcatcattct agtgcgggag 1920

acctcaggtt tttcctggct cggcggctcc tcagaggagc agattgcgat gtacaacgct 1980

ctggtgcaag atggaatcaa ggtggttctg ttggagctcg aaaagatcca ggattacgag 2040

aaaatgcccg agagcattaa gttcatcaaa caaaaacacg gagccattag atggagtggt 2100

gatttcacgc aaggaccgca gtccgccaag acacgtttct ggaaaaacgt gcgctatcat 2160

atgcccgtgc agaggagatc cccctccagt aaacatcagc tgttatctcc ggcgactaag 2220

gaaaagcttc agcgcgaagc ccatgttcct cttgga 2256

<210> 132
<211> 2250
<212> DNA
<213> Artificial Sequence

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

<400> 132

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ccggcgcctg tcagaagcct caactgcacg ctgagggact cacagcaaaa gagcctggtc 120

atgagtggcc cctacgagct gaaagcactc caccttcagg ggcaggacat ggaacaacag 180

gtggttttct ccatgtcttt cgtacaggga gaggagtcta acgataagat ccccgtggct 240

ttgggcttaa aagagaaaaa cctgtatctg agctgtgtgc taaaggacga taagcccaca 300

cttcagctcg agtccgttga tccaaaaaat tatccaaaga agaaaatgga aaagcggttt 360

gtgtttaaca agattgagat taataacaaa ttggaattcg aatcagccca gttccctaat 420

tggtacatca gtacctctca agccgaaaat atgccggtgt ttctgggagg gaccaagggt 480

ggccaggata taacagactt cactatgcag tttgtctcgt cctctggagg cggaagcggg 540

ggtggcggca gcggcggtgg aggatcaggt ggcggggggt ccgggggcgg aagtctgcag 600

tccgagcggt gcgatgattg gggcttagat accatgcggc agattcaggt gttcgaagac 660

gagcctgctc gcattaaatg cccgctcttt gagcacttcc tgaagtttaa ttacagcact 720

gctcactccg caggactcac actgatctgg tattggacac gccaagacag agatctggag 780

gagcccatta attttaggct ccccgagaac aggatctcta aggagaagga cgtgctgtgg 840

tttcggccga cactactgaa cgatactggg aattacacat gtatgcttcg aaatactacc 900

tattgctcca aggtggcttt tccacttgag gtggtgcaga aagacagctg ttttaatagc 960

ccaatgaaac tgcccgtgca caagctgtac atcgaatatg gcatacagag aatcacatgc 1020

cctaacgtcg acggctactt ccctagctca gttaagccga ccataacttg gtatatgggc 1080

tgctataaaa tacagaactt caataatgta atccccgagg gtatgaactt gagtttcctg 1140

atcgcactga tatctaacaa cgggaactac acctgtgtgg tgacttatcc cgagaacgga 1200

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gaactcctga tcccctgcac ggtgtacttc tctttttaa tggactcccg taatgaagtt 1380

tggtggacca tcgacggcaa aaaacctgat gatattacca tcgacgtgac aatcaacgag 1440

agcatttcac atagtcggac cgaagatgag acaagaaccc agattcttag cataaaaaaa 1500

gtgacttctg aagacctgaa gcgcagttac gtatgtcacg cgcgatccgc aaaaggggaa 1560

gttgccaagg ctgccaaggt gaagcagaaa gtccctgccc cacggtacac cgtagagctg 1620

gcctgtggct tcggagctac ggttttgctg gttgttatcc ttatcgtcgt ctatcatgtg 1680

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gtgctcttaa ccctgagggg agtactggaa aacgagtttg gctacaagtt gtgtattttt 1860

gacagagatt cactgccagg aggaattgtc actgacgaga cactctcatt catccagaaa 1920

tctaggaggt tgctcgttgt cctgagtcca aattatgtgc tccaaggcac ccaggccttg 1980

ctagaactga aggcggggct tgaaaacatg gcctctcgcg ggaacatcaa cgtaattctg 2040

gtgcagtaca aagcagtgaa ggagaccaaa gttaaagagc tgaaacgagc caagacagtc 2100

ctcactgtca tcaagtggaa aggtgaaaaa tcaaagtatc cacaagggag attctggaag 2160

cagcttcaag tcgctatgcc cgtgaagaag tccccccgtc gttcctcctc ggacgagcag 2220

ggcctgagct acagctctct caagaatgtc 2250

<210> 133
<211> 2301
<212> DNA
<213> Artificial Sequence

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

<400> 133
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ccgaactacc ccaaaaaaaa gatggagaag cggtttgttt ttaacaagat tgagatcaac 120

aataagctgg aattcgagtc tgcgcagttc ccaaactggt atattagcac atcgcaagca 180

gaaaatatgc ccgtgttcct cggcggaacc aaaggcgggc aggatatcac agactttacg 240

atgcagttcg tgtcatctgg tggtggtgga agcggcgggg gaggcagtgg gggaggcggg 300

tccgccccag tgaggtccct gaactgtacc ttaagagact cacagcaaaa gtccctggtc 360

atgtctggcc cctacgaact gaaagccctt cacctgcagg ggcaagatat ggagcagcag 420

gtggttttca gcatgagttt tgtacagggc gaagagagta atgacaagat acctgtggct 480

ctaggactca aggaaaagaa tttgtatctc agctgcgtcc tgaaggacga taaacctact 540

cttcagttgg agtccgtcga tccgaaatct ggaggcggaa gcgggggtgg cggcagcggc 600

ggtggaggat caggtggcgg ggggtccggg ggcggaagtc tgcagctcga ggccgataag 660

tgcaaagaaa gagaggaaaa aatcattctg gtttctagcg ccaacgaaat cgatgtccgc 720

ccctgtccac tgaatcctaa cgagcataag gggactataa catggtataa ggacgacagc 780

aagacccctg tgtctacaga acaagcaagc aggatacacc agcacaaaga aaagctttgg 840

tttgtaccag caaaggtcga ggacagcggg cattattatt gcgtggtacg aaacagttct 900

tactgcctca gaatcaagat ttccgctaag tttgtcgaga acgaacctaa cttatgttac 960

aacgcacagg ctatttttaa acagaagctc ccagttgctg gggatggcgg cctggtgtgt 1020

ccctacatgg agtttttaa aaatgagaat aatgagctac ctaaactgca atggtacaag 1080

gactgcaaac ccctttgct cgacaatatt cacttcagcg gagtgaaaga tcggctgatt 1140

gtgatgaacg tggctgagaa acaccgcggg aactatacat gccacgcctc ttatacgtac 1200

ctgggcaagc agtacccgat cactagagtg attgaattta taacactgga agagaacaag 1260

ccaactcgtc ctgtcatagt atcccccgca aacgaaacca tggaggtgga cttgggttct 1320

cagatccagc tgatttgcaa tgttaccggg caattgagtg atatcgccta ttggaagtgg 1380

aatggttctg tcattgacga agacgatcca gtgttaggag aggactatta tagcgtagaa 1440

aatcctgcga acaagaggcg gtcgactctg ataactgtcc tgaacatcag tgagatcgag 1500

agccgatttt ataaacatcc attcacatgt ttcgccaaaa atacacacgg gatcgacgcc 1560

gcctacattc agctgatcta ccccgtaacc aatttccaga agcacatgat cgggatatgc 1620

gtgacgctaa ccgtgatcat tgtttgctca gtgttcattt acaagatctt caagatcgac 1680

atcgtccttt ggtataggga tagctgttac gactttctgc ccattaaggc atcggatggc 1740

aaaacctacg acgcttacat cttgtaccca aagaccgtgg gagaaggctc aacctccgac 1800

tgtgacattt tcgtctttaa ggtgctccct gaggtcctcg agaaacagtg tggctataaa 1860

ctgttcatct atggccggga tgactacgtg ggcgaggata tagttgaagt cataaatgaa 1920

aatgttaaga aatcacggag gctgatcatc attctagtgc gggagacctc aggtttttcc 1980

tggctcggcg gctcctcaga ggagcagatt gcgatgtaca acgctctggt gcaagatgga 2040

atcaaggtgg ttctgttgga gctcgaaaag atccaggatt acgagaaaat gcccgagagc 2100

attaagttca tcaaacaaaa acacggagcc attagatgga gtggtgattt cacgcaagga 2160

ccgcagtccg ccaagacacg tttctggaaa aacgtgcgct atcatatgcc cgtgcagagg 2220

agatcccccc ccagtaaaca tcagctgtta tctccggcga ctaaggaaaa gcttcagcgc 2280

gaagcccatg ttcctcttgg a 2301

<210> 134
<211> 2295
<212> DNA
<213> Artificial Sequence

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

<400> 134
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aataagctgg aattcgagtc tgcgcagttc ccaaactggt atattagcac atcgcaagca 180

gaaaatatgc ccgtgttcct cggcggaacc aaaggcgggc aggatatcac agactttacg 240

atgcagttcg tgtcatctgg tggtggtgga agcggcgggg gaggcagtgg gggaggcggg 300

tccgccccag tgaggtccct gaactgtacc ttaagagact cacagcaaaa gtccctggtc 360

atgtctggcc cctacgaact gaaagccctt cacctgcagg ggcaagatat ggagcagcag 420

gtggttttca gcatgagttt tgtacagggc gaagagagta atgacaagat acctgtggct 480

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ggtggaggat caggtggcgg ggggtccggg ggcggaagtc tgcagtccga gcggtgcgat 660

gattggggct tagataccat gcggcagatt caggtgttcg aagacgagcc tgctcgcatt 720

aaatgcccgc tctttgagca cttcctgaag tttaattaca gcactgctca ctccgcagga 780

ctcacactga tctggtattg gacacgccaa gacagagatc tggaggagcc cattaatttt 840

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ctgaacgata ctgggaatta cacatgtatg cttcgaaata ctacctattg ctccaaggtg 960

gcttttccac ttgaggtggt gcagaaagac agctgtttta atagcccaat gaaactgccc 1020

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aacaacggga actacacctg tgtggtgact tatcccgaga acggacgcac attccatttg 1260

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cacagcccta atgatcacgt ggtgtatgaa aaagaaccag gtgaagaact cctgatcccc 1380

tgcacggtgt acttctcttt tttaatggac tcccgtaatg aagtttggtg gaccatcgac 1440

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cggaccgaag atgagacaag aacccagatt cttagcataa aaaaagtgac ttctgaagac 1560

ctgaagcgca gttacgtatg tcacgcgcga tccgcaaaag gggaagttgc caaggctgcc 1620

aaggtgaagc agaaagtccc tgccccacgg tacaccgtag agctggcctg tggcttcgga 1680

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gatatttacg tctcgtacgc cagaaatgcg gaggaagagg aattcgtgct cttaaccctg 1860

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gttgtcctga gtccaaatta tgtgctccaa ggcacccagg ccttgctaga actgaaggcg 2040

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gtgaaggaga ccaaagttaa agagctgaaa cgagccaaga cagtcctcac tgtcatcaag 2160

tggaaaggtg aaaaatcaaa gtatccacaa gggagattct ggaagcagct tcaagtcgct 2220

atgcccgtga agaagtcccc ccgtcgttcc tcctcggacg agcagggcct gagctacagc 2280

tctctcaaga atgtc 2295

<210> 135
<211> 2037
<212> DNA
<213> Artificial Sequence

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

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agcagcgaga gaatcgacaa gcaaataagg tatattcttg atggaatcag cgcgctgcga 180

aaggagacat gtaacaagtc gaatatgtgc gagtcttcca aagaagcact tgctgaaaat 240

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gagacttgtt tagtaaagat tataacgggc ttgttggaat tcgaagtcta cctagaatac 360

ctccaaaata gattcgagag tagtgaggaa caggcccgcg ctgttcagat gtcaacaaaa 420

gtgttgatcc aattcctgca gaaaaaagcc aagaacttag atgcaatcac cacacctgac 480

cccactacca atgcctctct gctcaccaag ctgcaagccc agaaccagtg gctgcaggac 540

atgactaccc atctaattct gcggtctttt aaggagttcc tccagtcatc cctgcgtgca 600

cttcggcaga tgtctggagg cggaagcggg ggtggcggca gcggcggtgg aggatcaggt 660

ggcggggggt ccgggggcgg aagtctgcag cttgcaccaa gacgctgtcc ggctcaggag 720

gtcgctaggg gagtgctgac ctcgctgccg ggcgactccg tgaccctgac atgtcctgga 780

gtggagcctg aggacaacgc aacagttcac tgggtgctac ggaagcccgc cgctggctcc 840

catccttcca ggtgggccgg gatggggcgc agactgcttc tcagatcagt gcagttacat 900

gatagcggta attacagctg ctaccgcgct ggaaggccgg caggcactgt gcacctccta 960

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gagagtcaga agttctcatg ccagcttgca gtcccggagg gtgactcatc cttctatatt 1200

gttagtatgt gcgtcgcctc gtctgtgggg tctaagttta gcaagactca aacttttcag 1260

ggctgcggca tcctccaacc agacccccct gccaacatta cagtgaccgc agttgccaga 1320

aaccctaggt ggttgagcgt gacgtggcag gatccccatt cctggaattc atcattctac 1380

agactgcggt tcgagctccg atacagggcg gaacgtagca agacattcac cacgtggatg 1440

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gccggagggt ctctggcgtt cgggacgttg ctctgtatag ccattgtgct gcgtttcaaa 1800

aagacctgga aactgcgcgc cttaaaggag ggaaaaacaa gcatgcaccc cccatattct 1860

cttgggcagc tggtgcccga acggcccaga ccaacaccag tcctggtgcc tcttatatcc 1920

ccccccgtga gcccctctag cctgggcagt gacaatacca gtagccataa taggcccgac 1980

gcccgagacc ctcgctcccc atacgatatc tcaaacacag attatttttt tccccgg 2037

<210> 136
<211> 3378
<212> DNA
<213> Artificial Sequence

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

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agcagcgaga gaatcgacaa gcaaataagg tatattcttg atggaatcag cgcgctgcga 180

aaggagacat gtaacaagtc gaatatgtgc gagtcttcca aagaagcact tgctgaaaat 240

aatctgaacc tcccaaaaat ggccgagaaa gacggctgct ttcagtccgg ttttaacgag 300

gagacttgtt tagtaaagat tataacgggc ttgttggaat tcgaagtcta cctagaatac 360

ctccaaaata gattcgagag tagtgaggaa caggcccgcg ctgttcagat gtcaacaaaa 420

gtgttgatcc aattcctgca gaaaaaagcc aagaacttag atgcaatcac cacacctgac 480

cccactacca atgcctctct gctcaccaag ctgcaagccc agaaccagtg gctgcaggac 540

atgactaccc atctaattct gcggtctttt aaggagttcc tccagtcatc cctgcgtgca 600

cttcggcaga tgtctggagg cggaagcggg ggtggcggca gcggcggtgg aggatcaggt 660

ggcgggggggt ccgggggcgg aagtctgcag gaactcctgg acccctgcgg gtatattagc 720

cccgagtctc ccgtggtgca actgcattct aacttcaccg cagtttgtgt gctcaaagaa 780

aagtgtatgg attacttcca tgttaacgcc aactacattg tgtggaaaac taatcatttt 840

acgataccaa aggagcagta cacaattatc aacagaaccg catcatccgt cacatttacc 900

gatatcgcct ccttgaacat tcagctgaca tgtaatatct taacattcgg tcaactggaa 960

caaaacgtgt atggcatcac catcatctct ggacttcctc cagaaaaacc caaaaatttg 1020

tcgtgtatcg tgaatgaggg aaaaaaaatg cgctgtgaat gggacggggg ccgggagact 1080

cacctcgaga cgaacttcac ccttaagtca gagtgggcga cacataaatt tgccgactgc 1140

aaagcaaaga gagatacccc cacttcctgc accgtcgact attcaactgt gtacttcgtc 1200

aacattgagg tgtgggtgga ggcggagaat gcccttggca aggttacttc cgaccacatc 1260

aactttgatc ccgtctacaa ggtgaaaccg aacccacccc acaacctgtc cgtcattaat 1320

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gtactgacta tccctgcttg tgactttcag gctacccacc ctgttatgga tctgaaggcc 1920

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cttatcaccg tcacgccagt ctacgccgac ggcccgggct ctccagagtc aatcaaggct 2160

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gtcgtcgaaa tagaagctaa tgataagaag ccctttcctg aagacctgaa atccttggac 2760

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gcggccgatg ctttcggccc tggcactgag ggtcaggtgg aaagattcga gacagtgggt 3300

atggaagccg ctacagatga gggaatgccc aaaagctacc tcccacaaac cgtgcggcag 3360

ggaggatata tgccacag 3378

<210> 137
<211> 3621
<212> DNA
<213> Artificial Sequence

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

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ctgctgctgc ataaaaaaga ggatggtatt tggagcactg atattctgaa agaccagaag 360

gaacccaaga acaaaacttt tctgcggtgt gaggccaaga attacagtgg aagattcacc 420

tgttggtggt taaccacaat ctctaccgat cttacctttt ccgtcaaatc aagtcgcggc 480

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ggtgacaaca aggaatacga gtactccgtt gagtgtcaag aagactctgc atgccctgcc 600

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aaagagacat ggcagtggat caaccctgta gacttccagg aggaggctag cctccaggaa 3480

gccctggttg tggaaatgtc atgggataag ggcgagagaa cggaacctct cgagaagact 3540

gaacttcccg agggagctcc tgagctcgca cttgacacag aactgtcttt agaggatggg 3600

gataggtgta aggctaagat g 3621

<210> 138
<211> 4221
<212> DNA
<213> Artificial Sequence

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

<400> 138
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ccaggggaga tggtggtgtt gacctgcgac acccccgaag aggacgggat tacatggact 180

ttggaccagt ccagtgaagt cctgggctcg ggaaagaccc tgactatcca ggtgaaggag 240

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gaacccaaga acaaaacttt tctgcggtgt gaggccaaga attacagtgg aagattcacc 420

tgttggtggt taaccacaat ctctaccgat cttacctttt ccgtcaaatc aagtcgcggc 480

agcagcgatc cacagggcgt gacgtgcggc gctgccacac taagcgcgga gagagtgcgg 540

ggtgacaaca aggaatacga gtactccgtt gagtgtcaag aagactctgc atgccctgcc 600

gcagaggaat cattaccgat cgaagtaatg gtggatgctg ttcacaaact gaagtatgaa 660

aactacactt cttcattttt cataagggac attatcaagc ctgatcctcc aaagaacctc 720

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agaatcaact tccatcacgg tcactctctg aattcgcagg tgacagggct gccgctgggt 1920

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gctgactctc tggaggaact ggagccccag cacatatccc tgtccgtttt cccatctagc 4140

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agatgcgatt ccctgatgct t 4221

<210> 139
<211> 2928
<212> DNA
<213> Artificial Sequence

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

<400> 139
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cagaaaactc tctgtacgga attgaccgtt accgatatct tcgcagctag taagaataca 180

actgaaaaag agacgttttg tcgtgccgcc acagtcctga ggcagtttta ttcacatcac 240

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ggcggtggag gatcaggtgg cgggggtcc gggggcggaa gtctgcagat gaaagtgctg 540

caggaaccga cctgcgtgag cgattatatg agcattagca cctgcgaatg gaaaatgaac 600

ggcccgacca actgcagcac cgaactgcgc ctgctgtatc agctggtgtt tctgctgagc 660

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gtgctgtggc cggaaagcat tagcgtggtg cgctgcgtgg aactgtttga agcgccggtg 1560

gaatgcgaag aagaagaaga agtggaagaa gaaaaaggca gcttttgcgc gagcccggaa 1620

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agcccgccgg cgagcccgac ccagagcccg gataacctga cctgcaccga aaccccgctg 1920

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ctggcgagca gcgcggtgag cccggaaaaa tgcggctttg gcgcgagcag cggcgaagaa 2340

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aaaagcagca gcagctttca tccggcgccg ggcaacgcgc agagcagcag ccagaccccg 2880

aaaattgtga actttgtgag cgtgggcccg acctatatgc gcgtgagc 2928

<210> 140
<211> 1569
<212> DNA
<213> Artificial Sequence

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

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cagaaaactc tctgtacgga attgaccgtt accgatatct tcgcagctag taagaataca 180

actgaaaaag agacgttttg tcgtgccgcc acagtcctga ggcagtttta ttcacatcac 240

gagaaagaca cccggtgcct tggggcaact gcccaacagt ttcatcgcca caaacagctg 300

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ttgcactact ggtataaaaa ctcagataac gacaaagtgc agaagtgttc ccactactta 780

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ttcaatcccc tgtgcgggtc cgcccaacac tggagtgagt ggtctcatcc tattcactgg 1200

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cctgaaact 1569

<210> 141
<211> 1746
<212> DNA
<213> Artificial Sequence

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

<400> 141
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actgaaaaag agacgttttg tcgtgccgcc acagtcctga ggcagtttta ttcacatcac 240

gagaaagaca cccggtgcct tggggcaact gcccaacagt ttcatcgcca caaacagctg 300

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cccgtgaagg aggcgaacca gagcactctg gagaacttcc tggaacgact taagacaatt 420

atgagagaga agtactccaa atgctcctct tctggaggcg gaagcggggg tggcggcagc 480

ggcggtggag gatcaggtgg cgggggtcc gggggcggaa gtctgcaggg cggcggcggc 540

gcggcgccga ccgaaaccca gccgccggtg accaacctga gcgtgagcgt ggaaaacctg 600

tgcaccgtga tttggacctg gaacccgccg gaaggcgcga gcagcaactg cagcctgtgg 660

tattttagcc attttggcga taaacaggat aaaaaaattg cgccggaaac ccgccgcagc 720

attgaagtgc cgctgaacga acgcatttgc ctgcaggtgg gcagccagtg cagcaccaac 780

gaaagcgaaa aaccgagcat tctggtggaa aaatgcatta gcccgccgga aggcgatccg 840

gaaagcgcgg tgaccgaact gcagtgcatt tggcataacc tgagctatat gaaatgcagc 900

tggctgccgg gccgcaacac cagcccggat accaactata ccctgtatta ttggcatcgc 960

agcctggaaa aaattcatca gtgcgaaaac atttttcgcg aaggccagta ttttggctgc 1020

agctttgatc tgaccaaagt gaaagatagc agctttgaac agcatagcgt gcagattatg 1080

gtgaaagata acgcgggcaa aattaaaccg agctttaaca ttgtgccgct gaccagccgc 1140

gtgaaaccgg atccgccgca tattaaaaac ctgagctttc ataacgatga tctgtatgtg 1200

cagtgggaaa acccgcagaa ctttattagc cgctgcctgt tttatgaagt ggaagtgaac 1260

aacagccaga ccgaaaccca taacgtgttt tatgtgcagg aagcgaaatg cgaaaacccg 1320

gaatttgaac gcaacgtgga aaacaccagc tgctttatgg tgccgggcgt gctgccggat 1380

accctgaaca ccgtgcgcat tcgcgtgaaa accaacaaac tgtgctatga agatgataaa 1440

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attaccatgc tgctgattgt gccggtgatt gtggcgggcg cgattattgt gctgctgctg 1560

tatctgaaac gcctgaaaat tattattttt ccgccgattc cggatccggg caaaattttt 1620

aaagaaatgt ttggcgatca gaacgatgat accctgcatt ggaaaaaata tgatatttat 1680

gaaaaacaga ccaaagaaga aaccgatagc gtggtgctga ttgaaaacct gaaaaaagcg 1740

agccag 1746

<210> 142
<211> 2943
<212> DNA
<213> Artificial Sequence

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

<400> 142

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aactcatgcc ccgtgaaaga agcgaatcag tccactcttg agaacttcct cgaaaggctc 300

aagacaatta tgcgcgaaaa gtacagcaag tgcagctctg gcggaaacgg tgggcacaag 360

tgtgatatta cgctccaaga aatcatcaag actctgaact ccctgaccga gcagaaaaca 420

ctttgcactg agttgacagt gaccgacata ttcgccgcta gcaaatctgg aggcggaagc 480

gggggtggcg gcagcggcgg tggaggatca ggtggcgggg ggtccggggg cggaagtctg 540

cagatgaaag tgctgcagga accgacctgc gtgagcgatt atatgagcat tagcacctgc 600

gaatggaaaa tgaacggccc gaccaactgc agcaccgaac tgcgcctgct gtatcagctg 660

gtgtttctgc tgagcgaagc gcatacctgc attccggaaa acaacggcgg cgcgggctgc 720

gtgtgccatc tgctgatgga tgatgtggtg agcgcggata actataccct ggatctgtgg 780

gcgggccagc agctgctgtg gaaaggcagc tttaaaccga gcgaacatgt gaaaccgcgc 840

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cataaagcgg cgaaagaaat gccgtttcag ggcagcggca aaagcgcgtg gtgcccggtg 1500

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tttgaagcgc cggtggaatg cgaagaagaa gaagaagtgg aagaagaaaa aggcagcttt 1620

tgcgcgagcc cggaaagcag ccgcgatgat tttcaggaag gccgcgaagg cattgtggcg 1680

cgcctgaccg aaagcctgtt tctggatctg ctgggcgaag aaaacggcgg cttttgccag 1740

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tgggatgaat ttccgagcgc gggcccgaaa gaagcgccgc cgtggggcaa agaacagccg 1860

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accgaaaccc cgctggtgat tgcgggcaac ccggcgtatc gcagctttag caacagcctg 1980

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gaagtggaac cggaaatgcc gtgcgtgccg cagctgagcg aaccgaccac cgtgccgcag 2100

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agc 2943

<210> 143
<211> 1584
<212> DNA
<213> Artificial Sequence

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

<400> 143
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agtcaccatg agaaagacac cagatgtctg ggggcaaccg ctcagcaatt ccatagacac 180

aagcagttaa tccgatttct gaagcggctt gatcgtaact tgtggggact agccggcctg 240

aactcatgcc ccgtgaaaga agcgaatcag tccactcttg agaacttcct cgaaaggctc 300

aagacaatta tgcgcgaaaa gtacagcaag tgcagctctg gcggaaacgg tgggcacaag 360

tgtgatatta cgctccaaga aatcatcaag actctgaact ccctgaccga gcagaaaaca 420

ctttgcactg agttgacagt gaccgacata ttcgccgcta gcaaatctgg aggcggaagc 480

gggggtggcg gcagcggcgg tggaggatca ggtggcgggg ggtccggggg cggaagtctg 540

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ctcactacta tgcccactga ttccctttcc gtgtcgacct tgccgctgcc agaagtgcag 660

tgcttcgtct ttaatgttga gtatatgaat tgtacatgga attctagcag cgaaccgcag 720

ccaaccaatt tgacattgca ctactggtat aaaaactcag ataacgacaa agtgcagaag 780

tgttcccact acttatttag cgaggaaata acctctgggt gccagctgca gaagaaggag 840

atccatctgt accagacctt cgtcgtgcag ctccaggatc cacgggaacc acgccggcaa 900

gctacccaaa tgctaaagct gcaaaatctc gttatcccat gggcacctga gaatttgaca 960

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gtcgattata gacacaaatt ctcactaccc tcagtggacg ggcagaagag gtacacattt 1140

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tggctggagc gaacaatgcc caggatcccc actctcaaaa atctggaaga ccttgtgacg 1380

gagtatcacg gcaacttcag cgcgtggtct ggcgtctcta aaggtcttgc cgagagcctg 1440

cagcctgatt acagtgagcg cttatgcctg gtgagcgaga taccacctaa aggaggagcc 1500

cttggtgaag gaccgggggc atccccctgt aatcaacact caccatactg ggccccccc 1560

tgctataccc taaagcctga aact 1584

<210> 144
<211> 1761
<212> DNA
<213> Artificial Sequence

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

<400> 144
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgaatacga ctgagaaaga gacctttgt agggctgcca cagtcctgcg gcagttctat 120

agtcaccatg agaaagacac cagatgtctg ggggcaaccg ctcagcaatt ccatagacac 180

aagcagttaa tccgatttct gaagcggctt gatcgtaact tgtggggact agccggcctg 240

aactcatgcc ccgtgaaaga agcgaatcag tccactcttg agaacttcct cgaaaggctc 300

aagacaatta tgcgcgaaaa gtacagcaag tgcagctctg gcggaaacgg tgggcacaag 360

tgtgatatta cgctccaaga aatcatcaag actctgaact ccctgaccga gcagaaaaca 420

ctttgcactg agttgacagt gaccgacata ttcgccgcta gcaaatctgg aggcggaagc 480

gggggtggcg gcagcggcgg tggaggatca ggtggcgggg ggtccggggg cggaagtctg 540

cagggcggcg gcggcgcggc gccgaccgaa acccagccgc cggtgaccaa cctgagcgtg 600

agcgtggaaa acctgtgcac cgtgatttgg acctggaacc cgccggaagg cgcgagcagc 660

aactgcagcc tgtggtattt tagccatttt ggcgataaac aggataaaaa aattgcgccg 720

gaaacccgcc gcagcattga agtgccgctg aacgaacgca tttgcctgca ggtgggcagc 780

cagtgcagca ccaacgaaag cgaaaaaccg agcattctgg tggaaaaatg cattagcccg 840

ccggaaggcg atccggaaag cgcggtgacc gaactgcagt gcatttggca taacctgagc 900

tatatgaaat gcagctggct gccgggccgc aacaccagcc cggataccaa ctataccctg 960

tattattggc atcgcagcct ggaaaaaatt catcagtgcg aaaacatttt tcgcgaaggc 1020

cagtattttg gctgcagctt tgatctgacc aaagtgaaag atagcagctt tgaacagcat 1080

agcgtgcaga ttatggtgaa agataacgcg ggcaaaatta aaccgagctt taacattgtg 1140

ccgctgacca gccgcgtgaa accggatccg ccgcatatta aaaacctgag ctttcataac 1200

gatgatctgt atgtgcagtg ggaaaacccg cagaacttta ttagccgctg cctgttttat 1260

gaagtggaag tgaacaacag ccagaccgaa acccataacg tgttttatgt gcaggaagcg 1320

aaatgcgaaa acccggaatt tgaacgcaac gtggaaaaca ccagctgctt tatggtgccg 1380

ggcgtgctgc cggataccct gaacaccgtg cgcattcgcg tgaaaaccaa caaactgtgc 1440

tatgaagatg ataaactgtg gagcaactgg agccaggaaa tgagcattgg caaaaaacgc 1500

aacagcaccc tgtatattac catgctgctg attgtgccgg tgattgtggc gggcgcgatt 1560

attgtgctgc tgctgtatct gaaacgcctg aaaattatta tttttccgcc gattccggat 1620

ccgggcaaaa tttttaaaga aatgtttggc gatcagaacg atgataccct gcattggaaa 1680

aaatatgata tttatgaaaa acagaccaaa gaagaaaccg atagcgtggt gctgattgaa 1740

aacctgaaaa aagcgagcca g 1761

<210> 145
<211> 2292
<212> DNA
<213> Artificial Sequence

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

<400> 145
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ccgtcacccg gacagggtac tcaatctgaa aatagttgca cccattttcc aggaaatctg 120

cctaacatgc tgagggactt acgcgatgca ttttcgcgtg taaaaacatt ctttcagatg 180

aaagatcaac tggataacct gttgctaaaa gagagcctgc ttgaggattt caagggctat 240

ctgggctgtc aggcgctctc cgaaatgatt caattctacc tcgaagaggt gatgccccag 300

gccgagaacc aggacccaga catcaaggcc cacgtgaatt ctctgggggа gaatctgaaa 360

acgctcagat tgcgactcag acggtgccac aggtttttac cttgtgaaaa caagagcaaa 420

gccgttgagc aggtcaagaa cgcttttaat aagcttcagg aaaaagggat ctataaggca 480

atgtccgagt tcgacatatt cattaattac attgaggctt acatgaccat gaagatccgg 540

aactctggag gcggaagcgg gggtggcggc agcggcggtg gaggatcagg tggcgggggg 600

tccgggggcg gaagtctgca gcatgggacc gagctcccca gtcctccttc tgtttggttc 660

gaagccgaat tctttcacca tattctgcac tggactccta tcccaaatca atcagaatca 720

acatgttacg aggtggcact gctgaggtac ggaatcgagt cttggaatag catttcaaac 780

tgtagccaaa ccctgtctta cgatcttacc gctgtgacgc tggacctgta tcatagcaac 840

ggctaccgtg ccagggttag ggcagttgat ggcagcagac actccaattg gacagttacg 900

aatacccgat tcagtgtcga cgaggtgact ttaactgtcg ggagtgttaa ccttgaaatt 960

cacaacgggt tcatattggg aaagatccag ctcccccggc caaaaatggc cccagccaac 1020

gacacatacg agagtatatt ttctcatttt agagagtatg agatcgcaat ccgcaaggtg 1080

cctgggaatt tcacatttac tcataagaag gtaaaacacg agaacttctc cttgctcacc 1140

tccggcgaag tgggggagtt ctgcgtgcag gtgaagccct cggtggcttc acgctccaat 1200

aaaggcatgt ggagcaaaga agaatgtatt tctctgactc ggcagtactt taccgtgact 1260

aacgtaatca tatttttgc cttcgtgctc ctgctgtctg gtgccctggc ctattgcctg 1320

gcgcttcaac tttatgtgcg gaggaggaag aagctgccgt ccgtgctgtt gtttaagaaa 1380

ccgtctccct tcatttttat cagccagcgc ccctcacccg aaacacagga tactattcac 1440

ccccttgacg aagaagcctt ccttaaagtg tcccccgagc taaaaaacct cgacctgcac 1500

gggtccaccg atagcgggtt tggtagcacc aaaccatcct tgcaaaccga ggagccccag 1560

ttcttgctcc ctgatccaca cccacaggct gacagaacgt tgggaaacag agagccccca 1620

gtcctggggg attcctgttc gtcagggtct agtaatagta ccgatagcgg gatttgcctg 1680

caggagccga gcctgtcacc ctcaaccggt ccgacctggg agcagcaagt aggatctaac 1740

tcccgcgggc aggatgactc cggcatagac ctcgtacaga attcggaagg ccgggcgggt 1800

gacacacagg gcggctccgc tctgggccac cattccccac cagagcccga ggtccctggc 1860

gaggaggacc ctgcagccgt cgcttttcaa ggctatctgc gtcagacacg atgtgctgaa 1920

gagaaagcta ctaagacggg atgtcttgaa gaggaatctc cgcttacaga cggattggga 1980

ccaaagttcg gcagatgcct agtggatgag gcgggactac atcctcccgc attagcaaag 2040

ggctacctga agcaggatcc actagaaatg acactggcct catctggcgc ccctacagga 2100

cagtggaacc agccaaccga agagtggtcc ttgctcgctt taagctcttg cagtgacctg 2160

ggtatctcag attggagttt tgcacacgac ctcgcccctc tgggttgcgt cgccgctcct 2220

ggtggactct taggaagttt caatagcgat ctcgtcactc tgcctctcat cagtagctta 2280

cagagcagcg aa 2292

<210> 146
<211> 1539
<212> DNA
<213> Artificial Sequence

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

<400> 146
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgtcacccg gacagggtac tcaatctgaa aatagttgca cccattttcc aggaaatctg 120

cctaacatgc tgagggactt acgcgatgca ttttcgcgtg taaaaacatt ctttcagatg 180

aaagatcaac tggataacct gttgctaaaa gagagcctgc ttgaggattt caagggctat 240

ctgggctgtc aggcgctctc cgaaatgatt caattctacc tcgaagaggt gatgccccag 300

gccgagaacc aggacccaga catcaaggcc cacgtgaatt ctctgggggа gaatctgaaa 360

acgctcagat tgcgactcag acggtgccac aggtttttac cttgtgaaaa caagagcaaa 420

gccgttgagc aggtcaagaa cgcttttaat aagcttcagg aaaaagggat ctataaggca 480

atgtccgagt tcgacatatt cattaattac attgaggctt acatgaccat gaagatccgg 540

aactctggag gcggaagcgg gggtggcggc agcggcggtg gaggatcagg tggcgggggg 600

tccgggggcg gaagtctgca gatggtacca ccacctgaaa atgtgaggat gaactctgtg 660

aattttaaga acattctcca gtgggaaagt cccgcttttg ctaaggggaa cctgaccttc 720

acagcccaat acttatccta ccgaatcttc caagacaagt gcatgaatac cactttaact 780

gaatgcgact tctcaagcct gtctaagtat ggcgatcata cactgcgggt tcgtgccgag 840

tttgccgacg agcactctga ctgggtgaat ataaccttct gccccgtcga tgatactata 900

attgggccac caggtatgca agttgaagtg ttggcagatt cgctgcacat gaggtttctc 960

gcccccaaaa tcgagaacga gtacgagacc tggacgatga agaatgtcta caactcttgg 1020

acatataatg ttcagtattg gaaaaacgga accgacgaga agtttcagat cactccgcag 1080

tatgatttcg aagtcctgag aaacctcgag ccttggacaa cttactgtgt ccaagtgcgc 1140

ggctttctcc ctgaccggaa caaggcagga gagtggtcag aaccggtgtg tgagcagacc 1200

acccacgacg agacagtacc cagctggatg gtagctgtga tccttatggc ctccgtgttc 1260

atggtttgtc tagctttgtt gggctgtttt gcccttctat ggtgcgtcta taaaaagacc 1320

aaatacgcgt tttcacctag aaacagcctt ccacagcacc tcaaggagtt cctggggcat 1380

cctcatcaca atacactgct gttcttctcc ttccccctga gtgacgaaaa cgatgtgttt 1440

gataaactgt ccgtgattgc agaagacagt gagtccggca aacagaatcc aggagatagt 1500

tgcagcctgg gtacgcctcc cggacagggc ccccagagc 1539

<210> 147
<211> 2310
<212> DNA
<213> Artificial Sequence

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

<400> 147
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgtcgcctg gccagggaac gcagagtgaa aatagctgta cccactttcc cggcaaccta 120

ccaaatatgc tcagagatct gcgggatgca ttctcccggg tgaagacatt tttccaaatg 180

aaggatcagt tggacaacct tctgttgaag gagtcactct tagaggactt caagggatac 240

ctggggtgcc aagccctgtc tgagatgatt cagttctacc tcgaagaggt aatgccacag 300

gccgaaaacc aggaccctga tataaaagct catgtcaata gtttaggcga gaatctgaaa 360

actctcaggc tgcgtctgcg aagatgccac cgctttctgc cctgtgagaa cgggggaggg 420

tctggtggca aaagcaaagc tgtggagcaa gttaaaaatg cattcaacaa acttcaggag 480

aagggtattt ataaggcgat gtccgaattt gacatcttta ttaattacat cgaagcctat 540

atgaccatga agatcaggaa ctctggaggc ggaagcgggg gtggcggcag cggcggtgga 600

ggatcaggtg gcgggggtc cgggggcgga agtctgcagc atgggaccga gctccccagt 660

cctccttctg tttggttcga agccgaattc tttcaccata ttctgcactg gactcctatc 720

ccaaatcaat cagaatcaac atgttacgag gtggcactgc tgaggtacgg aatcgagtct 780

tggaatagca tttcaaactg tagccaaacc ctgtcttacg atcttaccgc tgtgacgctg 840

gacctgtatc atagcaacgg ctaccgtgcc agggttaggg cagttgatgg cagcagacac 900

tccaattgga cagttacgaa tacccgattc agtgtcgacg aggtgacttt aactgtcggg 960

agtgttaacc ttgaaattca caacgggttc atattgggaa agatccagct cccccggcca 1020

aaaatggccc cagccaacga cacatacgag agtatatttt ctcattttag agagtatgag 1080

atcgcaatcc gcaaggtgcc tgggaatttc acatttactc ataagaaggt aaaacacgag 1140

aacttctcct tgctcacctc cggcgaagtg ggggagttct gcgtgcaggt gaagccctcg 1200

gtggcttcac gctccaataa aggcatgtgg agcaaagaag aatgtatttc tctgactcgg 1260

cagtacttta ccgtgactaa cgtaatcata ttttttgcct tcgtgctcct gctgtctggt 1320

gccctggcct attgcctggc gcttcaactt tatgtgcgga ggaggaagaa gctgccgtcc 1380

gtgctgttgt ttaagaaacc gtctcccttc atttttatca gccagcgccc ctcacccgaa 1440

acacaggata ctattcaccc ccttgacgaa gaagccttcc ttaaagtgtc ccccgagcta 1500

aaaaacctcg acctgcacgg gtccaccgat agcgggtttg gtagcaccaa accatccttg 1560

caaaccgagg agccccagtt cttgctccct gatccacacc cacaggctga cagaacgttg 1620

ggaaacagag agcccccagt cctgggggat tcctgttcgt cagggtctag taatagtacc 1680

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tcggaaggcc gggcgggtga cacacagggc ggctccgctc tgggccacca ttccccacca 1860

gagcccgagg tccctggcga ggaggaccct gcagccgtcg cttttcaagg ctatctgcgt 1920

cagacacgat gtgctgaaga gaaagctact aagacgggat gtcttgaaga ggaatctccg 1980

cttacagacg gattgggacc aaagttcggc agatgcctag tggatgaggc gggactacat 2040

cctcccgcat tagcaaaggg ctacctgaag caggatccac tagaaatgac actggcctca 2100

tctggcgccc ctacaggaca gtggaaccag ccaaccgaag agtggtcctt gctcgcttta 2160

agctcttgca gtgacctggg tatctcagat tggagttttg cacacgacct cgcccctctg 2220

ggttgcgtcg ccgctcctgg tggactctta ggaagtttca atagcgatct cgtcactctg 2280

cctctcatca gtagcttaca gagcagcgaa 2310

<210> 148
<211> 1557
<212> DNA
<213> Artificial Sequence

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

<400> 148
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgtcgcctg gccagggaac gcagagtgaa aatagctgta cccactttcc cggcaaccta 120

ccaaatatgc tcagagatct gcgggatgca ttctcccggg tgaagacatt tttccaaatg 180

aaggatcagt tggacaacct tctgttgaag gagtcactct tagaggactt caagggatac 240

ctggggtgcc aagccctgtc tgagatgatt cagttctacc tcgaagaggt aatgccacag 300

gccgaaaacc aggaccctga tataaaagct catgtcaata gtttaggcga gaatctgaaa 360

actctcaggc tgcgtctgcg aagatgccac cgctttctgc cctgtgagaa cgggggaggg 420

tctggtggca aaagcaaagc tgtggagcaa gttaaaaatg cattcaacaa acttcaggag 480

aagggtattt ataaggcgat gtccgaattt gacatcttta ttaattacat cgaagcctat 540

atgaccatga agatcaggaa ctctggaggc ggaagcgggg gtggcggcag cggcggtgga 600

ggatcaggtg gcgggggtc cgggggcgga agtctgcaga tggtaccacc acctgaaaat 660

gtgaggatga actctgtgaa ttttaagaac attctccagt gggaaagtcc cgcttttgct 720

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ctgcgggttc gtgccgagtt tgccgacgag cactctgact gggtgaatat aaccttctgc 900

cccgtcgatg atactataat tgggccacca ggtatgcaag ttgaagtgtt ggcagattcg 960

ctgcacatga ggtttctcgc ccccaaaatc gagaacgagt acgagacctg gacgatgaag 1020

aatgtctaca actcttggac atataatgtt cagtattgga aaaacggaac cgacgagaag 1080

tttcagatca ctccgcagta tgatttcgaa gtcctgagaa acctcgagcc ttggacaact 1140

tactgtgtcc aagtgcgcgg ctttctccct gaccggaaca aggcaggaga gtggtcagaa 1200

ccggtgtgtg agcagaccac ccacgacgag acagtaccca gctggatggt agctgtgatc 1260

cttatggcct ccgtgttcat ggtttgtcta gctttgttgg gctgttttgc ccttctatgg 1320

tgcgtctata aaaagaccaa atacgcgttt tcacctagaa acagccttcc acagcacctc 1380

aaggagttcc tggggcatcc tcatcacaat acactgctgt tcttctcctt ccccctgagt 1440

gacgaaaacg atgtgtttga taaactgtcc gtgattgcag aagacagtga gtccggcaaa 1500

cagaatccag gagatagttg cagcctgggt acgcctcccg gacagggccc ccagagc 1557

<210> 149
<211> 2337
<212> DNA
<213> Artificial Sequence

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

<400> 149
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgggttact tgggctgtca ggctctgagt gaaatgattc agttctatct tgaagaggtt 120

atgcctcagg cggagaacca agacccagac atcaaggccc atgtgaactc tctcggggag 180

aatctgaaaa cactgcgact gcggttaaga cgttgccaca ggttcctacc ctgcgaaaat 240

aaaagcaagg ccgtcgagca agtgaaaaac gcattcaata aactccagga aaagggaatt 300

tacaaggcca tgtccgagtt tgatatcttt ataaactata ttgaggctta catgaccatg 360

aagatccgca atggtggtgg tggaagcggc gggggaggca gtgggggagg cgggtcctcc 420

cctggccagg gaactcagtc agaaaatagc tgcacacact ttccagggaa tctccccaac 480

atgttgagag atctgaggga cgccttctct cgggtgaaaa ccttttcca aatgaaagac 540

cagctggaca acctccttct gaaggagagt ttactagagg atttcaagtc tggaggcgga 600

agcgggggtg gcggcagcgg cggtggagga tcaggtggcg gggggtccgg gggcggaagt 660

ctgcagcatg ggaccgagct ccccagtcct ccttctgttt ggttcgaagc cgaattcttt 720

caccatattc tgcactggac tcctatccca aatcaatcag aatcaacatg ttacgaggtg 780

gcactgctga ggtacggaat cgagtcttgg aatagcattt caaactgtag ccaaaccctg 840

tcttacgatc ttaccgctgt gacgctggac ctgtatcata gcaacggcta ccgtgccagg 900

gttagggcag ttgatggcag cagacactcc aattggacag ttacgaatac ccgattcagt 960

gtcgacgagg tgactttaac tgtcgggagt gttaaccttg aaattcacaa cgggttcata 1020

ttgggaaaga tccagctccc ccggccaaaa atggccccag ccaacgacac atacgagagt 1080

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tttactcata agaaggtaaa acacgagaac ttctccttgc tcacctccgg cgaagtgggg 1200

gagttctgcg tgcaggtgaa gccctcggtg gcttcacgct ccaataaagg catgtggagc 1260

aaagaagaat gtatttctct gactcggcag tactttaccg tgactaacgt aatcatattt 1320

tttgccttcg tgctcctgct gtctggtgcc ctggcctatt gcctggcgct tcaactttat 1380

gtgcggagga ggaagaagct gccgtccgtg ctgttgttta agaaaccgtc tcccttcatt 1440

tttatcagcc agcgcccctc acccgaaaca caggatacta ttcaccccct tgacgaagaa 1500

gccttcctta aagtgtcccc cgagctaaaa aacctcgacc tgcacgggtc caccgatagc 1560

gggtttggta gcaccaaacc atccttgcaa accgaggagc cccagttctt gctccctgat 1620

ccacacccac aggctgacag aacgttggga aacagagagc ccccagtcct gggggattcc 1680

tgttcgtcag ggtctagtaa tagtaccgat agcgggattt gcctgcagga gccgagcctg 1740

tcaccctcaa ccggtccgac ctgggagcag caagtaggat ctaactcccg cgggcaggat 1800

gactccggca tagacctcgt acagaattcg gaaggccggg cgggtgacac acagggcggc 1860

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agttttgcac acgacctcgc ccctctgggt tgcgtcgccg ctcctggtgg actcttagga 2280

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<210> 150
<211> 1584
<212> DNA
<213> Artificial Sequence

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

<400> 150
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgggttact tgggctgtca ggctctgagt gaaatgattc agttctatct tgaagaggtt 120

atgcctcagg cggagaacca agacccagac atcaaggccc atgtgaactc tctcggggag 180

aatctgaaaa cactgcgact gcggttaaga cgttgccaca ggttcctacc ctgcgaaaat 240

aaaagcaagg ccgtcgagca agtgaaaaac gcattcaata aactccagga aaagggaatt 300

tacaaggcca tgtccgagtt tgatatcttt ataaactata ttgaggctta catgaccatg 360

aagatccgca atggtggtgg tggaagcggc gggggaggca gtgggggagg cgggtcctcc 420

cctggccagg gaactcagtc agaaaatagc tgcacacact ttccagggaa tctccccaac 480

atgttgagag atctgaggga cgccttctct cgggtgaaaa ccttttcca aatgaaagac 540

cagctggaca acctccttct gaaggagagt ttactagagg atttcaagtc tggaggcgga 600

agcgggggtg gcggcagcgg cggtggagga tcaggtggcg gggggtccgg gggcggaagt 660

ctgcagatgg taccaccacc tgaaaatgtg aggatgaact ctgtgaattt taagaacatt 720

ctccagtggg aaagtcccgc ttttgctaag gggaacctga ccttcacagc ccaatactta 780

tcctaccgaa tcttccaaga caagtgcatg aataccactt taactgaatg cgacttctca 840

agcctgtcta agtatggcga tcatacactg cgggttcgtg ccgagtttgc cgacgagcac 900

tctgactggg tgaatataac cttctgcccc gtcgatgata ctataattgg gccaccaggt 960

atgcaagttg aagtgttggc agattcgctg cacatgaggt ttctcgcccc caaaatcgag 1020

aacgagtacg agacctggac gatgaagaat gtctacaact cttggacata taatgttcag 1080

tattggaaaa acggaaccga cgagaagttt cagatcactc cgcagtatga tttcgaagtc 1140

ctgagaaacc tcgagccttg gacaacttac tgtgtccaag tgcgcggctt tctccctgac 1200

cggaacaagg caggagagtg gtcagaaccg gtgtgtgagc agaccaccca cgacgagaca 1260

gtacccagct ggatggtagc tgtgatcctt atggcctccg tgttcatggt ttgtctagct 1320

ttgttgggct gttttgccct tctatggtgc gtctataaaa agaccaaata cgcgttttca 1380

cctagaaaca gccttccaca gcacctcaag gagttcctgg ggcatcctca tcacaataca 1440

ctgctgttct tctccttccc cctgagtgac gaaaacgatg tgtttgataa actgtccgtg 1500

attgcagaag acagtgagtc cggcaaacag aatccaggag atagttgcag cctgggtacg 1560

cctcccggac agggccccca gagc 1584

<210> 151
<211> 2817
<212> DNA
<213> Artificial Sequence

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

<400> 151
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgtctccgg gacagggaac ccagagcgaa aactcctgca ctcattttcc tggcaacctc 120

cccaatatgc tgcgagactt gcgcgacgca ttctcaaggg tgaagacgtt cttccagatg 180

aaggatcaac tggacaactt attgctgaaa gaatctctgc tcgaggattt caaaggatac 240

ctgggatgtc aggcactgag cgagatgatc caattttacc tggaggaggt catgcctcag 300

gctgagaatc aggatcctga catcaaggcc cacgtgaaca gtcttggaga gaatcttaag 360

acccttaggc tgagacttag acggtgtcac cgctttctgc cctgcgaaaa taaatcaaaa 420

gcggtggaac aggttaagaa cgcttttaat aagctgcagg aaaagggcat ttataaagct 480

atgagtgaat ttgacatttt cattaactat atcgaggcct atatgacaat gaaaattagg 540

aacgggggag gcgggagcgg gggcggcggc tcaggcggtg gggggtcctc tccaggtcaa 600

ggaacacaat ctgagaactc ctgcacacac ttccccggca atctaccaaa catgctcaga 660

gatctcaggg acgcgttcag tcgagtgaaa actttcttcc agatgaagga tcagctggac 720

aatctactgc tgaaagaaag cttgcttgag gattttaaag gctatctggg ttgtcaggcc 780

ttatcggaga tgatccagtt ttacttggag gaagttatgc ctcaggcaga aaaccaagac 840

cccgatatca aggctcatgt gaattccctc ggtgaaaacc taaagacctt acgcctgcgt 900

ctcagacggt gtcatcggtt tttgccatgc gagaataagt ccaaagccgt agagcaggtc 960

aagaatgcct tcaataagct ccaggagaag gggatataca aagcaatgag cgaatttgac 1020

attttcatca actacataga ggcctacatg accatgaaga tccggaactc tggaggcgga 1080

agcgggggtg gcggcagcgg cggtggagga tcaggtggcg gggggtccgg gggcggaagt 1140

ctgcagcatg ggaccgagct ccccagtcct ccttctgttt ggttcgaagc cgaattcttt 1200

caccatattc tgcactggac tcctatccca aatcaatcag aatcaacatg ttacgaggtg 1260

gcactgctga ggtacggaat cgagtcttgg aatagcattt caaactgtag ccaaaccctg 1320

tcttacgatc ttaccgctgt gacgctggac ctgtatcata gcaacggcta ccgtgccagg 1380

gttagggcag ttgatggcag cagacactcc aattggacag ttacgaatac ccgattcagt 1440

gtcgacgagg tgactttaac tgtcgggagt gttaaccttg aaattcacaa cgggttcata 1500

ttgggaaaga tccagctccc ccggccaaaa atggccccag ccaacgacac atacgagagt 1560

atattttctc attttagaga gtatgagatc gcaatccgca aggtgcctgg gaatttcaca 1620

tttactcata agaaggtaaa acacgagaac ttctccttgc tcacctccgg cgaagtgggg 1680

gagttctgcg tgcaggtgaa gccctcggtg gcttcacgct ccaataaagg catgtggagc 1740

aaagaagaat gtatttctct gactcggcag tactttaccg tgactaacgt aatcatattt 1800

tttgccttcg tgctcctgct gtctggtgcc ctggcctatt gcctggcgct tcaactttat 1860

gtgcggagga ggaagaagct gccgtccgtg ctgttgttta agaaaccgtc tcccttcatt 1920

tttatcagcc agcgcccctc acccgaaaca caggatacta ttcaccccct tgacgaagaa 1980

gccttcctta aagtgtcccc cgagctaaaa aacctcgacc tgcacgggtc caccgatagc 2040

gggtttggta gcaccaaacc atccttgcaa accgaggagc cccagttctt gctccctgat 2100

ccacacccac aggctgacag aacgttggga aacagagagc ccccagtcct gggggattcc 2160

tgttcgtcag ggtctagtaa tagtaccgat agcgggattt gcctgcagga gccgagcctg 2220

tcaccctcaa ccggtccgac ctgggagcag caagtaggat ctaactcccg cgggcaggat 2280

gactccggca tagacctcgt acagaattcg gaaggccggg cgggtgacac acagggcggc 2340

tccgctctgg gccaccattc cccaccagag cccgaggtcc ctggcgagga ggaccctgca 2400

gccgtcgctt ttcaaggcta tctgcgtcag acacgatgtg ctgaagagaa agctactaag 2460

acgggatgtc ttgaagagga atctccgctt acagacggat tgggaccaaa gttcggcaga 2520

tgcctagtgg atgaggcggg actacatcct cccgcattag caaagggcta cctgaagcag 2580

gatccactag aaatgacact ggcctcatct ggcgccccta caggacagtg gaaccagcca 2640

accgaagagt ggtccttgct cgctttaagc tcttgcagtg acctgggtat ctcagattgg 2700

agttttgcac acgacctcgc ccctctgggt tgcgtcgccg ctcctggtgg actcttagga 2760

agtttcaata gcgatctcgt cactctgcct ctcatcagta gcttacagag cagcgaa 2817

<210> 152
<211> 2064
<212> DNA
<213> Artificial Sequence

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

<400> 152
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgtctccgg gacagggaac ccagagcgaa aactcctgca ctcattttcc tggcaacctc 120

cccaatatgc tgcgagactt gcgcgacgca ttctcaaggg tgaagacgtt cttccagatg 180

aaggatcaac tggacaactt attgctgaaa gaatctctgc tcgaggattt caaaggatac 240

ctgggatgtc aggcactgag cgagatgatc caattttacc tggaggaggt catgcctcag 300

gctgagaatc aggatcctga catcaaggcc cacgtgaaca gtcttggaga gaatcttaag 360

acccttaggc tgagacttag acggtgtcac cgctttctgc cctgcgaaaa taaatcaaaa 420

gcggtggaac aggttaagaa cgcttttaat aagctgcagg aaaagggcat ttataaagct 480

atgagtgaat ttgacatttt cattaactat atcgaggcct atatgacaat gaaaattagg 540

aacgggggag gcgggagcgg gggcggcggc tcaggcggtg gggggtcctc tccaggtcaa 600

ggaacacaat ctgagaactc ctgcacacac ttccccggca atctaccaaa catgctcaga 660

gatctcaggg acgcgttcag tcgagtgaaa actttcttcc agatgaagga tcagctggac 720

aatctactgc tgaaagaaag cttgcttgag gattttaaag gctatctggg ttgtcaggcc 780

ttatcggaga tgatccagtt ttacttggag gaagttatgc ctcaggcaga aaaccaagac 840

cccgatatca aggctcatgt gaattccctc ggtgaaaacc taaagacctt acgcctgcgt 900

ctcagacggt gtcatcggtt tttgccatgc gagaataagt ccaaagccgt agagcaggtc 960

aagaatgcct tcaataagct ccaggagaag gggatataca aagcaatgag cgaatttgac 1020

attttcatca actacataga ggcctacatg accatgaaga tccggaactc tggaggcgga 1080

agcgggggtg gcggcagcgg cggtggagga tcaggtggcg gggggtccgg gggcggaagt 1140

ctgcagatgg taccaccacc tgaaaatgtg aggatgaact ctgtgaattt taagaacatt 1200

ctccagtggg aaagtcccgc ttttgctaag gggaacctga ccttcacagc ccaatactta 1260

tcctaccgaa tcttccaaga caagtgcatg aataccactt taactgaatg cgacttctca 1320

agcctgtcta agtatggcga tcatacactg cgggttcgtg ccgagtttgc cgacgagcac 1380

tctgactggg tgaatataac cttctgcccc gtcgatgata ctataattgg gccaccaggt 1440

atgcaagttg aagtgttggc agattcgctg cacatgaggt ttctcgcccc caaaatcgag 1500

aacgagtacg agacctggac gatgaagaat gtctacaact cttggacata taatgttcag 1560

tattggaaaa acggaaccga cgagaagttt cagatcactc cgcagtatga tttcgaagtc 1620

ctgagaaacc tcgagccttg gacaacttac tgtgtccaag tgcgcggctt tctccctgac 1680

cggaacaagg caggagagtg gtcagaaccg gtgtgtgagc agaccaccca cgacgagaca 1740

gtacccagct ggatggtagc tgtgatcctt atggcctccg tgttcatggt ttgtctagct 1800

ttgttgggct gttttgccct tctatggtgc gtctataaaa agaccaaata cgcgttttca 1860

cctagaaaca gccttccaca gcacctcaag gagttcctgg ggcatcctca tcacaataca 1920

ctgctgttct tctccttccc cctgagtgac gaaaacgatg tgtttgataa actgtccgtg 1980

attgcagaag acagtgagtc cggcaaacag aatccaggag atagttgcag cctgggtacg 2040

cctcccggac agggccccca gagc 2064

<210> 153
<211> 1725
<212> DNA
<213> Artificial Sequence

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

<400> 153
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgttaacat gtctgggcgg gttcgcctca cctggaccag ttccccttc aaccgctctc 120

agagaactga ttgaggagct cgtcaatatc acccagaacc aaaaagcccc actctgcaat 180

ggaagtatgg tgtggtctat taacttgact gccggcatgt actgtgccgc actggagtct 240

ttgatcaacg tgtccgggtg cagtgcaatc gaaaagacgc agcggatgct gagcggcttt 300

tgcccccaca aggtgagcgc tggtcagttt tccagccttc acgtgcgaga tacaaagata 360

gaagtagcgc agttcgtcaa ggacctgctg ctgcatctta aaaaactatt tcgcgagggt 420

aggttcaatt ctggaggcgg aagcgggggt ggcggcagcg gcggtggagg atcaggtggc 480

gggggtccg ggggcggaag tctgcagggc ggcggcggcg cggcgccgac cgaaacccag 540

ccgccggtga ccaacctgag cgtgagcgtg gaaaacctgt gcaccgtgat ttggacctgg 600

aacccgccgg aaggcgcgag cagcaactgc agcctgtggt attttagcca ttttggcgat 660

aaacaggata aaaaaattgc gccggaaacc cgccgcagca ttgaagtgcc gctgaacgaa 720

cgcatttgcc tgcaggtggg cagccagtgc agcaccaacg aaagcgaaaa accgagcatt 780

ctggtggaaa aatgcattag cccgccggaa ggcgatccgg aaagcgcggt gaccgaactg 840

cagtgcattt ggcataacct gagctatatg aaatgcagct ggctgccggg ccgcaacacc 900

agcccggata ccaactatac cctgtattat tggcatcgca gcctggaaaa aattcatcag 960

tgcgaaaaca tttttcgcga aggccagtat tttggctgca gctttgatct gaccaaagtg 1020

aaagatagca gctttgaaca gcatagcgtg cagattatgg tgaaagataa cgcgggcaaa 1080

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attaaaaacc tgagctttca taacgatgat ctgtatgtgc agtgggaaaa cccgcagaac 1200

tttattagcc gctgcctgtt ttatgaagtg gaagtgaaca acagccagac cgaaacccat 1260

aacgtgtttt atgtgcagga agcgaaatgc gaaaacccgg aatttgaacg caacgtggaa 1320

aacaccagct gctttatggt gccgggcgtg ctgccggata ccctgaacac cgtgcgcatt 1380

cgcgtgaaaa ccaacaaact gtgctatgaa gatgataaac tgtggagcaa ctggagccag 1440

gaaatgagca ttggcaaaaa acgcaacagc accctgtata ttaccatgct gctgattgtg 1500

ccggtgattg tggcgggcgc gattattgtg ctgctgctgt atctgaaacg cctgaaaatt 1560

attatttttc cgccgattcc ggatccgggc aaaattttta aagaaatgtt tggcgatcag 1620

aacgatgata ccctgcattg gaaaaaatat gatatttatg aaaaacagac caaagaagaa 1680

accgatagcg tggtgctgat tgaaaacctg aaaaaagcga gccag 1725

<210> 154
<211> 2907
<212> DNA
<213> Artificial Sequence

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

<400> 154
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgttaacat gtctgggcgg gttcgcctca cctggaccag ttccccccttc aaccgctctc 120

agagaactga ttgaggagct cgtcaatatc acccagaacc aaaaagcccc actctgcaat 180

ggaagtatgg tgtggtctat taacttgact gccggcatgt actgtgccgc actggagtct 240

ttgatcaacg tgtccgggtg cagtgcaatc gaaaagacgc agcggatgct gagcggcttt 300

tgcccccaca aggtgagcgc tggtcagttt tccagccttc acgtgcgaga tacaaagata 360

gaagtagcgc agttcgtcaa ggacctgctg ctgcatctta aaaaactatt tcgcgagggt 420

aggttcaatt ctggaggcgg aagcgggggt ggcggcagcg gcggtggagg atcaggtggc 480

ggggggtccg ggggcggaag tctgcagatg aaagtgctgc aggaaccgac ctgcgtgagc 540

gattatatga gcattagcac ctgcgaatgg aaaatgaacg gcccgaccaa ctgcagcacc 600

gaactgcgcc tgctgtatca gctggtgttt ctgctgagcg aagcgcatac ctgcattccg 660

gaaaacaacg gcggcgcggg ctgcgtgtgc catctgctga tggatgatgt ggtgagcgcg 720

gataactata ccctggatct gtgggcgggc cagcagctgc tgtggaaagg cagctttaaa 780

ccgagcgaac atgtgaaacc gcgcgcgccg ggcaacctga ccgtgcatac caacgtgagc 840

gataccctgc tgctgacctg gagcaacccg tatccgccgg ataactatct gtataaccat 900

ctgacctatg cggtgaacat ttggagcgaa aacgatccgg cggattttcg catttataac 960

gtgacctatc tggaaccgag cctgcgcatt gcggcgagca ccctgaaaag cggcattagc 1020

tatcgcgcgc gcgtgcgcgc gtgggcgcag tgctataaca ccacctggag cgaatggagc 1080

ccgagcacca aatggcataa cagctatcgc gaaccgtttg aacagcatct gctgctgggc 1140

gtgagcgtga gctgcattgt gattctggcg gtgtgcctgc tgtgctatgt gagcattacc 1200

aaaattaaaa aagaatggtg ggatcagatt ccgaacccgg cgcgcagccg cctggtggcg 1260

attattattc aggatgcgca gggcagccag tgggaaaaac gcagccgcgg ccaggaaccg 1320

gcgaaatgcc cgcattggaa aaactgcctg accaaactgc tgccgtgctt tctggaacat 1380

aacatgaaac gcgatgaaga tccgcataaa gcggcgaaag aaatgccgtt tcagggcagc 1440

ggcaaaagcg cgtggtgccc ggtggaaatt agcaaaaccg tgctgtggcc ggaaagcatt 1500

agcgtggtgc gctgcgtgga actgtttgaa gcgccggtgg aatgcgaaga agaagaagaa 1560

gtggaagaag aaaaaggcag cttttgcgcg agcccggaaa gcagccgcga tgattttcag 1620

gaaggccgcg aaggcattgt ggcgcgcctg accgaaagcc tgtttctgga tctgctgggc 1680

gaagaaaacg gcggcttttg ccagcaggat atgggcgaaa gctgcctgct gccgccgagc 1740

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cagagcccgg ataacctgac ctgcaccgaa accccgctgg tgattgcggg caacccggcg 1920

tatcgcagct ttagcaacag cctgagccag agcccgtgcc cgcgcgaact gggcccggat 1980

ccgctgctgg cgcgccatct ggaagaagtg gaaccggaaa tgccgtgcgt gccgcagctg 2040

agcgaaccga ccaccgtgcc gcagccggaa ccggaaacct gggaacagat tctgcgccgc 2100

aacgtgctgc agcatggcgc ggcggcggcg ccggtgagcg cgccgaccag cggctatcag 2160

gaatttgtgc atgcggtgga acagggcggc acccaggcga gcgcggtggt gggcctgggc 2220

ccgccgggcg aagcgggcta taaagcgttt agcagcctgc tggcgagcag cgcggtgagc 2280

ccggaaaaat gcggctttgg cgcgagcagc ggcgaagaag gctataaacc gtttcaggat 2340

ctgattccgg gctgcccggg cgatccggcg ccggtgccgg tgccgctgtt tacctttggc 2400

ctggatcgcg aaccgccgcg cagcccgcag agcagccatc tgccgagcag cagcccggaa 2460

catctgggcc tggaaccggg cgaaaaagtg gaagatatgc cgaaaccgcc gctgccgcag 2520

gaacaggcga ccgatccgct ggtggatagc ctgggcagcg gcattgtgta tagcgcgctg 2580

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accccgctgc gcgcgccgga tccgagcccg ggcggcgtgc cgctggaagc gagcctgtgc 2760

ccggcgagcc tggcgccgag cggcattagc gaaaaaagca aaagcagcag cagctttcat 2820

ccggcgccgg gcaacgcgca gagcagcagc cagaccccga aaattgtgaa ctttgtgagc 2880

gtgggcccga cctatatgcg cgtgagc 2907

<210> 155
<211> 1740
<212> DNA
<213> Artificial Sequence

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

<400> 155
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggtgagcg cgggccagtt tagcagcctg catgtgcgcg ataccaaaat tgaagtggcg 120

cagtttgtga aagatctgct gctgcatctg aaaaaactgt ttcgcgaagg ccgctttaac 180

ggaggaggtg gatctctgac ctgcctgggc ggctttgcga gcccgggccc ggtgccgccg 240

agcaccgcgc tgcgcgaact gattgaagaa ctggtgaaca ttacccagaa ccagaaagcg 300

ccgctgtgca acggcagcat ggtgtggagc attaacctga ccgcgggcat gtattgcgcg 360

gcgctggaaa gcctgattaa cgtgagcggc tgcagcgcga ttgaaaaaac ccagcgcatg 420

ctgagcggct tttgcccgca taaatctgga ggcggaagcg ggggtggcgg cagcggcggt 480

ggaggatcag gtggcggggg gtccgggggc ggaagtctgc agggcggcgg cggcgcggcg 540

ccgaccgaaa cccagccgcc ggtgaccaac ctgagcgtga gcgtggaaaa cctgtgcacc 600

gtgatttgga cctggaaccc gccggaaggc gcgagcagca actgcagcct gtggtatttt 660

agccattttg gcgataaaca ggataaaaaa attgcgccgg aaacccgccg cagcattgaa 720

gtgccgctga acgaacgcat ttgcctgcag gtgggcagcc agtgcagcac caacgaaagc 780

gaaaaaccga gcattctggt ggaaaaatgc attagcccgc cggaaggcga tccggaaagc 840

gcggtgaccg aactgcagtg catttggcat aacctgagct atatgaaatg cagctggctg 900

ccgggccgca acaccagccc ggataccaac tataccctgt attattggca tcgcagcctg 960

gaaaaaattc atcagtgcga aaacattttt cgcgaaggcc agtattttgg ctgcagcttt 1020

gatctgacca aagtgaaaga tagcagcttt gaacagcata gcgtgcagat tatggtgaaa 1080

gataacgcgg gcaaaattaa accgagcttt aacattgtgc cgctgaccag ccgcgtgaaa 1140

ccggatccgc cgcatattaa aaacctgagc tttcataacg atgatctgta tgtgcagtgg 1200

gaaaacccgc agaactttat tagccgctgc ctgttttatg aagtggaagt gaacaacagc 1260

cagaccgaaa cccataacgt gttttatgtg caggaagcga aatgcgaaaa cccggaattt 1320

gaacgcaacg tggaaaacac cagctgcttt atggtgccgg gcgtgctgcc ggataccctg 1380

aacaccgtgc gcattcgcgt gaaaaccaac aaactgtgct atgaagatga taaactgtgg 1440

agcaactgga gccaggaaat gagcattggc aaaaaacgca acagcaccct gtatattacc 1500

atgctgctga ttgtgccggt gattgtggcg ggcgcgatta ttgtgctgct gctgtatctg 1560

aaacgcctga aaattattat ttttccgccg attccggatc cgggcaaaat ttttaaagaa 1620

atgtttggcg atcagaacga tgataccctg cattggaaaa aatatgatat ttatgaaaaa 1680

cagaccaaag aagaaaccga tagcgtggtg ctgattgaaa acctgaaaaa agcgagccag 1740

<210> 156
<211> 2922
<212> DNA
<213> Artificial Sequence

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

<400> 156
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggtgagcg cgggccagtt tagcagcctg catgtgcgcg ataccaaaat tgaagtggcg 120

cagtttgtga aagatctgct gctgcatctg aaaaaactgt ttcgcgaagg ccgctttaac 180

ggaggaggtg gatctctgac ctgcctgggc ggctttgcga gcccgggccc ggtgccgccg 240

agcaccgcgc tgcgcgaact gattgaagaa ctggtgaaca ttacccagaa ccagaaagcg 300

ccgctgtgca acggcagcat ggtgtggagc attaacctga ccgcgggcat gtattgcgcg 360

gcgctggaaa gcctgattaa cgtgagcggc tgcagcgcga ttgaaaaaac ccagcgcatg 420

ctgagcggct tttgcccgca taaatctgga ggcggaagcg ggggtggcgg cagcggcggt 480

ggaggatcag gtggcggggg gtccgggggc ggaagtctgc agatgaaagt gctgcaggaa 540

ccgacctgcg tgagcgatta tatgagcatt agcacctgcg aatggaaaat gaacggcccg 600

accaactgca gcaccgaact gcgcctgctg tatcagctgg tgtttctgct gagcgaagcg 660

catacctgca ttccggaaaa caacggcggc gcgggctgcg tgtgccatct gctgatggat 720

gatgtggtga gcgcggataa ctataccctg gatctgtggg cgggccagca gctgctgtgg 780

aaaggcagct ttaaaccgag cgaacatgtg aaaccgcgcg cgccgggcaa cctgaccgtg 840

cataccaacg tgagcgatac cctgctgctg acctggagca acccgtatcc gccggataac 900

tatctgtata accatctgac ctatgcggtg aacatttgga gcgaaaacga tccggcggat 960

tttcgcattt ataacgtgac ctatctggaa ccgagcctgc gcattgcggc gagcaccctg 1020

aaaagcggca ttagctatcg cgcgcgcgtg cgcgcgtggg cgcagtgcta taacaccacc 1080

tggagcgaat ggagcccgag caccaaatgg cataacagct atcgcgaacc gtttgaacag 1140

catctgctgc tgggcgtgag cgtgagctgc attgtgattc tggcggtgtg cctgctgtgc 1200

tatgtgagca ttaccaaaat taaaaaagaa tggtgggatc agattccgaa cccggcgcgc 1260

agccgcctgg tggcgattat tattcaggat gcgcagggca gccagtggga aaaacgcagc 1320

cgcggccagg aaccggcgaa atgcccgcat tggaaaaact gcctgaccaa actgctgccg 1380

tgctttctgg aacataacat gaaacgcgat gaagatccgc ataaagcggc gaaagaaatg 1440

ccgtttcagg gcagcggcaa aagcgcgtgg tgcccggtgg aaattagcaa aaccgtgctg 1500

tggccggaaa gcattagcgt ggtgcgctgc gtggaactgt ttgaagcgcc ggtggaatgc 1560

gaagaagaag aagaagtgga agaagaaaaa ggcagctttt gcgcgagccc ggaaagcagc 1620

cgcgatgatt ttcaggaagg ccgcgaaggc attgtggcgc gcctgaccga aagcctgttt 1680

ctggatctgc tgggcgaaga aaacggcggc ttttgccagc aggatatggg cgaaagctgc 1740

ctgctgccgc cgagcggcag caccagcgcg catatgccgt gggatgaatt tccgagcgcg 1800

ggcccgaaag aagcgccgcc gtggggcaaa gaacagccgc tgcatctgga accgagcccg 1860

ccggcgagcc cgacccagag cccggataac ctgacctgca ccgaaacccc gctggtgatt 1920

gcgggcaacc cggcgtatcg cagctttagc aacagcctga gccagagccc gtgcccgcgc 1980

gaactgggcc cggatccgct gctggcgcgc catctggaag aagtggaacc ggaaatgccg 2040

tgcgtgccgc agctgagcga accgaccacc gtgccgcagc cggaaccgga aacctgggaa 2100

cagattctgc gccgcaacgt gctgcagcat ggcgcggcgg cggcgccggt gagcgcgccg 2160

accagcggct atcaggaatt tgtgcatgcg gtggaacagg gcggcaccca ggcgagcgcg 2220

gtggtgggcc tgggcccgcc gggcgaagcg ggctataaag cgtttagcag cctgctggcg 2280

agcagcgcgg tgagcccgga aaaatgcggc tttggcgcga gcagcggcga agaaggctat 2340

aaaccgtttc aggatctgat tccgggctgc ccgggcgatc cggcgccggt gccggtgccg 2400

ctgtttacct ttggcctgga tcgcgaaccg ccgcgcagcc cgcagagcag ccatctgccg 2460

agcagcagcc cggaacatct gggcctggaa ccgggcgaaa aagtggaaga tatgccgaaa 2520

ccgccgctgc cgcaggaaca ggcgaccgat ccgctggtgg atagcctggg cagcggcatt 2580

gtgtatagcg cgctgacctg ccatctgtgc ggccatctga aacagtgcca tggccaggaa 2640

gatggcggcc agaccccggt gatggcgagc ccgtgctgcg gctgctgctg cggcgatcgc 2700

agcagcccgc cgaccacccc gctgcgcgcg ccggatccga gcccgggcgg cgtgccgctg 2760

gaagcgagcc tgtgcccggc gagcctggcg ccgagcggca ttagcgaaaa aagcaaaagc 2820

agcagcagct ttcatccggc gccgggcaac gcgcagagca gcagccagac cccgaaaatt 2880

gtgaactttg tgagcgtggg cccgacctat atgcgcgtga gc 2922

<210> 157
<211> 2181
<212> DNA
<213> Artificial Sequence

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

<400> 157
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgtattttg gcaaactcga aagtaagctg agcgtgattc ggaatcttaa cgatcaggtg 120

ttattcatcg atcaaggcaa cagaccactc tttgaagata tgacagattc agactgtagg 180

gataatgccc ctaggaccat ctttattata agcatgtata aggactctca gccccgcggt 240

atggcagtaa cgattagcgt taagtgcgag aagatttcta cactttcatg cgaaaacaaa 300

atcatctcct tcaaagagat gaaccctccc gataatatca aagataccaa gtcggacata 360

attttctttc agagatccgt cccaggacac gacaataaga tgcaattcga atccagcagt 420

tacgagggat actttctggc ttgtgagaag gaacgtgact tgttcaaact gatcctgaag 480

aaagaggacg agctagggga ccgatctatc atgttcactg tgcagaacga ggactctgga 540

ggcggaagcg ggggtggcgg cagcggcggt ggaggatcag gtggcggggg gtccgggggc 600

ggaagtctgc aggccgagag ctgcactagc cggccccata taactgtggt cgaaggggag 660

ccattctatc tgaaacattg ttcctgctcc cttgcccatg aaattgaaac cacaaccaag 720

agctggtaca aatctagtgg gtctcaagag cacgtcgagt tgaacccaag atcatctagt 780

aggatcgccc tgcatgactg cgttctagag ttttggccgg tggaattaaa tgacaccgga 840

tcttacttct tccagatgaa gaattacacc cagaaatgga agctgaacgt gatacgacgc 900

aacaagcact catgcttcac agaacgtcag gtgacctcga aaatcgtgga agtgaaaaag 960

ttctttcaga ttacatgcga gaacagttac tatcaaacgc tagtgaatag cacgagcctg 1020

tacaaaaact gtaagaaact tctgctggag aacaataaaa accctactat caaaaaaaat 1080

gcagaattcg aggatcaggg ctattacagt tgtgtgcatt ttctccacca caatggtaag 1140

ctattcaata tcaccaagac gttcaacatc accattgtgg aggatcgctc caacatagta 1200

cctgtgttat tgggtcctaa acttaaccac gtggcagtgg agctggggaa aaacgtgaga 1260

ctcaattgct cagccttgct gaacgaagag gatgttattt attggatgtt tggggaagaa 1320

aatggaagtg acccgaacat tcacgaagag aaggagatgc gaatcatgac accagagggg 1380

aaatggcacg cgagtaaggt cctcagaatt gaaaatattg gcgaatcaaa tctcaacgtc 1440

ctctataact gtaccgtagc atccacaggc ggcactgata ctaagtcctt tatccttgtg 1500

cgtaaggccg atatggctga catccccggc cacgtattca cacggggaat gatcattgct 1560

gttctgatcc tggtggcagt agtgtgtttg gttactgtat gtgttatcta ccgcgtggac 1620

ttagttctgt tttataggca cctgacccga agagacgaaa cccttacaga tggcaagact 1680

tatgacgcgt tcgtgtcgta tcttaaagaa tgccggcccg agaatggaga ggagcacacg 1740

tttgctgtcg aaattctccc cagagtcctg gagaagcatt ttggttacaa gctgtgcatc 1800

ttcgaaagag acgtcgtgcc cggtggcgcc gtggtcgacg agatacattc cctgatcgag 1860

aagtcccgca ggttgatcat agtcctctca aagtcttaca tgagcaatga ggtgcggtac 1920

gaactcgaga gcggactgca tgaggcttta gtcgagagga agattaagat tattttgatc 1980

gagtttacac ctgtgactga ctttaccttc ctccctcagt cactgaaact ccttaagtct 2040

cacagggtac tgaagtggaa agctgataaa tccctctctt ataatagccg gttttggaag 2100

aacctattgt acctgatgcc agccaaaaca gtcaagcctg gacgcgatga gcccgaagtt 2160

ctgccagttc tgagcgagtc c 2181

<210> 158
<211> 2352
<212> DNA
<213> Artificial Sequence

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

<400> 158
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgtattttg gcaaactcga aagtaagctg agcgtgattc ggaatcttaa cgatcaggtg 120

ttattcatcg atcaaggcaa cagaccactc tttgaagata tgacagattc agactgtagg 180

gataatgccc ctaggaccat ctttattata agcatgtata aggactctca gccccgcggt 240

atggcagtaa cgattagcgt taagtgcgag aagatttcta cactttcatg cgaaaacaaa 300

atcatctcct tcaaagagat gaaccctccc gataatatca aagataccaa gtcggacata 360

attttctttc agagatccgt cccaggacac gacaataaga tgcaattcga atccagcagt 420

tacgagggat actttctggc ttgtgagaag gaacgtgact tgttcaaact gatcctgaag 480

aaagaggacg agctagggga ccgatctatc atgttcactg tgcagaacga ggactctgga 540

ggcggaagcg ggggtggcgg cagcggcggt ggaggatcag gtggcggggg gtccgggggc 600

ggaagtctgc agtttaatat ctctggatgc agtacgaaga aattgctctg gacatactct 660

actaggagcg aggaagagtt cgtgcttttc tgcgatttac cagaaccaca gaaatcccat 720

ttttgtcaca gaaatcgtct ttctcctaag caggttcccg aacacctgcc cttcatgggc 780

tccaacgacc ttagtgacgt tcaatggtac cagcaaccaa gcaatggcga ccctctggaa 840

gacatacgca agagttaccc ccatattatc caggataaat gcacgctaca tttcctgacc 900

ccaggcgtca acaacagtgg atcttatata tgtaggccta agatgatcaa atccccctac 960

gacgtggctt gttgcgtcaa gatgattctc gaggtgaagc cccagaccaa tgcctcatgt 1020

gagtactccg cctctcacaa acaggacctt ctgctggggt cgaccggcag tataagctgc 1080

ccatcgctct cttgtcagag tgatgcgcag agccctgctg tgacatggta caaaaacgga 1140

aagctactgt cagtggagcg ctcaaaccgt attgtagtag acgaagtcta cgactatcac 1200

caaggcacct acgtgtgcga ttatacacag tctgatacgg tctccagttg gactgtgcgg 1260

gccgtggtgc aggtacggac catcgtgggg gacacaaaac tgaagcccga catccttgat 1320

ccagttgagg acaccctgga ggtggagctc gggaagcccc tgactatctc ctgtaaagca 1380

agatttggct tcgagcgagt atttaaccct gttatcaagt ggtatattaa agatagcgat 1440

ctcgagtggg aggtatcagt gcctgaagcc aaatccatca aatcaactct gaaggatgaa 1500

atcattgagc gaaatattat tcttgagaag gttacccagc gcgatctccg ccgcaaattt 1560

gtctgcttcg tgcaaaacag cataggcaat actactcaga gcgtgcagct gaaagagaag 1620

cgtggtgtcg tcttgttgta catcctgctc ggaacaattg gtacactcgt agccgtgttg 1680

gccgcctcag ccctgctcta caggcattgg attgaaatcg tgttgcttta caggacatat 1740

cagagcaagg accagactct gggcgacaaa aaggatttcg atgcattcgt tagctatgct 1800

aaatggtctt catttcctag cgaagctaca tcctccctga gcgaggaaca cttagcctta 1860

tcactgtttc cagatgtgtt agaaaataaa tatggctata gcctgtgttt gctggagcgc 1920

gacgttgcac cagggggggt gtatgctgaa gacatcgtca gcatcatcaa gcggtccagg 1980

aggggaatat ttatattaag ccctaactac gtcaacggtc catcgatttt cgaactgcag 2040

gctgcagtga acttggcgct cgatgaccag acgctcaagc tgattctcat caagttctgc 2100

tactttcaag agcccgagtc tcttcctcac ctagtcaaga aggcgctgag agtcctgccg 2160

accgtgacat ggcgaggact aaagtctgtg ccgccgaatt ccagattctg ggcaaagatg 2220

cggtatcata tgcccgttaa aaattcccaa ggttttactt ggaaccagct gcggattacc 2280

agtcggatct tccagtggaa ggggctgtct agaaccgaga ccaccggaag atccagtcaa 2340

cccaaagaat gg 2352

<210> 159
<211> 246
<212> PRT
<213> Artificial Sequence

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

<400> 159
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

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

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

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

Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp
145                 150                 155                 160

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

Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe
            180                 185                 190

Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn
        195                 200                 205

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly
    210                 215                 220

Gly Asp Gly Phe Tyr Ala Met Asp Val Trp Gly Gln Gly Thr Leu Val
225                 230                 235                 240

Thr Val Ser Ser Ser Gly
                245


<210> 160
<211> 45
<212> PRT
<213> Artificial Sequence

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

<400> 160
Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1               5                   10                  15
```

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
35 40 45

<210> 161
<211> 24
<212> PRT
<213> Artificial Sequence

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

<400> 161
Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
1 5 10 15

Ser Leu Val Ile Thr Leu Tyr Cys
20

<210> 162
<211> 112
<212> PRT
<213> Artificial Sequence

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

<400> 162
Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys

```
    50                  55                  60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65                  70                  75                  80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
                85                  90                  95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            100                 105                 110

<210> 163
<211> 448
<212> PRT
<213> Artificial Sequence

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

<400> 163
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
            20                  25                  30

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

Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
    50                  55                  60

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

Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His
```

```
            100                 105                 110

Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115                 120                 125

Arg Thr Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
    130                 135                 140

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
145                 150                 155                 160

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp
                165                 170                 175

Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
            180                 185                 190

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

Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala
    210                 215                 220

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
225                 230                 235                 240

Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Val Trp Gly
                245                 250                 255

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Thr Thr Thr Pro Ala
            260                 265                 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
        275                 280                 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
    290                 295                 300
```

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305 310 315 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
325 330 335

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
340 345 350

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
355 360 365

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
370 375 380

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
385 390 395 400

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
405 410 415

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
420 425 430

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
435 440 445

<210> 164
<211> 63
<212> DNA
<213> Artificial Sequence

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

<400> 164
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccg 63

<210> 165
<211> 738
<212> DNA
<213> Artificial Sequence

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

<400> 165
gacattcaaa tgacacagag tccctcatcc ctcagtgcca gcgtgggcga tcgggtgact 60

ataacctgca gagcttctca ggacgtgaat accgctgtgg cgtggtacca gcagaagcca 120

ggcaaagcgc ctaagcttct catttatagt gccagcttcc tgtactcagg tgttccgtct 180

cgcttttctg gaagtagaag tgggaccgat ttcacattga cgatcagcag cttgcagccc 240

gaagatttcg ccacctacta ctgtcagcag cactacacta ccccaccgac atttggtcaa 300

ggcacaaaag tagagattaa acgcactggt tccaccagcg ggagcgggaa acccggctct 360

ggggagggga gcgaggtcca gctggtggaa tccgggggtg gtcttgtgca gccaggagga 420

tccttgaggt tgtcctgcgc cgcaagcggc tttaacatca aagatacata catccattgg 480

gtccgacagg cccctggaaa gggcctggag tgggtcgccc ggatctaccc aactaacggg 540

tacactcgct acgctgatag cgtcaagggt cggtttacta tttctgccga cacctcaaaa 600

aacacagcct acctccagat gaactctctc agagctgagg atacagccgt gtactattgc 660

agccggtggg gaggcgacgg gttctacgct atggatgtgt gggggcaggg cacactggtc 720

accgtgagct catccgga 738

<210> 166
<211> 135
<212> DNA
<213> Artificial Sequence

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

<400> 166
accacgacgc cagcgccgcg accaccaaca ccggcgccca ccatcgcgtc gcagcccctg 60

tccctgcgcc cagaggcgtg ccggccagcg gcgggggcg cagtgcacac gagggggctg 120

gacttcgcct gtgat 135

<210> 167
<211> 72
<212> DNA
<213> Artificial Sequence

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

<400> 167
atctacatct gggcgccctt ggccgggact tgtggggtcc ttctcctgtc actggttatc 60

acccttact gc 72

<210> 168
<211> 336
<212> DNA
<213> Artificial Sequence

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

<400> 168
agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagctc 60

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 120

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 300

tacgacgccc ttcacatgca ggccctgccc cctcgc 336

<210> 169
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 169
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggacattc aaatgacaca gagtccctca tccctcagtg ccagcgtggg cgatcgggtg 120

actataacct gcagagcttc tcaggacgtg aataccgctg tggcgtggta ccagcagaag 180

ccaggcaaag cgcctaagct tctcatttat agtgccagct tcctgtactc aggtgttccg 240

tctcgctttt ctggaagtag aagtgggacc gatttcacat tgacgatcag cagcttgcag 300

cccgaagatt tcgccaccta ctactgtcag cagcactaca ctaccccacc gacatttggt 360

caaggcacaa aagtagagat taaacgcact ggttccacca gcgggagcgg gaaacccggc 420

tctggggagg ggagcgaggt ccagctggtg gaatccgggg gtggtcttgt gcagccagga 480

ggatccttga ggttgtcctg cgccgcaagc ggctttaaca tcaaagatac atacatccat 540

tgggtccgac aggcccctgg aaagggcctg gagtgggtcg cccggatcta cccaactaac 600

gggtacactc gctacgctga tagcgtcaag ggtcggttta ctatttctgc cgacacctca 660

aaaaacacag cctacctcca gatgaactct ctcagagctg aggatacagc cgtgtactat 720

tgcagccggt ggggaggcga cgggttctac gctatggatg tgtgggggca gggcacactg 780

gtcaccgtga gctcatccgg aaccacgacg ccagcgccgc gaccaccaac accggcgccc 840

accatcgcgt cgcagcccct gtccctgcgc ccagaggcgt gccggccagc ggcgggggggc 900

gcagtgcaca cgagggggct ggacttcgcc tgtgatatct acatctgggc gcccttggcc 960

gggacttgtg gggtccttct cctgtcactg gttatcaccc tttactgcag agtgaagttc 1020

agcaggagcg cagacgcccc cgcgtaccag cagggccaga accagctcta taacgagctc 1080

aatctaggac gaagagagga gtacgatgtt ttggacaaga gacgtggccg ggaccctgag 1140

atgggggggaa agccgagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa 1200

gataagatgg cggaggccta cagtgagatt gggatgaaag gcgagcgccg gaggggcaag 1260

gggcacgatg gcctttacca gggtctcagt acagccacca aggacaccta cgacgccctt 1320

cacatgcagg ccctgccccc tcgc 1344

<210> 170
<211> 25
<212> PRT
<213> Artificial Sequence

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

<220>
<221> SITE
<222> (1)..(25)
<223> This sequence may encompass 1-5 "Gly Gly Gly Gly Ser" repeating units

<400> 170
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 171
<211> 15
<212> PRT
<213> Artificial Sequence

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

<400> 171
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 172
<211> 18
<212> PRT
<213> Artificial Sequence

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

<400> 172

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
1 5 10 15

Lys Gly

<210> 173
<211> 26
<212> PRT
<213> Artificial Sequence

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

<400> 173
Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln
20 25

<210> 174
<211> 21
<212> PRT
<213> Artificial Sequence

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

<400> 174
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro
20

<210> 175
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 175
Gly Gly Gly Gly Ser
1 5

<210> 176
<211> 400
<212> RNA
<213> Artificial Sequence

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

<220>
<221> misc_feature
<222> (1)..(400)
<223> This sequence may encompass 10-400 nucleotides

<220>
<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 176
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 120

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 180

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 240

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 300

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 360

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 400

<210> 177
<211> 200
<212> RNA
<213> Artificial Sequence

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

polynucleotide

<220>
<221> misc_feature
<222> (1)..(200)
<223> This sequence may encompass 10-200 nucleotides

<220>
<223> See specification as filed for detailed description of substitutions and preferred embodiments

<400> 177
ccccccccccc ccccccccccc ccccccccccc ccccccccccc ccccccccccc ccccccccccc 60

ccccccccccc ccccccccccc ccccccccccc ccccccccccc ccccccccccc ccccccccccc 120

ccccccccccc ccccccccccc ccccccccccc ccccccccccc ccccccccccc ccccccccccc 180

ccccccccccc ccccccccccc 200

<210> 178
<211> 98
<212> PRT
<213> Homo sapiens

<400> 178
Met Ala Leu Leu Leu Ala Leu Ser Leu Leu Val Leu Trp Thr Ser Pro
1 5 10 15

Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala Glu Asp Cys Cys Leu Ser
20 25 30

Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile Val Arg Asn Phe His Tyr
35 40 45

Leu Leu Ile Lys Asp Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr
50 55 60

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

Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser Ala Lys Met Lys Arg Arg
85 90 95

Ser Ser

<210> 179
<211> 89
<212> PRT
<213> Homo sapiens

<400> 179
Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu
1 5 10 15

Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys
            20 25 30

Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys
        35 40 45

Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys
    50 55 60

Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
65 70 75 80

Glu Tyr Leu Glu Lys Ala Leu Asn Lys
                85