SEQUENCE LISTING

<110> Adamed Sp. z o.o.

<120> przeciwnowotworowe bia³ko fuzyjne

<130> PL

<150> PL397167
<151> 2011-11-28

<160> 208

<170> PatentIn version 3.5

<210> 1
<211> 430
<212> PRT
<213> Artificial Sequence

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Tyr Asn Thr Val Ser Phe Asn Leu Gly Glu Ala Tyr Glu Tyr Pro Thr
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Phe Ile Gln Asp Leu Arg Asn Glu Leu Ala Lys Gly Thr Pro Val Cys
            20                  25                  30

Gln Leu Pro Val Thr Leu Gln Thr Ile Ala Asp Asp Lys Arg Phe Val
        35                  40                  45

Leu Val Asp Ile Thr Thr Thr Ser Lys Lys Thr Val Lys Val Ala Ile
    50                  55                  60

Asp Val Thr Asp Val Tyr Val Val Gly Tyr Gln Asp Lys Trp Asp Gly
65                  70                  75                  80

Lys Asp Arg Ala Val Phe Leu Asp Lys Val Pro Thr Val Ala Thr Ser
                85                  90                  95

Lys Leu Phe Pro Gly Val Thr Asn Arg Val Thr Leu Thr Phe Asp Gly
            100                 105                 110

Ser Tyr Gln Lys Leu Val Asn Ala Ala Lys Val Asp Arg Lys Asp Leu
        115                 120                 125

Glu Leu Gly Val Tyr Lys Leu Glu Phe Ser Ile Glu Ala Ile His Gly
    130                 135                 140

Lys Thr Ile Asn Gly Gln Glu Ile Ala Lys Phe Phe Leu Ile Val Ile
145                 150                 155                 160
```

```
Gln Met Val Ser Glu Ala Ala Arg Phe Lys Tyr Ile Glu Thr Glu Val
                165                 170                 175

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

Asn Leu Glu Asn Asn Trp Gly Asp Ile Ser Asp Ala Ile His Lys Ser
        195                 200                 205

Ser Pro Gln Cys Thr Thr Ile Asn Pro Ala Leu Gln Leu Ile Ser Pro
    210                 215                 220

Ser Asn Asp Pro Trp Val Val Asn Lys Val Ser Gln Ile Ser Pro Asp
225                 230                 235                 240

Met Gly Ile Leu Lys Phe Lys Ser Gly Gly Gly Gly Ser Arg Lys Lys
                245                 250                 255

Arg Ala Ser Gly Cys Gly Pro Glu Gly Gly Gly Gly Ser Arg Val Ala
            260                 265                 270

Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro
        275                 280                 285

Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu
    290                 295                 300

Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn
305                 310                 315                 320

Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln
                325                 330                 335

Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp
            340                 345                 350

Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro
        355                 360                 365

Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala
    370                 375                 380

Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys
385                 390                 395                 400

Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp
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405 410 415

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

<210> 2
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<213> Artificial Sequence

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<223> none

<400> 2

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
115 120 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
130 135 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145 150 155 160

Gly Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Arg Lys Lys
165 170 175

Arg Gly Gly Gly Gly Ser Glu Asp Asn Asn Ile Phe Pro Lys Gln Tyr
180 185 190

```
Pro Ile Ile Asn Phe Thr Thr Ala Gly Ala Thr Val Gln Ser Tyr Thr
        195                 200                 205

Asn Phe Ile Arg Ala Val Arg Gly Arg Leu Thr Thr Gly Ala Asp Val
    210                 215                 220

Arg His Glu Ile Pro Val Leu Pro Asn Arg Val Gly Leu Pro Ile Asn
225                 230                 235                 240

Gln Arg Phe Ile Leu Val Glu Leu Ser Asn His Ala Glu Leu Ser Val
                245                 250                 255

Thr Leu Ala Leu Asp Val Thr Asn Ala Tyr Val Val Gly Tyr Arg Ala
            260                 265                 270

Gly Asn Ser Ala Tyr Phe Phe His Pro Asp Asn Gln Glu Asp Ala Glu
        275                 280                 285

Ala Ile Thr His Leu Phe Thr Asp Val Gln Asn Arg Tyr Thr Phe Ala
    290                 295                 300

Phe Gly Gly Asn Tyr Asp Arg Leu Glu Gln Leu Ala Gly Ser Leu Arg
305                 310                 315                 320

Glu Asn Ile Glu Leu Gly Asn Gly Pro Leu Glu Glu Ala Ile Ser Ala
                325                 330                 335

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

Ser Phe Ile Val Cys Ile Gln Met Ile Ser Glu Ala Ala Arg Phe Gln
        355                 360                 365

Tyr Ile Glu Gly Glu Met Arg Thr Arg Ile Arg Tyr Asn Arg Arg Ser
    370                 375                 380

Ala Pro Asp Pro Ser Val Ile Thr Leu Glu Asn Ser Trp Gly Arg Leu
385                 390                 395                 400

Ser Thr Ala Ile Gln Glu Ser Asn Gln Gly Ala Phe Ala Ser Pro Ile
                405                 410                 415

Gln Leu Gln Arg Arg Asn Gly Ser Lys Phe Ser Val Tyr Asp Val Ser
            420                 425                 430

Ile Leu Ile Pro Ile Ile Ala Leu Met Val Tyr Arg Cys Ala Pro Pro
```

435 440 445

Pro Lys Asp Glu Leu
450

<210> 3
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<213> Artificial Sequence

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<223> none

<400> 3

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
115 120 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
130 135 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145 150 155 160

Gly Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Arg Lys Lys
165 170 175

Arg Gly Gly Gly Gly Ser Gly Pro Gly Pro Lys Gln Tyr Pro Ile Ile
180 185 190

```
Asn Phe Thr Thr Ala Gly Ala Thr Val Gln Ser Tyr Thr Asn Phe Ile
        195                 200                 205

Arg Ala Val Arg Gly Arg Leu Thr Thr Gly Ala Asp Val Arg His Glu
    210                 215                 220

Ile Pro Val Leu Pro Asn Arg Val Gly Leu Pro Ile Asn Gln Arg Phe
225                 230                 235                 240

Ile Leu Val Glu Leu Ser Asn His Ala Glu Leu Ser Val Thr Leu Ala
                245                 250                 255

Leu Asp Val Thr Asn Ala Tyr Val Val Gly Tyr Arg Ala Gly Asn Ser
            260                 265                 270

Ala Tyr Phe Phe His Pro Asp Asn Gln Glu Asp Ala Glu Ala Ile Thr
        275                 280                 285

His Leu Phe Thr Asp Val Gln Asn Arg Tyr Thr Phe Ala Phe Gly Gly
    290                 295                 300

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

Glu Leu Gly Asn Gly Pro Leu Glu Glu Ala Ile Ser Ala Leu Tyr Tyr
                325                 330                 335

Tyr Ser Thr Gly Gly Thr Gln Leu Pro Thr Leu Ala Arg Ser Phe Ile
            340                 345                 350

Ile Cys Ile Gln Met Ile Ser Glu Ala Ala Arg Phe Gln Tyr Ile Glu
        355                 360                 365

Gly Glu Met Arg Val Pro Lys Asp Glu Leu
    370                 375
```

<210> 4
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<213> Artificial Sequence

<220>
<223> none

<400> 4

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

```
Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
            20                  25                  30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
        35                  40                  45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
    50                  55                  60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65                  70                  75                  80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
                85                  90                  95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Gly Gly Gly
                165                 170                 175

Gly Ser Ala Ile Asn Thr Ile Thr Phe Asp Ala Gly Asn Ala Thr Ile
            180                 185                 190

Asn Lys Tyr Ala Thr Phe Met Glu Ser Leu Arg Asn Gln Ala Lys Asp
        195                 200                 205

Pro Lys Leu Lys Cys Tyr Gly Ile Pro Met Leu Pro Asp Thr Asn Ser
    210                 215                 220

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

Ile Thr Leu Met Leu Arg Arg Asn Asn Leu Tyr Val Met Gly Tyr Ser
                245                 250                 255

Asp Pro Phe Asn Gly Asn Lys Cys Arg Tyr His Ile Phe Asn Asp Ile
            260                 265                 270
```

```
Thr Ser Thr Glu Arg Thr Asp Val Glu Asn Thr Leu Cys Ser Ser Ser
        275                 280                 285

Ser Ser Arg Val Ala Met Ser Ile Asn Tyr Asn Ser Leu Tyr Pro Thr
    290                 295                 300

Met Glu Lys Lys Ala Glu Val Asn Ser Arg Asn Gln Val Gln Leu Gly
305                 310                 315                 320

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

Phe Pro Val Lys Thr Glu Ala Phe Phe Leu Leu Val Ala Ile Gln Met
            340                 345                 350

Val Ser Glu Ala Ala Arg Phe Lys Tyr Ile Glu Asn Gln Val Lys Thr
        355                 360                 365

Asn Phe Asn Arg Ala Phe Tyr Pro Asp Pro Lys Val Ile Asn Leu Glu
    370                 375                 380

Glu Lys Trp Gly Lys Ile Ser Glu Ala Ile His Asn Ala Lys Asn Gly
385                 390                 395                 400

Ala Leu Pro Lys Pro Leu Glu Leu Val Asp Ala Lys Gly Thr Lys Trp
                405                 410                 415

Ile Val Leu Arg Val Asp Glu Ile Asn Arg Asp Val Ala Leu Leu Lys
            420                 425                 430

Tyr Val Asn Gly Thr Cys Gln Thr Thr Tyr Gln Asn Ala Met Phe Ser
        435                 440                 445

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

Leu Phe Glu Gly Phe Lys Asp Glu Leu
465                 470
```

<210> 5
<211> 430
<212> PRT
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<223> none

<400> 5

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Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1               5                  10                  15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
            20                  25                  30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
        35                  40                  45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
    50                  55                  60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65                  70                  75                  80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
                85                  90                  95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Gly Gly Gly
                165                 170                 175

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

Gln Tyr Ser Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro
        195                 200                 205

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

Lys Asp Lys Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val
225                 230                 235                 240

Ser Leu Gly Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala
                245                 250                 255
```

```
Met Asp Asn Thr Asn Val Asn Arg Ala Tyr Tyr Phe Lys Ser Glu Ile
            260                 265                 270

Thr Ser Ala Glu Leu Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn
        275                 280                 285

Gln Lys Ala Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn
    290                 295                 300

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

Ile Asp Leu Leu Leu Thr Phe Met Glu Ala Val Asn Lys Lys Ala Arg
                325                 330                 335

Val Val Lys Asn Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr
            340                 345                 350

Ala Glu Val Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Thr Lys Asn
        355                 360                 365

Phe Pro Asn Lys Phe Asp Ser Asp Asn Lys Val Ile Gln Phe Glu Val
    370                 375                 380

Ser Trp Arg Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly
385                 390                 395                 400

Val Phe Asn Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val
                405                 410                 415

Lys Asp Leu Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro
            420                 425                 430
```

<210> 6
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 6

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Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr
1               5                   10                  15

Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys
            20                  25                  30
```

```
Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His
        35                  40                  45

Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His
    50                  55                  60

Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln
65                  70                  75                  80

Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr
                85                  90                  95

Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser
            100                 105                 110

Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser
        115                 120                 125

Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe
    130                 135                 140

Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser
145                 150                 155                 160

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Lys Lys Arg Val Thr
            180                 185                 190

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

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

Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser Lys Asp Lys Phe
225                 230                 235                 240

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

Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala Met Asp Asn Thr
            260                 265                 270

Asn Val Asn Arg Ala Tyr Tyr Phe Lys Ser Glu Ile Thr Ser Ala Glu
        275                 280                 285
```

```
Leu Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys Ala Leu
    290                 295                 300

Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln Ile Thr
305                 310                 315                 320

Gln Gly Asp Lys Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp Leu Leu
                325                 330                 335

Leu Thr Phe Met Glu Ala Val Asn Lys Lys Ala Arg Val Val Lys Asn
            340                 345                 350

Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu Val Ala
        355                 360                 365

Arg Phe Arg Tyr Ile Gln Asn Leu Val Thr Lys Asn Phe Pro Asn Lys
    370                 375                 380

Phe Asp Ser Asp Asn Lys Val Ile Gln Phe Glu Val Ser Trp Arg Lys
385                 390                 395                 400

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

Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu Gln
            420                 425                 430

Met Gly Leu Leu Met Tyr Leu Gly Lys Pro
        435                 440


<210>  7
<211>  429
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  none

<400>  7

Asp Val Ser Phe Arg Leu Ser Gly Ala Thr Ser Ser Ser Tyr Gly Val
1               5                   10                  15

Phe Ile Ser Asn Leu Arg Lys Ala Leu Pro Asn Glu Arg Lys Leu Tyr
            20                  25                  30

Asp Ile Pro Leu Leu Arg Ser Ser Leu Pro Gly Ser Gln Arg Tyr Ala
        35                  40                  45
```

```
Leu Ile His Leu Thr Asn Tyr Ala Asp Glu Thr Ile Ser Val Ala Ile
    50                  55                  60

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

Tyr Phe Phe Asn Glu Ala Ser Ala Thr Glu Ala Ala Lys Tyr Val Phe
                85                  90                  95

Lys Asp Ala Met Arg Lys Val Thr Leu Pro Tyr Ser Gly Asn Tyr Glu
            100                 105                 110

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

Leu Pro Ala Leu Asp Ser Ala Ile Thr Thr Leu Phe Tyr Tyr Asn Ala
    130                 135                 140

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

Ala Ala Arg Tyr Lys Phe Ile Glu Gln Gln Ile Gly Lys Arg Val Asp
                165                 170                 175

Lys Thr Phe Leu Pro Ser Leu Ala Ile Ile Ser Leu Glu Asn Ser Trp
            180                 185                 190

Ser Ala Leu Ser Lys Gln Ile Gln Ile Ala Ser Thr Asn Asn Gly Gln
        195                 200                 205

Phe Glu Ser Pro Val Val Leu Ile Asn Ala Gln Asn Gln Arg Val Thr
    210                 215                 220

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

Leu Asn Arg Asn Asn Met Ala Gly Gly Gly Gly Ser Arg Lys Lys Arg
                245                 250                 255

Ala Ser Gly Cys Gly Pro Glu Gly Gly Gly Gly Ser Arg Val Ala Ala
            260                 265                 270

His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn
        275                 280                 285

Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser
    290                 295                 300
```

Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly
305 310 315 320

Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr
325 330 335

Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys
340 345 350

Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile
355 360 365

Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu
370 375 380

Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu
385 390 395 400

Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met
405 410 415

Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
420 425

<210> 8
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<223> brak

<400> 8

Asp Val Ser Phe Asp Leu Ser Thr Ala Thr Lys Lys Ser Tyr Ser Ser
1 5 10 15

Phe Ile Thr Gln Leu Arg Asp Ala Leu Pro Thr Gln Gly Thr Val Cys
20 25 30

Gly Ile Pro Leu Leu Pro Ser Thr Ala Ser Gly Ser Gln Trp Phe Arg
35 40 45

Phe Phe Asn Leu Thr Asn Tyr Asn Asp Glu Thr Val Thr Val Ala Val
50 55 60

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

```
Tyr Phe Phe Glu Asp Thr Pro Ala Glu Ala Phe Lys Leu Ile Phe Ala
                85                  90                  95

Gly Thr Lys Thr Val Lys Leu Pro Tyr Ser Gly Asn Tyr Asp Lys Leu
            100                 105                 110

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

Ala Leu Ser Ser Ala Ile Thr Asn Met Val Tyr Tyr Asp Tyr Gln Ser
    130                 135                 140

Thr Ala Ala Ala Leu Leu Val Leu Ile Gln Cys Thr Ala Glu Ala Ala
145                 150                 155                 160

Arg Tyr Lys Tyr Ile Glu Gln Gln Val Ser Ser His Ile Ser Ser Asn
                165                 170                 175

Phe Tyr Pro Asn Gln Ala Val Ile Ser Leu Glu Asn Lys Trp Gly Ala
            180                 185                 190

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

Glu Asn Pro Val Glu Leu Tyr Asn Pro Asp Gly Thr Arg Phe Ser Val
    210                 215                 220

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

Tyr Tyr Lys Ala Ser Gly Gly Gly Gly Ser Arg Lys Lys Arg Ala Ser
                245                 250                 255

Gly Cys Gly Pro Glu Gly Gly Gly Gly Ser Arg Val Ala Ala His Ile
            260                 265                 270

Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys
        275                 280                 285

Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg
    290                 295                 300

Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu
305                 310                 315                 320

Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe
                325                 330                 335
```

```
Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met
            340                 345                 350

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

Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly
    370                 375                 380

Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp
385                 390                 395                 400

Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His
                405                 410                 415

Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
            420                 425
```

<210> 9
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 9

```
Tyr Glu Arg Leu Arg Leu Arg Val Thr His Gln Thr Thr Gly Glu Glu
1               5                   10                  15

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

Phe Ser Asn Glu Ile Pro Leu Leu Arg Gln Ser Thr Ile Pro Val Ser
        35                  40                  45

Asp Ala Gln Arg Phe Val Leu Val Glu Leu Thr Asn Glu Gly Gly Asp
    50                  55                  60

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

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

Glu Thr His Leu Phe Thr Gly Thr Thr Arg Ser Ser Leu Pro Phe Asn
            100                 105                 110
```

```
Gly Ser Tyr Pro Asp Leu Glu Arg Tyr Ala Gly His Arg Asp Gln Ile
        115                 120                 125

Pro Leu Gly Ile Asp Gln Leu Ile Gln Ser Val Thr Ala Leu Arg Phe
    130                 135                 140

Pro Gly Gly Ser Thr Arg Thr Gln Ala Arg Ser Ile Leu Ile Leu Ile
145                 150                 155                 160

Gln Met Ile Ser Glu Ala Ala Arg Phe Asn Pro Ile Leu Trp Arg Ala
                165                 170                 175

Arg Gln Tyr Ile Asn Ser Gly Ala Ser Phe Leu Pro Asp Val Tyr Met
            180                 185                 190

Leu Glu Leu Glu Thr Ser Trp Gly Gln Gln Ser Thr Gln Val Gln Gln
        195                 200                 205

Ser Thr Asp Gly Val Phe Asn Asn Pro Ile Arg Leu Ala Ile Pro Pro
    210                 215                 220

Gly Asn Phe Val Thr Leu Thr Asn Val Arg Asp Val Ile Ala Ser Leu
225                 230                 235                 240

Ala Ile Met Leu Phe Val Cys Gly Glu Gly Gly Gly Gly Gly Ser Ala
                245                 250                 255

Ser Gly Cys Gly Pro Glu Gly Gly Gly Gly Ser Arg Val Ala Ala His
            260                 265                 270

Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser
        275                 280                 285

Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser
    290                 295                 300

Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu
305                 310                 315                 320

Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr
                325                 330                 335

Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln
            340                 345                 350

Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu
        355                 360                 365
```

```
Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr
    370                 375                 380

Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn
385                 390                 395                 400

Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp
                405                 410                 415

His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
            420                 425
```

<210> 10
<211> 462
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 10

```
Ile Asp Tyr Pro Ser Val Ser Phe Asn Leu Ala Gly Ala Lys Ser Thr
1               5                   10                  15

Thr Tyr Arg Asp Phe Leu Lys Asn Leu Arg Asp Arg Val Ala Thr Gly
            20                  25                  30

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

Gln Val Lys Asn Arg Phe Val Leu Val Arg Leu Thr Asn Tyr Asn Gly
    50                  55                  60

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

Phe Ser Ala Asn Gly Asn Ser Tyr Phe Phe Lys Asp Ala Thr Glu Leu
                85                  90                  95

Gln Lys Ser Asn Leu Phe Leu Gly Thr Thr Gln His Thr Leu Ser Phe
            100                 105                 110

Thr Gly Asn Tyr Asp Asn Leu Glu Thr Ala Ala Gly Thr Arg Arg Glu
        115                 120                 125

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

```
Trp Tyr Asp Gly Gly Val Ala Arg Ser Leu Leu Val Leu Ile Gln Met
145                 150                 155                 160

Val Pro Glu Ala Ala Arg Phe Arg Tyr Ile Glu Gln Glu Val Arg Arg
                165                 170                 175

Ser Leu Gln Gln Leu Thr Ser Phe Thr Pro Asn Ala Leu Met Leu Ser
            180                 185                 190

Met Glu Asn Asn Trp Ser Ser Met Ser Leu Glu Val Gln Leu Ser Gly
        195                 200                 205

Asp Asn Val Ser Pro Phe Ser Gly Thr Val Gln Leu Gln Asn Tyr Asp
    210                 215                 220

His Thr Pro Arg Leu Val Asp Asn Phe Glu Glu Leu Tyr Lys Ile Thr
225                 230                 235                 240

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

Asn Ala Ile Arg Met Pro His Val Leu Val Gly Glu Asp Asn Lys Phe
            260                 265                 270

Asn Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Arg Lys Lys
        275                 280                 285

Arg Gly Gly Gly Gly Val Arg Glu Arg Gly Pro Gln Arg Arg Val Ala
    290                 295                 300

Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro
305                 310                 315                 320

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

Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn
            340                 345                 350

Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln
        355                 360                 365

Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp
    370                 375                 380

Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro
385                 390                 395                 400
```

```
Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala
                405                 410                 415

Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys
            420                 425                 430

Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp
        435                 440                 445

Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
    450                 455                 460
```

<210> 11
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 11

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

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

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

Gln Val Lys Ser Arg Phe Val Leu Val Pro Leu Thr Asn Tyr Asn Gly
    50                  55                  60

Asn Thr Val Thr Leu Ala Val Asp Val Thr Asn Leu Tyr Val Val Ala
65                  70                  75                  80

Phe Ser Gly Asn Ala Asn Ser Tyr Phe Phe Lys Asp Ala Thr Glu Val
                85                  90                  95

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

Thr Gly Asn Tyr Asp Asn Leu Glu Thr Ala Ala Asn Thr Arg Arg Glu
        115                 120                 125

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

```
Tyr His Gly Asp Ser Val Ala Arg Ser Leu Leu Val Val Ile Gln Met
145                 150                 155                 160

Val Ser Glu Ala Ala Arg Phe Arg Tyr Ile Glu Gln Glu Val Arg Arg
                165                 170                 175

Ser Leu Gln Gln Ala Thr Ser Phe Thr Pro Asn Ala Leu Met Leu Ser
            180                 185                 190

Met Glu Asn Asn Trp Ser Ser Met Ser Leu Glu Ile Gln Gln Ala Gly
        195                 200                 205

Asn Asn Val Ser Pro Phe Phe Gly Thr Val Gln Leu Leu Asn Tyr Asp
    210                 215                 220

His Thr His Arg Leu Val Asp Asn Phe Glu Glu Leu Tyr Lys Ile Thr
225                 230                 235                 240

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

Ala Ile Arg Met Pro Leu Asp Leu Ala Gly Glu Asp Asn Lys Tyr Asn
            260                 265                 270

Gly Gly Gly Gly Ser Arg Lys Lys Arg Ala Ser Gly Cys Gly Pro Glu
        275                 280                 285

Gly Gly Gly Gly Ser Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly
    290                 295                 300

Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu
305                 310                 315                 320

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

Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys
            340                 345                 350

Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu
        355                 360                 365

Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr
    370                 375                 380

Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg
385                 390                 395                 400
```

```
Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr
                405                 410                 415

Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser
            420                 425                 430

Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe
        435                 440                 445

Gly Ala Phe Leu Val Gly
    450
```

<210> 12
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 12

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

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
            20                  25                  30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
        35                  40                  45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
    50                  55                  60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65                  70                  75                  80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
                85                  90                  95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140
```

```
Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

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

Thr Glu Tyr Glu Ala Cys Arg Val Arg Cys Gln Val Ala Glu His Gly
            180                 185                 190

Val Glu Arg Gln Arg Arg Cys Gln Gln Val Cys Glu Lys Arg Leu Arg
        195                 200                 205

Glu Arg Glu Gly Arg Arg Glu Val Asp Lys Asp Glu Leu
    210                 215                 220
```

<210> 13
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 13

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

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
            20                  25                  30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
        35                  40                  45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
    50                  55                  60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65                  70                  75                  80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
                85                  90                  95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125
```

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
130 135 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145 150 155 160

Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Arg Lys Lys Arg
165 170 175

Ala Ser Gly Gly Pro Arg Gly Ser Pro Arg Thr Glu Tyr Glu Ala Cys
180 185 190

Arg Val Arg Cys Gln Val Ala Glu His Gly Val Glu Arg Gln Arg Arg
195 200 205

Cys Gln Gln Val Cys Glu Lys Arg Leu Arg Glu Arg Glu Gly Arg Arg
210 215 220

Glu Val Asp
225

<210> 14
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 14

Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile
1 5 10 15

Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile
20 25 30

Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys
35 40 45

Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg
50 55 60

Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu
65 70 75 80

Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe
85 90 95

Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met

100 105 110

Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu
115 120 125

Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly
130 135 140

Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp
145 150 155 160

Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His
165 170 175

Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Gly Gly Gly Ser
180 185 190

Ala Ser Gly Cys Gly Pro Glu Arg Lys Lys Arg Pro Arg Gly Ser Pro
195 200 205

Arg Thr Glu Tyr Glu Ala Cys Arg Val Arg Cys Gln Val Ala Glu His
210 215 220

Gly Val Glu Arg Gln Arg Arg Cys Gln Gln Val Cys Glu Lys Arg Leu
225 230 235 240

Arg Glu Arg Glu Gly Arg Arg Glu Val Asp Lys Asp Glu Leu
245 250

<210> 15
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 15

Val Phe Pro Lys Val Pro Phe Asp Val Pro Lys Ala Thr Val Glu Ser
1 5 10 15

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

Ser Pro Gln Gly Ile Arg Arg Leu Arg Asn Pro Ala Glu Ile Gln Pro
35 40 45

Ser Gln Gly Phe Ile Leu Ile Gln Leu Thr Gly Tyr Val Gly Ser Val
50 55 60

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

His Asn Val Leu Tyr His Phe Asn Asp Val Ser Ala Ser Ser Ile Ala
                85                  90                  95

Ser Val Phe Pro Asp Ala Gln Arg Arg Gln Leu Pro Phe Gly Gly Gly
            100                 105                 110

Tyr Pro Ser Met Arg Asn Tyr Ala Pro Glu Arg Asp Gln Ile Asp His
        115                 120                 125

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

Asn Asn Asn Gln Ile Ala Leu Gly Leu Val Ile Cys Ala Gly Met Val
145                 150                 155                 160

Ala Glu Ala Ser Arg Phe Arg Tyr Ile Glu Gly Leu Val Arg Gln Ser
                165                 170                 175

Ile Val Gly Pro Gly Asp Tyr Arg Thr Phe Arg Pro Asp Ala Leu Met
            180                 185                 190

Tyr Ser Ile Val Thr Gln Trp Gln Thr Leu Ser Glu Arg Ile Gln Gly
        195                 200                 205

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

Pro Phe Tyr Trp Asp Asn Val Ala Gln Ala Ile Thr Arg Leu Ser Leu
225                 230                 235                 240

Met Leu Phe Val Ser Arg Ser Thr Asp Gly Gly Gly Gly Ser Arg Val
                245                 250                 255

Lys Arg Ala Ser Gly Cys Gly Pro Glu Gly Gly Gly Gly Ser Val Arg
            260                 265                 270

Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly
        275                 280                 285

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

Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe
```

305 310 315 320

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

Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu
340 345 350

Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr
355 360 365

Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg
370 375 380

Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr
385 390 395 400

Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser
405 410 415

Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe
420 425 430

Gly Ala Phe Leu Val Gly
435

<210> 16
<211> 431
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 16

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
115 120 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
130 135 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145 150 155 160

Gly Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Gly Gly Gly
165 170 175

Gly Ser Val Phe Pro Lys Val Pro Phe Asp Val Pro Lys Ala Thr Val
180 185 190

Glu Ser Tyr Thr Arg Phe Ile Arg Val Leu Arg Asp Glu Leu Ala Gly
195 200 205

Gly Val Ser Pro Gln Gly Ile Arg Arg Leu Arg Asn Pro Ala Glu Ile
210 215 220

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

Ser Val Thr Leu Ile Met Asp Val Arg Asn Ala Tyr Leu Leu Gly Tyr
245 250 255

Leu Ser His Asn Val Leu Tyr His Phe Asn Asp Val Ser Ala Ser Ser
260 265 270

Ile Ala Ser Val Phe Pro Asp Ala Gln Arg Arg Gln Leu Pro Phe Gly
275 280 285

Gly Gly Tyr Pro Ser Met Arg Asn Tyr Ala Pro Glu Arg Asp Gln Ile
290 295 300

Asp His Gly Ile Val Glu Leu Ala Tyr Ala Val Asp Arg Leu Tyr Tyr
305 310 315 320

Ser Gln Asn Asn Asn Gln Ile Ala Leu Gly Leu Val Ile Cys Ala Gly

325 330 335

Met Val Ala Glu Ala Ser Arg Phe Arg Tyr Ile Glu Gly Leu Val Arg
340 345 350

Gln Ser Ile Val Gly Pro Gly Asp Tyr Arg Thr Phe Arg Pro Asp Ala
355 360 365

Leu Met Tyr Ser Ile Val Thr Gln Trp Gln Thr Leu Ser Glu Arg Ile
370 375 380

Gln Gly Ser Phe Asn Gly Ala Phe Gln Pro Val Gln Leu Gly Tyr Ala
385 390 395 400

Ser Asp Pro Phe Tyr Trp Asp Asn Val Ala Gln Ala Ile Thr Arg Leu
405 410 415

Ser Leu Met Leu Phe Val Ser Arg Ser Thr Asp Lys Asp Glu Leu
420 425 430

<210> 17
<211> 428
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 17

Asp Val Ser Phe Arg Leu Ser Gly Ala Asp Pro Arg Ser Tyr Gly Met
1 5 10 15

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

Asn Ile Pro Leu Leu Leu Pro Ser Val Ser Gly Ala Gly Arg Tyr Leu
35 40 45

Leu Met His Leu Phe Asn Tyr Asp Gly Lys Thr Ile Thr Val Ala Leu
50 55 60

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

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

Arg Asp Ala Arg Arg Lys Ile Thr Leu Pro Tyr Ser Gly Asn Tyr Glu
100 105 110

```
Arg Leu Gln Ile Ala Ala Gly Lys Pro Arg Glu Lys Ile Pro Ile Gly
        115                 120                 125

Leu Pro Ala Leu Asp Ser Ala Ile Ser Thr Leu Leu His Tyr Asp Ser
    130                 135                 140

Thr Ala Ala Ala Gly Ala Leu Leu Val Leu Ile Gln Thr Thr Ala Glu
145                 150                 155                 160

Ala Ala Arg Phe Lys Tyr Ile Glu Gln Gln Ile Gln Glu Arg Ala Tyr
                165                 170                 175

Arg Asp Glu Val Pro Ser Leu Ala Thr Ile Ser Leu Glu Asn Ser Trp
            180                 185                 190

Ser Gly Leu Ser Lys Gln Ile Gln Leu Ala Gln Gly Asn Asn Gly Ile
        195                 200                 205

Phe Arg Thr Pro Ile Val Leu Val Asp Asn Lys Gly Asn Arg Val Gln
    210                 215                 220

Ile Thr Asn Val Thr Ser Lys Val Val Thr Ser Asn Ile Gln Leu Leu
225                 230                 235                 240

Leu Asn Thr Arg Asn Ile Gly Gly Gly Gly Ser Arg Lys Lys Arg Ala
                245                 250                 255

Ser Gly Cys Gly Pro Glu Gly Gly Gly Gly Ser Arg Val Ala Ala His
            260                 265                 270

Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser
        275                 280                 285

Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser
    290                 295                 300

Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu
305                 310                 315                 320

Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr
                325                 330                 335

Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln
            340                 345                 350

Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu
```

355 360 365

Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr
370 375 380

Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn
385 390 395 400

Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp
405 410 415

His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
420 425

<210> 18
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 18

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
115 120 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
130 135 140

```
Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Ser Ala Ser Gly Gly Pro Glu Gly Gly Ser Leu Ala
                165                 170                 175

Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr
            180                 185                 190

Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr
        195                 200                 205

Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp
    210                 215                 220

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

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

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

Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Gly Pro Ala Asp Ser
        275                 280                 285

Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe Leu
    290                 295                 300

Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn Trp
305                 310                 315                 320

Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Ala Gly
                325                 330                 335

Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser
            340                 345                 350

Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile
        355                 360                 365

Trp Ala Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr
    370                 375                 380

Ala Gln Asp Gln Glu Pro Asp Ala Ala Gly Arg Ile Arg Asn Gly Ala
```

385 390 395 400

Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Ala
405 410 415

Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg
420 425 430

Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro
435 440 445

Glu Glu Ser Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala
450 455 460

Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn
465 470 475 480

Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Ser Glu Gln Ala
485 490 495

Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Lys
500 505 510

Asp Glu Leu
515

<210> 19
<211> 528
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 19

Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn
1 5 10 15

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

Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn
35 40 45

Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr
50 55 60

Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu
65 70 75 80

```
Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr
                85                  90                  95

Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys
            100                 105                 110

Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly
        115                 120                 125

Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn
    130                 135                 140

Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe
145                 150                 155                 160

Leu Val Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Arg Lys
                165                 170                 175

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

Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr Arg His Arg
        195                 200                 205

Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln
    210                 215                 220

Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val
225                 230                 235                 240

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

Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu
            260                 265                 270

Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg Gln Gly Thr Gly
        275                 280                 285

Asn Asp Glu Ala Gly Ala Ala Asn Gly Pro Ala Asp Ser Gly Asp Ala
    290                 295                 300

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

Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn Trp Thr Val Glu
```

325 330 335

Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Ala Gly Tyr Val Phe
340 345 350

Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile Val Phe
355 360 365

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

Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp
385 390 395 400

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

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

Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly
435 440 445

His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Ser
450 455 460

Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr
465 470 475 480

Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn Val Gly Gly
485 490 495

Asp Leu Asp Pro Ser Ser Ile Pro Asp Ser Glu Gln Ala Ile Ser Ala
500 505 510

Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Lys Asp Glu Leu
515 520 525

<210> 20
<211> 526
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 20

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

```
Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
            20                  25                  30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
        35                  40                  45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
    50                  55                  60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65                  70                  75                  80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
                85                  90                  95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Arg Lys Lys Arg
                165                 170                 175

Ala Ser Gly Gly Pro Glu Gly Gly Ser Leu Ala Ala Leu Thr Ala His
            180                 185                 190

Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro
        195                 200                 205

Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu
    210                 215                 220

Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln
225                 230                 235                 240

Val Ile Ala Asn Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly
                245                 250                 255

Glu Ala Ile Arg Glu Ser Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu
```

260 265 270

Ala Ala Ala Glu Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Asp
275 280 285

Glu Ala Gly Ala Ala Asn Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu
290 295 300

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

Val Ser Phe Ser Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu
325 330 335

Leu Gln Ala His Arg Gln Leu Glu Glu Ala Gly Tyr Val Phe Val Gly
340 345 350

Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly
355 360 365

Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile Trp Ala Gly Phe Tyr
370 375 380

Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu
385 390 395 400

Pro Asp Ala Ala Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr
405 410 415

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

Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro
435 440 445

Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Ser Gly Gly
450 455 460

Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val
465 470 475 480

Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn Val Gly Gly Asp Leu
485 490 495

Asp Pro Ser Ser Ile Pro Asp Ser Glu Gln Ala Ile Ser Ala Leu Pro
500 505 510

Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Lys Asp Glu Leu
515 520 525

<210> 21
<211> 534
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 21

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
115 120 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
130 135 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145 150 155 160

Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Arg Lys Lys Arg
165 170 175

Ala Ser Gly Gly Pro Glu Gly Gly Ser Leu Ala Ala Leu Thr Ala His
180 185 190

Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro

195 200 205

Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu
210 215 220

Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln
225 230 235 240

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

Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu
260 265 270

Ala Ala Ala Glu Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Val
275 280 285

Val Ser Leu Thr Cys Pro Val Ala Ala Gly Glu Cys Ala Gly Pro Ala
290 295 300

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

Phe Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln
325 330 335

Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu
340 345 350

Arg Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala
355 360 365

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

Ala Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr
385 390 395 400

Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg Asn
405 410 415

Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe
420 425 430

Tyr Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val
435 440 445

Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr
450 455 460

Gly Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro
465 470 475 480

Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro
485 490 495

Arg Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu
500 505 510

Gln Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro
515 520 525

Pro Arg Glu Asp Leu Lys
530

<210> 22
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 22

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Asn Phe Lys Phe Arg Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe

115 120 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu Arg
130 135 140

Leu Arg Asp Met His His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145 150 155 160

Gly Gly Gly Gly Ser Ala Ser Gly Gly Pro Glu Gly Gly Ser Leu Ala
165 170 175

Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr
180 185 190

Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr
195 200 205

Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp
210 215 220

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

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

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

Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Gly Pro Ala Asp Ser
275 280 285

Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe Leu
290 295 300

Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn Trp
305 310 315 320

Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg Gly
325 330 335

Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser
340 345 350

Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile
355 360 365

Trp Ala Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr
370 375 380

Ala Gln Asp Gln Glu Pro Asp Ala Ala Gly Arg Ile Arg Asn Gly Ala
385 390 395 400

Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Ala
405 410 415

Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg
420 425 430

Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro
435 440 445

Glu Glu Ser Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala
450 455 460

Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn
465 470 475 480

Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Ser Glu Gln Ala
485 490 495

Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Lys
500 505 510

Asp Glu Leu
515

<210> 23
<211> 528
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 23

Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn
1 5 10 15

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

Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn
35 40 45

Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr

50 55 60

Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu
65 70 75 80

Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr
85 90 95

Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys
100 105 110

Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly
115 120 125

Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn
130 135 140

Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe
145 150 155 160

Leu Val Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Arg Lys
165 170 175

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

Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr Arg His Arg
195 200 205

Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln
210 215 220

Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val
225 230 235 240

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

Leu Gly Glu Ala Ile Arg Glu Ser Pro Glu Gln Ala Arg Leu Ala Leu
260 265 270

Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg Gln Gly Thr Gly
275 280 285

Asn Asp Glu Ala Gly Ala Ala Asn Gly Pro Ala Asp Ser Gly Asp Ala
290 295 300

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

Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn Trp Thr Val Glu
325 330 335

Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg Gly Tyr Val Phe
340 345 350

Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile Val Phe
355 360 365

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

Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp
385 390 395 400

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

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

Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly
435 440 445

His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Ser
450 455 460

Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr
465 470 475 480

Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn Val Gly Gly
485 490 495

Asp Leu Asp Pro Ser Ser Ile Pro Asp Ser Glu Gln Ala Ile Ser Ala
500 505 510

Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Lys Asp Glu Leu
515 520 525

<210> 24
<211> 526
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 24

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

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
            20                  25                  30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
        35                  40                  45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
    50                  55                  60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65                  70                  75                  80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
                85                  90                  95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Arg Lys Lys Arg
                165                 170                 175

Ala Ser Gly Gly Pro Glu Gly Gly Ser Leu Ala Ala Leu Thr Ala His
            180                 185                 190

Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro
        195                 200                 205

Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu
    210                 215                 220

Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln
225                 230                 235                 240
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```
Val Ile Ala Asn Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly
                245                 250                 255

Glu Ala Ile Arg Glu Ser Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu
            260                 265                 270

Ala Ala Ala Glu Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Asp
        275                 280                 285

Glu Ala Gly Ala Ala Asn Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu
    290                 295                 300

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

Val Ser Phe Ser Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu
                325                 330                 335

Leu Gln Ala His Arg Gln Leu Glu Glu Arg Gly Tyr Val Phe Val Gly
            340                 345                 350

Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly
        355                 360                 365

Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile Trp Ala Gly Phe Tyr
    370                 375                 380

Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu
385                 390                 395                 400

Pro Asp Ala Ala Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr
                405                 410                 415

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

Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro
        435                 440                 445

Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Ser Gly Gly
    450                 455                 460

Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val
465                 470                 475                 480

Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn Val Gly Gly Asp Leu
                485                 490                 495
```

Asp Pro Ser Ser Ile Pro Asp Ser Glu Gln Ala Ile Ser Ala Leu Pro
500 505 510

Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Lys Asp Glu Leu
515 520 525

<210> 25
<211> 423
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 25

Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser
1 5 10 15

Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser
20 25 30

Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp Asn
35 40 45

Leu Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe
50 55 60

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

Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser
85 90 95

His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp Ser
100 105 110

Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly Met
115 120 125

Gln Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser
130 135 140

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

Phe Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg
165 170 175

```
Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val Met
            180                 185                 190

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

Val Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val Gly Arg Ile
    210                 215                 220

Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala Leu Ile Leu
225                 230                 235                 240

Asn Ser His His Ala Ser Gly Gly Gly Gly Ser Arg Val Lys Arg Val
                245                 250                 255

Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg
            260                 265                 270

Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala
        275                 280                 285

Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser
    290                 295                 300

Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu
305                 310                 315                 320

Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu
                325                 330                 335

Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile
            340                 345                 350

Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala
        355                 360                 365

Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile
    370                 375                 380

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

Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe
                405                 410                 415

Phe Gly Ala Phe Leu Val Gly
            420
```

<210> 26
<211> 432
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 26

```
Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr
1               5                   10                  15

Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile
            20                  25                  30

Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu
        35                  40                  45

His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr
    50                  55                  60

Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn
65                  70                  75                  80

Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser
                85                  90                  95

Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp
            100                 105                 110

Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile
        115                 120                 125

Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu
    130                 135                 140

His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu
145                 150                 155                 160

Val Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Arg Lys Lys
                165                 170                 175

Arg Gly Gly Gly Gly Ser Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala
            180                 185                 190

Lys Thr Tyr Val Asp Ser Leu Asn Val Ile Arg Ser Ala Ile Gly Thr
        195                 200                 205
```

Pro Leu Gln Thr Ile Ser Ser Gly Gly Thr Ser Leu Leu Met Ile Asp
210 215 220

Ser Gly Thr Gly Asp Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp
225 230 235 240

Pro Glu Glu Gly Arg Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn
245 250 255

Asn Leu Tyr Val Thr Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr
260 265 270

Arg Phe Ala Asp Phe Ser His Val Thr Phe Pro Gly Thr Thr Ala Val
275 280 285

Thr Leu Ser Gly Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly
290 295 300

Ile Ser Arg Thr Gly Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser
305 310 315 320

Tyr Leu Asp Leu Met Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val
325 330 335

Ala Arg Ala Met Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg
340 345 350

Phe Arg Gln Ile Gln Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser
355 360 365

Gly Arg Ser Tyr Val Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn
370 375 380

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

Val Arg Val Gly Arg Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly
405 410 415

Ser Val Ala Leu Ile Leu Asn Ser His His Ala Ser Lys Asp Glu Leu
420 425 430

<210> 27
<211> 338
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 27

```
Ala Thr Trp Thr Cys Ile Asn Gln Gln Leu Asn Pro Lys Thr Asn Lys
1               5                  10                  15

Trp Glu Asp Lys Arg Leu Leu Tyr Ser Gln Ala Lys Ala Glu Ser Asn
            20                  25                  30

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

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

Arg Thr Pro Ile Lys Phe Gly Lys Ala Asp Cys Asp Arg Pro Pro Lys
65                  70                  75                  80

His Ser Gln Asn Gly Met Gly Lys Asp Asp His Tyr Leu Leu Glu Phe
                85                  90                  95

Pro Thr Phe Pro Asp Gly His Asp Tyr Lys Phe Asp Ser Lys Lys Pro
            100                 105                 110

Lys Glu Asp Pro Gly Pro Ala Arg Val Ile Tyr Thr Tyr Pro Asn Lys
        115                 120                 125

Val Phe Cys Gly Ile Val Ala His Gln Arg Gly Asn Gln Gly Asp Leu
    130                 135                 140

Arg Leu Cys Ser His Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg
145                 150                 155                 160

Lys Lys Arg Ala Ser Gly Cys Gly Pro Glu Val Arg Glu Arg Gly Pro
                165                 170                 175

Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr
            180                 185                 190

Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile
        195                 200                 205

Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu
    210                 215                 220

His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr
225                 230                 235                 240
```

Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn
245 250 255

Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser
260 265 270

Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp
275 280 285

Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile
290 295 300

Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu
305 310 315 320

His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu
325 330 335

Val Gly

<210> 28
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 28

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser

100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
115 120 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
130 135 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145 150 155 160

Gly Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Arg Lys Lys
165 170 175

Arg Gly Gly Gly Gly Ser Ala Thr Trp Thr Cys Ile Asn Gln Gln Leu
180 185 190

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

Ala Lys Ala Glu Ser Asn Ser His His Ala Pro Leu Ser Asp Gly Lys
210 215 220

Thr Gly Ser Ser Tyr Pro His Trp Phe Thr Asn Gly Tyr Asp Gly Asn
225 230 235 240

Gly Lys Leu Ile Lys Gly Arg Thr Pro Ile Lys Phe Gly Lys Ala Asp
245 250 255

Cys Asp Arg Pro Pro Lys His Ser Gln Asn Gly Met Gly Lys Asp Asp
260 265 270

His Tyr Leu Leu Glu Phe Pro Thr Phe Pro Asp Gly His Asp Tyr Lys
275 280 285

Phe Asp Ser Lys Lys Pro Lys Glu Asp Pro Gly Pro Ala Arg Val Ile
290 295 300

Tyr Thr Tyr Pro Asn Lys Val Phe Cys Gly Ile Val Ala His Gln Arg
305 310 315 320

Gly Asn Gln Gly Asp Leu Arg Leu Cys Ser His Lys Asp Glu Leu
325 330 335

<210> 29
<211> 319
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 29

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

Phe Lys Val Asp Val Ala Thr Ala Gln Ala Gln Ala Arg Lys Ala Gly
            20                  25                  30

Leu Thr Thr Gly Lys Ser Gly Asp Pro His Arg Tyr Phe Ala Gly Asp
        35                  40                  45

His Ile Arg Trp Gly Val Asn Asn Cys Asp Lys Ala Asp Ala Ile Leu
    50                  55                  60

Trp Glu Tyr Pro Ile Tyr Trp Val Gly Lys Asn Ala Glu Trp Ala Lys
65                  70                  75                  80

Asp Val Lys Thr Ser Gln Gln Lys Gly Gly Pro Thr Pro Ile Arg Val
                85                  90                  95

Val Tyr Ala Asn Ser Arg Gly Ala Val Gln Tyr Cys Gly Val Met Thr
            100                 105                 110

His Ser Lys Val Asp Lys Asn Asn Gln Gly Lys Glu Phe Phe Glu Lys
        115                 120                 125

Cys Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Lys Lys Arg
    130                 135                 140

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

Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser
                165                 170                 175

Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp
            180                 185                 190

Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg
        195                 200                 205

Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser
    210                 215                 220

Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn
```

225 230 235 240

Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp
245 250 255

Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp
260 265 270

Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu
275 280 285

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

Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
305 310 315

<210> 30
<211> 290
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 30

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
115 120 125

```
Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Arg Lys Lys
                165                 170                 175

Arg Glu Arg Gly Glu Ile Trp Leu Val Ser Leu Asp Pro Thr Ala Gly
            180                 185                 190

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

Phe Asn Arg Val Thr Arg Leu Pro Val Val Val Pro Val Thr Ser Gly
    210                 215                 220

Gly Asn Phe Ala Arg Thr Ala Gly Phe Ala Val Ser Leu Asp Gly Val
225                 230                 235                 240

Gly Ile Arg Thr Thr Gly Val Val Arg Cys Asp Gln Pro Arg Thr Ile
                245                 250                 255

Asp Met Lys Ala Arg Gly Gly Lys Arg Leu Glu Arg Val Pro Glu Thr
            260                 265                 270

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

Glu Leu
    290
```

<210> 31
<211> 277
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 31

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

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
            20                  25                  30
```

```
Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
        35                  40                  45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
    50                  55                  60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65                  70                  75                  80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
                85                  90                  95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Arg Lys Lys
                165                 170                 175

Arg Gln Phe Lys Val Tyr Thr Tyr Lys Arg Glu Ser Arg Tyr Arg Leu
            180                 185                 190

Phe Val Asp Val Gln Ser Asp Ile Ile Asp Thr Pro Gly Arg Arg Met
        195                 200                 205

Val Ile Pro Leu Ala Ser Ala Arg Leu Leu Ser Asp Lys Val Ser Arg
    210                 215                 220

Glu Leu Tyr Pro Val Val His Ile Gly Asp Glu Ser Trp Arg Met Met
225                 230                 235                 240

Thr Thr Asp Met Ala Ser Val Pro Val Ser Val Ile Gly Glu Glu Val
                245                 250                 255

Ala Asp Leu Ser His Arg Glu Asn Asp Ile Lys Asn Ala Ile Asn Leu
            260                 265                 270

Met Phe Trp Gly Ile
        275
```

<210> 32
<211> 228
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 32

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

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
            20                  25                  30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
        35                  40                  45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
    50                  55                  60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65                  70                  75                  80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
                85                  90                  95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Arg Lys Lys
                165                 170                 175

Arg Gln Phe Lys Val Tyr Thr Tyr Lys Gly Gly Ser Gly Gly Arg Leu
            180                 185                 190

Leu Ser Asp Lys Val Ser Arg Glu Leu Gly Gly Ser Gly Gly Ser His
        195                 200                 205
```

Arg Glu Asn Asp Ile Lys Asn Ala Ile Asn Leu Met Phe Trp Gly Ile
210 215 220

Lys Asp Glu Leu
225

<210> 33
<211> 275
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 33

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
115 120 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
130 135 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145 150 155 160

Gly Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Arg Lys Lys
165 170 175

Arg Ala Tyr Phe Leu Asp Phe Asp Glu Arg Ala Leu Lys Glu Trp Arg
180 185 190

Lys Leu Gly Ser Thr Val Arg Glu Gln Leu Lys Lys Lys Leu Val Glu
195 200 205

Val Leu Glu Ser Pro Arg Ile Glu Ala Asn Lys Leu Arg Gly Met Pro
210 215 220

Asp Cys Tyr Lys Ile Lys Leu Arg Ser Ser Gly Tyr Arg Leu Val Tyr
225 230 235 240

Gln Val Ile Asp Glu Lys Val Val Val Phe Val Ile Ser Val Gly Lys
245 250 255

Arg Glu Arg Ser Glu Val Tyr Ser Glu Ala Val Lys Arg Ile Leu Lys
260 265 270

Asp Glu Leu
275

<210> 34
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 34

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser

100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
115 120 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
130 135 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145 150 155 160

Gly Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Arg Lys Lys
165 170 175

Arg Pro Glu Leu Glu Trp Lys Ala Ala Ala Val Ala Asp Leu Leu Ala
180 185 190

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

Met Glu Glu Ile Gln Asp Lys Val Ala Gln Leu Pro Ala His Pro Lys
210 215 220

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

Pro Asn Tyr Leu Val Val Tyr Ala Glu Thr Pro Ala Val Val Thr Ile
245 250 255

Leu Arg Val Leu His Ala Ala Gln Met Trp Pro Lys Asp Glu Leu
260 265 270

<210> 35
<211> 429
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 35

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

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

Asn Ser His Gly Ile Pro Leu Leu Arg Lys Lys Ala Asp Asp Pro Gly
35 40 45

```
Lys Ala Phe Val Leu Val Ala Leu Ser Asn Asp Asn Gly Gln Leu Ala
    50                  55                  60

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

Arg Asn Arg Ser Tyr Phe Phe Lys Asp Ala Pro Asp Ala Ala Tyr Glu
                85                  90                  95

Gly Leu Phe Lys Asn Thr Ile Lys Thr Arg Leu His Phe Gly Gly Ser
            100                 105                 110

Tyr Pro Ser Leu Glu Gly Glu Lys Ala Tyr Arg Glu Thr Thr Asp Leu
        115                 120                 125

Gly Ile Glu Pro Leu Arg Ile Gly Ile Lys Lys Leu Asp Glu Asn Ala
    130                 135                 140

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

Ile Gln Met Val Ser Glu Ala Ala Arg Phe Thr Phe Ile Glu Asn Gln
                165                 170                 175

Ile Arg Asn Asn Phe Gln Gln Arg Ile Arg Pro Ala Asn Asn Thr Ile
            180                 185                 190

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

Gly Ala Asn Gly Met Phe Ser Glu Ala Val Glu Leu Glu Arg Ala Asn
    210                 215                 220

Gly Lys Lys Tyr Tyr Val Thr Ala Val Asp Gln Val Lys Pro Lys Ile
225                 230                 235                 240

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

Gly Gly Gly Gly Ser Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala
            260                 265                 270

His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn
        275                 280                 285

Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser
```

290 295 300

Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly
305 310 315 320

Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr
325 330 335

Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys
340 345 350

Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile
355 360 365

Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu
370 375 380

Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu
385 390 395 400

Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met
405 410 415

Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
420 425

<210> 36
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 36

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

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

Asn Ser His Gly Ile Pro Leu Leu Arg Lys Lys Ala Asp Asp Pro Gly
35 40 45

Lys Ala Phe Val Leu Val Ala Leu Ser Asn Asp Asn Gly Gln Leu Ala
50 55 60

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

```
Arg Asn Arg Ser Tyr Phe Phe Lys Asp Ala Pro Asp Ala Ala Tyr Glu
                85                  90                  95

Gly Leu Phe Lys Asn Thr Ile Lys Thr Arg Leu His Phe Gly Gly Ser
            100                 105                 110

Tyr Pro Ser Leu Glu Gly Glu Lys Ala Tyr Arg Glu Thr Thr Asp Leu
        115                 120                 125

Gly Ile Glu Pro Leu Arg Ile Gly Ile Lys Lys Leu Asp Glu Asn Ala
    130                 135                 140

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

Ile Gln Met Val Ser Glu Ala Ala Arg Phe Thr Phe Ile Glu Asn Gln
                165                 170                 175

Ile Arg Asn Asn Phe Gln Gln Arg Ile Arg Pro Ala Asn Asn Thr Ile
            180                 185                 190

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

Gly Ala Asn Gly Met Phe Ser Glu Ala Val Glu Leu Glu Arg Ala Asn
    210                 215                 220

Gly Lys Lys Tyr Tyr Val Thr Ala Val Asp Gln Val Lys Pro Lys Ile
225                 230                 235                 240

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

Arg Lys Lys Arg Ala Ser Gly Cys Gly Pro Glu Gly Gly Gly Gly Ser
            260                 265                 270

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

Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile
    290                 295                 300

Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu
305                 310                 315                 320

His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr
```

325 330 335

Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn
340 345 350

Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser
355 360 365

Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp
370 375 380

Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile
385 390 395 400

Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu
405 410 415

His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu
420 425 430

Val Gly

<210> 37
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 37

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

```
Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Ala Ser Gly Cys Gly Pro Glu Gly Gly Gly Gly Ser Gly Leu Asp
                165                 170                 175

Thr Val Ser Phe Ser Thr Lys Gly Ala Thr Tyr Ile Thr Tyr Val Asn
            180                 185                 190

Phe Leu Asn Glu Leu Arg Val Lys Leu Lys Pro Glu Gly Asn Ser His
        195                 200                 205

Gly Ile Pro Leu Leu Arg Lys Lys Ala Asp Asp Pro Gly Lys Ala Phe
    210                 215                 220

Val Leu Val Ala Leu Ser Asn Asp Asn Gly Gln Leu Ala Glu Ile Ala
225                 230                 235                 240

Ile Asp Val Thr Ser Val Tyr Val Val Gly Tyr Gln Val Arg Asn Arg
                245                 250                 255

Ser Tyr Phe Phe Lys Asp Ala Pro Asp Ala Ala Tyr Glu Gly Leu Phe
            260                 265                 270

Lys Asn Thr Ile Lys Thr Arg Leu His Phe Gly Gly Ser Tyr Pro Ser
        275                 280                 285

Leu Glu Gly Glu Lys Ala Tyr Arg Glu Thr Thr Asp Leu Gly Ile Glu
    290                 295                 300

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

Tyr Lys Pro Thr Glu Ile Ala Ser Ser Leu Leu Val Val Ile Gln Met
                325                 330                 335

Val Ser Glu Ala Ala Arg Phe Thr Phe Ile Glu Asn Gln Ile Arg Asn
```

340 345 350

Asn Phe Gln Gln Arg Ile Arg Pro Ala Asn Asn Thr Ile Ser Leu Glu
355 360 365

Asn Lys Trp Gly Lys Leu Ser Phe Gln Ile Arg Thr Ser Gly Ala Asn
370 375 380

Gly Met Phe Ser Glu Ala Val Glu Leu Glu Arg Ala Asn Gly Lys Lys
385 390 395 400

Tyr Tyr Val Thr Ala Val Asp Gln Val Lys Pro Lys Ile Ala Leu Leu
405 410 415

Lys Phe Val Asp Lys Asp Pro Lys Asp Glu Leu
420 425

<210> 38
<211> 433
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 38

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

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

Asn Ser His Gly Ile Pro Leu Leu Arg Lys Lys Ala Asp Asp Pro Gly
35 40 45

Lys Ala Phe Val Leu Val Ala Leu Ser Asn Asp Asn Gly Gln Leu Ala
50 55 60

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

Arg Asn Arg Ser Tyr Phe Phe Lys Asp Ala Pro Asp Ala Ala Tyr Glu
85 90 95

Gly Leu Phe Lys Asn Thr Ile Lys Thr Arg Leu His Phe Gly Gly Ser
100 105 110

Tyr Pro Ser Leu Glu Gly Glu Lys Ala Tyr Arg Glu Thr Thr Asp Leu
115 120 125

```
Gly Ile Glu Pro Leu Arg Ile Gly Ile Lys Lys Leu Asp Glu Asn Ala
    130                 135                 140

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

Ile Gln Met Val Ser Glu Ala Ala Arg Phe Thr Phe Ile Glu Asn Gln
                165                 170                 175

Ile Arg Asn Asn Phe Gln Gln Arg Ile Arg Pro Ala Asn Asn Thr Ile
            180                 185                 190

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

Gly Ala Asn Gly Met Phe Ser Glu Ala Val Glu Leu Glu Arg Ala Asn
    210                 215                 220

Gly Lys Lys Tyr Tyr Val Thr Ala Val Asp Gln Val Lys Pro Lys Ile
225                 230                 235                 240

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

Arg Lys Lys Arg Ala Ser Gly Cys Gly Pro Glu Gly Gly Gly Gly Ser
            260                 265                 270

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
        275                 280                 285

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
    290                 295                 300

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
305                 310                 315                 320

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
                325                 330                 335

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
            340                 345                 350

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
        355                 360                 365

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
```

370 375 380

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
385 390 395 400

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
405 410 415

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
420 425 430

Gly

<210> 39
<211> 558
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 39

Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met Glu Asn
1 5 10 15

Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val Asp Ser Ile Gln
20 25 30

Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp Asp
35 40 45

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

Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly Val
65 70 75 80

Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val
85 90 95

Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu
100 105 110

Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe Gly
115 120 125

Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly Ser
130 135 140

```
Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu Ser
145                 150                 155                 160

Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln Asp
                165                 170                 175

Ala Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn Arg Val Arg
            180                 185                 190

Arg Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val
        195                 200                 205

Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly
    210                 215                 220

Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val Ser Glu
225                 230                 235                 240

Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu Glu
                245                 250                 255

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

Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln Val
        275                 280                 285

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

Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala
305                 310                 315                 320

Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser
                325                 330                 335

Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val Asp
            340                 345                 350

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

Gln Val Val His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly His
    370                 375                 380

Lys Thr His Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Val Ala
```

385 390 395 400

Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro
405 410 415

Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu
420 425 430

Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn
435 440 445

Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln
450 455 460

Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp
465 470 475 480

Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro
485 490 495

Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala
500 505 510

Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys
515 520 525

Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp
530 535 540

Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
545 550 555

<210> 40
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 40

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

```
Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
    50                  55                  60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65                  70                  75                  80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
                85                  90                  95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Lys Lys Arg Pro Glu
                165                 170                 175

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

Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu
        195                 200                 205

Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala
    210                 215                 220

Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu
225                 230                 235                 240

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

Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu
            260                 265                 270

Arg Phe Val Arg Gln Gly Thr Gly Asn Gly Gly Gly Gly Ala Asp Asp
        275                 280                 285

Val Val Asp Ser Ser Lys Ser Phe Val Met Glu Asn Phe Ser Ser Tyr
```

290 295 300

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

Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp Asp Asp Trp Lys Gly
325 330 335

Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala Gly Tyr Ser Val Asp
340 345 350

Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly Val Val Lys Val Thr
355 360 365

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

Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu Pro Leu Met Glu
385 390 395 400

Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe Gly Asp Gly Ala Ser
405 410 415

Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly Ser Ser Ser Val Glu
420 425 430

Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu Ser Val Glu Leu Glu
435 440 445

Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln Asp Ala Met Tyr Glu
450 455 460

Tyr Met Ala Gln Ala Cys Ala Gly Asn Arg Val Arg Arg Lys Asp Glu
465 470 475 480

Leu

<210> 41
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 41

Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met Glu Asn
1 5 10 15

```
Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val Asp Ser Ile Gln
            20                  25                  30

Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp Asp
        35                  40                  45

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

Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly Val
65                  70                  75                  80

Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val
                85                  90                  95

Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu
            100                 105                 110

Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe Gly
        115                 120                 125

Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly Ser
    130                 135                 140

Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu Ser
145                 150                 155                 160

Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln Asp
                165                 170                 175

Ala Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn Arg Lys Lys
            180                 185                 190

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

Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr Arg His Arg
    210                 215                 220

Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln
225                 230                 235                 240

Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val
                245                 250                 255

Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp
```

260 265 270

Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu
275 280 285

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

Asn Gly Arg Lys Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
305 310 315 320

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
325 330 335

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
340 345 350

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
355 360 365

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
370 375 380

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
385 390 395 400

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
405 410 415

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
420 425 430

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
435 440 445

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
450 455 460

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
465 470 475 480

Gly

<210> 42
<211> 433
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 42

```
Ala Arg His Met Glu Asp Arg Pro Ile Lys Phe Ser Thr Glu Gly Ala
1               5                  10                  15

Thr Ser Gln Ser Tyr Lys Gln Phe Ile Glu Ala Leu Arg Glu Arg Leu
            20                  25                  30

Arg Gly Gly Leu Ile His Asp Ile Pro Val Leu Pro Asp Pro Thr Thr
        35                  40                  45

Leu Gln Glu Arg Asn Arg Tyr Ile Thr Val Glu Leu Ser Asn Ser Asp
    50                  55                  60

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

Ala Tyr Arg Ala Gly Thr Gln Ser Tyr Phe Leu Arg Asp Ala Pro Ser
                85                  90                  95

Ser Ala Ser Asp Tyr Leu Phe Thr Gly Thr Asp Gln His Ser Leu Pro
            100                 105                 110

Phe Tyr Gly Thr Tyr Gly Asp Leu Glu Arg Trp Ala His Gln Ser Arg
        115                 120                 125

Gln Gln Ile Pro Leu Gly Leu Gln Ala Leu Thr His Gly Ile Ser Phe
    130                 135                 140

Phe Arg Ser Gly Gly Asn Asp Asn Glu Glu Lys Ala Arg Thr Leu Ile
145                 150                 155                 160

Val Ile Ile Gln Met Val Ala Glu Ala Ala Arg Phe Arg Tyr Ile Ser
                165                 170                 175

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

Ala Ala Met Ile Ser Leu Glu Asn Asn Trp Asp Asn Leu Ser Arg Gly
        195                 200                 205

Val Gln Glu Ser Val Gln Asp Thr Phe Pro Asn Gln Val Thr Leu Thr
    210                 215                 220

Asn Ile Arg Asn Glu Pro Val Ile Val Asp Ser Leu Ser His Pro Thr
```

225 230 235 240

Val Ala Val Leu Ala Leu Met Leu Phe Val Cys Asn Pro Pro Asn Gly
245 250 255

Gly Gly Gly Ser Gly Gly Gly Gly Ser Val Arg Glu Arg Gly Pro Gln
260 265 270

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
275 280 285

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
290 295 300

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
305 310 315 320

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
325 330 335

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
340 345 350

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
355 360 365

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
370 375 380

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
385 390 395 400

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
405 410 415

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
420 425 430

Gly

<210> 43
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 43

```
Ala Arg His Met Glu Asp Arg Pro Ile Lys Phe Ser Thr Glu Gly Ala
1               5                  10                  15

Thr Ser Gln Ser Tyr Lys Gln Phe Ile Glu Ala Leu Arg Glu Arg Leu
            20                  25                  30

Arg Gly Gly Leu Ile His Asp Ile Pro Val Leu Pro Asp Pro Thr Thr
        35                  40                  45

Leu Gln Glu Arg Asn Arg Tyr Ile Thr Val Glu Leu Ser Asn Ser Asp
    50                  55                  60

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

Ala Tyr Arg Ala Gly Thr Gln Ser Tyr Phe Leu Arg Asp Ala Pro Ser
                85                  90                  95

Ser Ala Ser Asp Tyr Leu Phe Thr Gly Thr Asp Gln His Ser Leu Pro
            100                 105                 110

Phe Tyr Gly Thr Tyr Gly Asp Leu Glu Arg Trp Ala His Gln Ser Arg
        115                 120                 125

Gln Gln Ile Pro Leu Gly Leu Gln Ala Leu Thr His Gly Ile Ser Phe
    130                 135                 140

Phe Arg Ser Gly Gly Asn Asp Asn Glu Glu Lys Ala Arg Thr Leu Ile
145                 150                 155                 160

Val Ile Ile Gln Met Val Ala Glu Ala Ala Arg Phe Arg Tyr Ile Ser
                165                 170                 175

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

Ala Ala Met Ile Ser Leu Glu Asn Asn Trp Asp Asn Leu Ser Arg Gly
        195                 200                 205

Val Gln Glu Ser Val Gln Asp Thr Phe Pro Asn Gln Val Thr Leu Thr
    210                 215                 220

Asn Ile Arg Asn Glu Pro Val Ile Val Asp Ser Leu Ser His Pro Thr
225                 230                 235                 240

Val Ala Val Leu Ala Leu Met Leu Phe Val Cys Asn Pro Pro Asn Gly
```

245 250 255

Gly Gly Gly Ser Cys Phe Cys Asp Gly Arg Cys Asp Cys Ala Arg Val
260 265 270

Val Arg Gly Gly Gly Gly Ser Val Arg Glu Arg Gly Pro Gln Arg Val
275 280 285

Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser
290 295 300

Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp
305 310 315 320

Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg
325 330 335

Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser
340 345 350

Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn
355 360 365

Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp
370 375 380

Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp
385 390 395 400

Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu
405 410 415

Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile
420 425 430

Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
435 440 445

<210> 44
<211> 433
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 44

Glu Asp Arg Pro Ile Lys Phe Ser Thr Glu Gly Ala Thr Ser Gln Ser
1 5 10 15

```
Tyr Lys Gln Phe Ile Glu Ala Leu Arg Glu Arg Leu Arg Gly Gly Leu
            20                  25                  30

Ile His Asp Ile Pro Val Leu Pro Asp Pro Thr Thr Leu Gln Glu Arg
        35                  40                  45

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

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

Gly Thr Gln Ser Tyr Phe Leu Arg Asp Ala Pro Ser Ser Ala Ser Asp
                85                  90                  95

Tyr Leu Phe Thr Gly Thr Asp Gln His Ser Leu Pro Phe Tyr Gly Thr
            100                 105                 110

Tyr Gly Asp Leu Glu Arg Trp Ala His Gln Ser Arg Gln Gln Ile Pro
        115                 120                 125

Leu Gly Leu Gln Ala Leu Thr His Gly Ile Ser Phe Phe Arg Ser Gly
    130                 135                 140

Gly Asn Asp Asn Glu Glu Lys Ala Arg Thr Leu Ile Val Ile Ile Gln
145                 150                 155                 160

Met Val Ala Glu Ala Ala Arg Phe Arg Tyr Ile Ser Asn Arg Val Arg
                165                 170                 175

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

Ser Leu Glu Asn Asn Trp Asp Asn Leu Ser Arg Gly Val Gln Glu Ser
        195                 200                 205

Val Gln Asp Thr Phe Pro Asn Gln Val Thr Leu Thr Asn Ile Arg Asn
    210                 215                 220

Glu Pro Val Ile Val Asp Ser Leu Ser His Pro Thr Val Ala Val Leu
225                 230                 235                 240

Ala Leu Met Leu Phe Val Cys Asn Pro Pro Asn Gly Gly Gly Gly Ser
                245                 250                 255

Gly Gly Gly Gly Ser Arg Val Val Arg Val Arg Glu Arg Gly Pro Gln
```

260 265 270

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
275 280 285

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
290 295 300

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
305 310 315 320

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
325 330 335

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
340 345 350

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
355 360 365

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
370 375 380

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
385 390 395 400

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
405 410 415

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
420 425 430

Gly

<210> 45
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 45

Glu Asp Arg Pro Ile Lys Phe Ser Thr Glu Gly Ala Thr Ser Gln Ser
1 5 10 15

Tyr Lys Gln Phe Ile Glu Ala Leu Arg Glu Arg Leu Arg Gly Gly Leu
20 25 30

```
Ile His Asp Ile Pro Val Leu Pro Asp Pro Thr Thr Leu Gln Glu Arg
        35                  40                  45

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

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

Gly Thr Gln Ser Tyr Phe Leu Arg Asp Ala Pro Ser Ser Ala Ser Asp
                85                  90                  95

Tyr Leu Phe Thr Gly Thr Asp Gln His Ser Leu Pro Phe Tyr Gly Thr
            100                 105                 110

Tyr Gly Asp Leu Glu Arg Trp Ala His Gln Ser Arg Gln Gln Ile Pro
        115                 120                 125

Leu Gly Leu Gln Ala Leu Thr His Gly Ile Ser Phe Phe Arg Ser Gly
    130                 135                 140

Gly Asn Asp Asn Glu Glu Lys Ala Arg Thr Leu Ile Val Ile Ile Gln
145                 150                 155                 160

Met Val Ala Glu Ala Ala Arg Phe Arg Tyr Ile Ser Asn Arg Val Arg
                165                 170                 175

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

Ser Leu Glu Asn Asn Trp Asp Asn Leu Ser Arg Gly Val Gln Glu Ser
        195                 200                 205

Val Gln Asp Thr Phe Pro Asn Gln Val Thr Leu Thr Asn Ile Arg Asn
    210                 215                 220

Glu Pro Val Ile Val Asp Ser Leu Ser His Pro Thr Val Ala Val Leu
225                 230                 235                 240

Ala Leu Met Leu Phe Val Cys Asn Pro Pro Asn Arg Arg Arg Arg Arg
                245                 250                 255

Arg Arg Arg Arg Val Val Arg Gly Gly Gly Ser Gly Gly Gly Gly
            260                 265                 270

Ser Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly
```

275 280 285

Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
290 295 300

Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
305 310 315 320

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

His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
340 345 350

Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
355 360 365

Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
370 375 380

Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
385 390 395 400

Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
405 410 415

Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
420 425 430

Ser Phe Phe Gly Ala Phe Leu Val Gly
435 440

<210> 46
<211> 550
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 46

Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr
1 5 10 15

Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys
20 25 30

Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His
35 40 45

```
Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His
    50                  55                  60

Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln
65                  70                  75                  80

Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr
                85                  90                  95

Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser
            100                 105                 110

Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser
        115                 120                 125

Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe
    130                 135                 140

Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser
145                 150                 155                 160

Phe Phe Gly Ala Phe Leu Val Gly Gly Gly Gly Gly Ser Gly Gly Gly
                165                 170                 175

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

Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr Arg His Arg
        195                 200                 205

Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln
    210                 215                 220

Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val
225                 230                 235                 240

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

Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu
            260                 265                 270

Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg Gln Gly Thr Gly
        275                 280                 285

Asn Gly Gly Gly Gly Gly Ser Arg Lys Lys Arg Glu Asp Arg Pro Ile
```

290 295 300

Lys Phe Ser Thr Glu Gly Ala Thr Ser Gln Ser Tyr Lys Gln Phe Ile
305 310 315 320

Glu Ala Leu Arg Glu Arg Leu Arg Gly Gly Leu Ile His Asp Ile Pro
325 330 335

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

Val Glu Leu Ser Asn Ser Asp Thr Glu Ser Ile Glu Val Gly Ile Asp
355 360 365

Val Thr Asn Ala Tyr Val Val Ala Tyr Arg Ala Gly Thr Gln Ser Tyr
370 375 380

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

Thr Asp Gln His Ser Leu Pro Phe Tyr Gly Thr Tyr Gly Asp Leu Glu
405 410 415

Arg Trp Ala His Gln Ser Arg Gln Gln Ile Pro Leu Gly Leu Gln Ala
420 425 430

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

Glu Lys Ala Arg Thr Leu Ile Val Ile Ile Gln Met Val Ala Glu Ala
450 455 460

Ala Arg Phe Arg Tyr Ile Ser Asn Arg Val Arg Val Ser Ile Gln Thr
465 470 475 480

Gly Thr Ala Phe Gln Pro Asp Ala Ala Met Ile Ser Leu Glu Asn Asn
485 490 495

Trp Asp Asn Leu Ser Arg Gly Val Gln Glu Ser Val Gln Asp Thr Phe
500 505 510

Pro Asn Gln Val Thr Leu Thr Asn Ile Arg Asn Glu Pro Val Ile Val
515 520 525

Asp Ser Leu Ser His Pro Thr Val Ala Val Leu Ala Leu Met Leu Phe
530 535 540

Val Cys Asn Pro Pro Asn
545 550

<210> 47
<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 47

Glu Asp Arg Pro Ile Lys Phe Ser Thr Glu Gly Ala Thr Ser Gln Ser
1 5 10 15

Tyr Lys Gln Phe Ile Glu Ala Leu Arg Glu Arg Leu Arg Gly Gly Leu
20 25 30

Ile His Asp Ile Pro Val Leu Pro Asp Pro Thr Thr Leu Gln Glu Arg
35 40 45

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

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

Gly Thr Gln Ser Tyr Phe Leu Arg Asp Ala Pro Ser Ser Ala Ser Asp
85 90 95

Tyr Leu Phe Thr Gly Thr Asp Gln His Ser Leu Pro Phe Tyr Gly Thr
100 105 110

Tyr Gly Asp Leu Glu Arg Trp Ala His Gln Ser Arg Gln Gln Ile Pro
115 120 125

Leu Gly Leu Gln Ala Leu Thr His Gly Ile Ser Phe Phe Arg Ser Gly
130 135 140

Gly Asn Asp Asn Glu Glu Lys Ala Arg Thr Leu Ile Val Ile Ile Gln
145 150 155 160

Met Val Ala Glu Ala Ala Arg Phe Arg Tyr Ile Ser Asn Arg Val Arg
165 170 175

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

Ser Leu Glu Asn Asn Trp Asp Asn Leu Ser Arg Gly Val Gln Glu Ser

195 200 205

Val Gln Asp Thr Phe Pro Asn Gln Val Thr Leu Thr Asn Ile Arg Asn
210 215 220

Glu Pro Val Ile Val Asp Ser Leu Ser His Pro Thr Val Ala Val Leu
225 230 235 240

Ala Leu Met Leu Phe Val Cys Asn Pro Pro Asn Gly Gly Gly Gly Ser
245 250 255

Gly Gly Gly Gly Ser Arg Lys Lys Arg Ala Ser Gly Cys Gly Pro Glu
260 265 270

Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile
275 280 285

Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile
290 295 300

Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys
305 310 315 320

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

Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu
340 345 350

Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe
355 360 365

Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met
370 375 380

Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu
385 390 395 400

Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly
405 410 415

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

Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His
435 440 445

Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
450 455

<210> 48
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 48

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
115 120 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
130 135 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145 150 155 160

Gly Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Arg Lys Lys
165 170 175

Arg Gly Gly Gly Gly Ser Ala Arg His Met Glu Asp Arg Pro Ile Lys
180 185 190

Phe Ser Thr Glu Gly Ala Thr Ser Gln Ser Tyr Lys Gln Phe Ile Glu

195 200 205

Ala Leu Arg Glu Arg Leu Arg Gly Gly Leu Ile His Asp Ile Pro Val
210 215 220

Leu Pro Asp Pro Thr Thr Leu Gln Glu Arg Asn Arg Tyr Ile Thr Val
225 230 235 240

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

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

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

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

Trp Ala His Gln Ser Arg Gln Gln Ile Pro Leu Gly Leu Gln Ala Leu
305 310 315 320

Thr His Gly Ile Ser Phe Phe Arg Ser Gly Gly Asn Asp Asn Glu Glu
325 330 335

Lys Ala Arg Thr Leu Ile Val Ile Ile Gln Met Val Ala Glu Ala Ala
340 345 350

Arg Phe Arg Tyr Ile Ser Asn Arg Val Arg Val Ser Ile Gln Thr Gly
355 360 365

Thr Ala Phe Gln Pro Asp Ala Ala Met Ile Ser Leu Glu Asn Asn Trp
370 375 380

Asp Asn Leu Ser Arg Gly Val Gln Glu Ser Val Gln Asp Thr Phe Pro
385 390 395 400

Asn Gln Val Thr Leu Thr Asn Ile Arg Asn Glu Pro Val Ile Val Asp
405 410 415

Ser Leu Ser His Pro Thr Val Ala Val Leu Ala Leu Met Leu Phe Val
420 425 430

Cys Asn Pro Pro Asn Val Arg Glu Arg Gly Pro
435 440

<210> 49
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 49

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

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
            20                  25                  30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
        35                  40                  45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
    50                  55                  60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65                  70                  75                  80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
                85                  90                  95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Arg Lys Lys
                165                 170                 175

Arg Gly Gly Gly Gly Ser Ala Arg His Met Glu Asp Arg Pro Ile Lys
            180                 185                 190

Phe Ser Thr Glu Gly Ala Thr Ser Gln Ser Tyr Lys Gln Phe Ile Glu
        195                 200                 205

Ala Leu Arg Glu Arg Leu Arg Gly Gly Leu Ile His Asp Ile Pro Val
```

210 215 220

Leu Pro Asp Pro Thr Thr Leu Gln Glu Arg Asn Arg Tyr Ile Thr Val
225 230 235 240

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

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

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

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

Trp Ala His Gln Ser Arg Gln Gln Ile Pro Leu Gly Leu Gln Ala Leu
305 310 315 320

Thr His Gly Ile Ser Phe Phe Arg Ser Gly Gly Asn Asp Asn Glu Glu
325 330 335

Lys Ala Arg Thr Leu Ile Val Ile Ile Gln Met Val Ala Glu Ala Ala
340 345 350

Arg Phe Arg Tyr Ile Ser Asn Arg Val Arg Val Ser Ile Gln Thr Gly
355 360 365

Thr Ala Phe Gln Pro Asp Ala Ala Met Ile Ser Leu Glu Asn Asn Trp
370 375 380

Asp Asn Leu Ser Arg Gly Val Gln Glu Ser Val Gln Asp Thr Phe Pro
385 390 395 400

Asn Gln Val Thr Leu Thr Asn Ile Arg Asn Glu Pro Val Ile Val Asp
405 410 415

Ser Leu Ser His Pro Thr Val Ala Val Leu Ala Leu Met Leu Phe Val
420 425 430

Cys Asn Pro Pro Asn Val Arg Glu Arg Gly Pro Lys Asp Glu Leu
435 440 445

<210> 50
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 50

```
Glu Asp Arg Pro Ile Lys Phe Ser Thr Glu Gly Ala Thr Ser Gln Ser
1               5                   10                  15

Tyr Lys Gln Phe Ile Glu Ala Leu Arg Glu Arg Leu Arg Gly Gly Leu
            20                  25                  30

Ile His Asp Ile Pro Val Leu Pro Asp Pro Thr Thr Leu Gln Glu Arg
        35                  40                  45

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

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

Gly Thr Gln Ser Tyr Phe Leu Arg Asp Ala Pro Ser Ser Ala Ser Asp
                85                  90                  95

Tyr Leu Phe Thr Gly Thr Asp Gln His Ser Leu Pro Phe Tyr Gly Thr
            100                 105                 110

Tyr Gly Asp Leu Glu Arg Trp Ala His Gln Ser Arg Gln Gln Ile Pro
        115                 120                 125

Leu Gly Leu Gln Ala Leu Thr His Gly Ile Ser Phe Phe Arg Ser Gly
    130                 135                 140

Gly Asn Asp Asn Glu Glu Lys Ala Arg Thr Leu Ile Val Ile Ile Gln
145                 150                 155                 160

Met Val Ala Glu Ala Ala Arg Phe Arg Tyr Ile Ser Asn Arg Val Arg
                165                 170                 175

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

Ser Leu Glu Asn Asn Trp Asp Asn Leu Ser Arg Gly Val Gln Glu Ser
        195                 200                 205

Val Gln Asp Thr Phe Pro Asn Gln Val Thr Leu Thr Asn Ile Arg Asn
    210                 215                 220

Glu Pro Val Ile Val Asp Ser Leu Ser His Pro Thr Val Ala Val Leu
```

225 230 235 240

Ala Leu Met Leu Phe Val Cys Asn Pro Pro Asn Gly Gly Gly Gly Ser
245 250 255

Gly Gly Gly Gly Ser Arg Lys Lys Arg Ala Ser Gly Cys Gly Pro Glu
260 265 270

Cys Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly
275 280 285

Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
290 295 300

Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
305 310 315 320

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

His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
340 345 350

Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
355 360 365

Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
370 375 380

Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
385 390 395 400

Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
405 410 415

Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
420 425 430

Ser Phe Phe Gly Ala Phe Leu Val Gly
435 440

<210> 51
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 51

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Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1               5                  10                  15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
            20                  25                  30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
        35                  40                  45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
    50                  55                  60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65                  70                  75                  80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
                85                  90                  95

Pro His Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Ser Ala Ser Gly Gly Pro Glu Gly Gly Ser Leu Ala
                165                 170                 175

Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr
            180                 185                 190

Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr
        195                 200                 205

Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp
    210                 215                 220

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

Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Ser Pro Glu Gln Ala Arg
```

245 250 255

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

Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Gly Pro Ala Asp Ser
275 280 285

Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe Leu
290 295 300

Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn Trp
305 310 315 320

Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg Gly
325 330 335

Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser
340 345 350

Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile
355 360 365

Trp Ala Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr
370 375 380

Ala Gln Asp Gln Glu Pro Asp Ala Ala Gly Arg Ile Arg Asn Gly Ala
385 390 395 400

Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Ala
405 410 415

Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg
420 425 430

Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro
435 440 445

Glu Glu Ser Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala
450 455 460

Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn
465 470 475 480

Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Ser Glu Gln Ala
485 490 495

Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Lys
500 505 510

Asp Glu Leu
515

<210> 52
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 52

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Asn Phe Lys Phe Arg Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
115 120 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu Arg
130 135 140

Leu Arg Asp Met His His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145 150 155 160

Gly Gly Gly Gly Ser Ala Ser Gly Gly Pro Glu Gly Gly Ser Leu Ala
165 170 175

Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr

180 185 190

Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr
195 200 205

Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp
210 215 220

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

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

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

Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Gly Pro Ala Asp Ser
275 280 285

Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe Leu
290 295 300

Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn Trp
305 310 315 320

Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg Gly
325 330 335

Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser
340 345 350

Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile
355 360 365

Trp Ala Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr
370 375 380

Ala Gln Asp Gln Glu Pro Asp Ala Ala Gly Arg Ile Arg Asn Gly Ala
385 390 395 400

Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Ala
405 410 415

Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg
420 425 430

Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro
435 440 445

Glu Glu Ser Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala
450 455 460

Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn
465 470 475 480

Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Ser Glu Gln Ala
485 490 495

Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Lys
500 505 510

Asp Glu Leu
515

<210> 53
<211> 519
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 53

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro His Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe

115 120 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
130 135 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145 150 155 160

Gly Gly Gly Gly Ser Gly Ala Ser Gly Cys Gly Pro Glu Pro Glu Gly
165 170 175

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

Glu Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu
195 200 205

Gln Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala
210 215 220

Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Ala Asn Ala Leu Ala
225 230 235 240

Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Ser Pro
245 250 255

Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg
260 265 270

Phe Val Arg Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Gly
275 280 285

Pro Ala Asp Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly
290 295 300

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

Thr Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu
325 330 335

Glu Glu Arg Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu
340 345 350

Ala Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp
355 360 365

Leu Asp Ala Ile Trp Ala Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu
370 375 380

Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Ala Gly Arg Ile
385 390 395 400

Arg Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro
405 410 415

Gly Phe Tyr Ala Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly
420 425 430

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

Ile Thr Gly Pro Glu Glu Ser Gly Gly Arg Leu Glu Thr Ile Leu Gly
450 455 460

Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr
465 470 475 480

Asp Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp
485 490 495

Ser Glu Gln Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly
500 505 510

Lys Pro Pro Lys Asp Glu Leu
515

<210> 54
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> none

<400> 54

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile

50 55 60

Tyr Ser Gln Thr Asn Phe Lys Phe Arg Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
115 120 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu Arg
130 135 140

Leu Arg Asp Met His His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145 150 155 160

Gly Gly Gly Gly Ser Ala Ser Gly Gly Pro Glu Gly Gly Ser Leu Ala
165 170 175

Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr
180 185 190

Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr
195 200 205

Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp
210 215 220

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

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

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

Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Gly Pro Ala Asp Ser
275 280 285

Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe Leu
290 295 300

Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn Trp
305 310 315 320

Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg Gly
325 330 335

Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser
340 345 350

Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile
355 360 365

Trp Ala Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr
370 375 380

Ala Gln Asp Gln Glu Pro Asp Ala Ala Gly Arg Ile Arg Asn Gly Ala
385 390 395 400

Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Ala
405 410 415

Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg
420 425 430

Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro
435 440 445

Glu Glu Ser Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala
450 455 460

Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn
465 470 475 480

Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Ser Glu Gln Ala
485 490 495

Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Lys
500 505 510

Asp Glu Leu
515

<210> 55
<211> 248
<212> PRT
<213> Bougainvillea spectabilis

<300>
<308> GenBank/AAL35962.1

SEQ LISTING

<309> 2001-11-29
<313> (27)..(247)

<400> 55

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

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

Gln Leu Pro Val Thr Leu Gln Thr Ile Ala Asp Asp Lys Arg Phe Val
        35                  40                  45

Leu Val Asp Ile Thr Thr Thr Ser Lys Lys Thr Val Lys Val Ala Ile
    50                  55                  60

Asp Val Thr Asp Val Tyr Val Val Gly Tyr Gln Asp Lys Trp Asp Gly
65                  70                  75                  80

Lys Asp Arg Ala Val Phe Leu Asp Lys Val Pro Thr Val Ala Thr Ser
                85                  90                  95

Lys Leu Phe Pro Gly Val Thr Asn Arg Val Thr Leu Thr Phe Asp Gly
            100                 105                 110

Ser Tyr Gln Lys Leu Val Asn Ala Ala Lys Val Asp Arg Lys Asp Leu
        115                 120                 125

Glu Leu Gly Val Tyr Lys Leu Glu Phe Ser Ile Glu Ala Ile His Gly
    130                 135                 140

Lys Thr Ile Asn Gly Gln Glu Ile Ala Lys Phe Phe Leu Ile Val Ile
145                 150                 155                 160

Gln Met Val Ser Glu Ala Ala Arg Phe Lys Tyr Ile Glu Thr Glu Val
                165                 170                 175

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

Asn Leu Glu Asn Asn Trp Gly Asp Ile Ser Asp Ala Ile His Lys Ser
        195                 200                 205

Ser Pro Gln Cys Thr Thr Ile Asn Pro Ala Leu Gln Leu Ile Ser Pro
    210                 215                 220

Ser Asn Asp Pro Trp Val Val Asn Lys Val Ser Gln Ile Ser Pro Asp
225                 230                 235                 240
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Met Gly Ile Leu Lys Phe Lys Ser
245

<210> 56
<211> 267
<212> PRT
<213> Ricinus communis

<300>
<308> GenBank/ABG65738.1
<309> 2006-07-16
<313> (1)..(267)

<400> 56

Glu Asp Asn Asn Ile Phe Pro Lys Gln Tyr Pro Ile Ile Asn Phe Thr
1 5 10 15

Thr Ala Gly Ala Thr Val Gln Ser Tyr Thr Asn Phe Ile Arg Ala Val
20 25 30

Arg Gly Arg Leu Thr Thr Gly Ala Asp Val Arg His Glu Ile Pro Val
35 40 45

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

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

Thr Asn Ala Tyr Val Val Gly Tyr Arg Ala Gly Asn Ser Ala Tyr Phe
85 90 95

Phe His Pro Asp Asn Gln Glu Asp Ala Glu Ala Ile Thr His Leu Phe
100 105 110

Thr Asp Val Gln Asn Arg Tyr Thr Phe Ala Phe Gly Gly Asn Tyr Asp
115 120 125

Arg Leu Glu Gln Leu Ala Gly Ser Leu Arg Glu Asn Ile Glu Leu Gly
130 135 140

Asn Gly Pro Leu Glu Glu Ala Ile Ser Ala Leu Tyr Tyr Tyr Ser Thr
145 150 155 160

Gly Gly Thr Gln Leu Pro Thr Leu Ala Arg Ser Phe Ile Val Cys Ile
165 170 175

Gln Met Ile Ser Glu Ala Ala Arg Phe Gln Tyr Ile Glu Gly Glu Met

180 185 190

Arg Thr Arg Ile Arg Tyr Asn Arg Arg Ser Ala Pro Asp Pro Ser Val
195 200 205

Ile Thr Leu Glu Asn Ser Trp Gly Arg Leu Ser Thr Ala Ile Gln Glu
210 215 220

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

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

Ala Leu Met Val Tyr Arg Cys Ala Pro Pro Pro
260 265

<210> 57
<211> 192
<212> PRT
<213> Ricinus communis

<300>
<308> GenBank/ACZ56254.1
<309> 2009-12-05
<313> (1)..(192)

<400> 57

Gly Pro Gly Pro Lys Gln Tyr Pro Ile Ile Asn Phe Thr Thr Ala Gly
1 5 10 15

Ala Thr Val Gln Ser Tyr Thr Asn Phe Ile Arg Ala Val Arg Gly Arg
20 25 30

Leu Thr Thr Gly Ala Asp Val Arg His Glu Ile Pro Val Leu Pro Asn
35 40 45

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

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

Tyr Val Val Gly Tyr Arg Ala Gly Asn Ser Ala Tyr Phe Phe His Pro
85 90 95

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

Gln Asn Arg Tyr Thr Phe Ala Phe Gly Gly Asn Tyr Asp Arg Leu Glu
115 120 125

Gln Leu Ala Gly Asn Leu Arg Glu Asn Ile Glu Leu Gly Asn Gly Pro
130 135 140

Leu Glu Glu Ala Ile Ser Ala Leu Tyr Tyr Tyr Ser Thr Gly Gly Thr
145 150 155 160

Gln Leu Pro Thr Leu Ala Arg Ser Phe Ile Ile Cys Ile Gln Met Ile
165 170 175

Ser Glu Ala Ala Arg Phe Gln Tyr Ile Glu Gly Glu Met Arg Val Pro
180 185 190

<210> 58
<211> 290
<212> PRT
<213> Phytolacca americana

<300>
<308> GenBank/CAA66702.1
<309> 2005-04-18
<313> (25)..(314)

<400> 58

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

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

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

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

Met Leu Arg Arg Asn Asn Leu Tyr Val Met Gly Tyr Ser Asp Pro Phe
65 70 75 80

Asn Gly Asn Lys Cys Arg Tyr His Ile Phe Asn Asp Ile Thr Ser Thr
85 90 95

Glu Arg Thr Asp Val Glu Asn Thr Leu Cys Ser Ser Ser Ser Ser Arg
100 105 110

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

Lys Ala Glu Val Asn Ser Arg Asn Gln Val Gln Leu Gly Ile Gln Ile
130 135 140

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

Lys Thr Glu Ala Phe Phe Leu Leu Val Ala Ile Gln Met Val Ser Glu
165 170 175

Ala Ala Arg Phe Lys Tyr Ile Glu Asn Gln Val Lys Thr Asn Phe Asn
180 185 190

Arg Ala Phe Tyr Pro Asp Pro Lys Val Ile Asn Leu Glu Glu Lys Trp
195 200 205

Gly Lys Ile Ser Glu Ala Ile His Asn Ala Lys Asn Gly Ala Leu Pro
210 215 220

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

Arg Val Asp Glu Ile Asn Arg Asp Val Ala Leu Leu Lys Tyr Val Asn
245 250 255

Gly Thr Cys Gln Thr Thr Tyr Gln Asn Ala Met Phe Ser Gln Val Ile
260 265 270

Ile Ser Thr Tyr Tyr Asn Tyr Met Ser Asn Leu Gly Asp Leu Phe Glu
275 280 285

Gly Phe
290

<210> 59
<211> 252
<212> PRT
<213> Saponaria officinalis

<300>
<308> GenBank/CAA48886.1
<309> 2005-04-18
<313> (1)..(251)

<400> 59

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

Ser Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro Asn Leu
20 25 30

```
Lys Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser Lys Asp
        35                  40                  45

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

Gly Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala Met Asp
65                  70                  75                  80

Asn Thr Asn Val Asn Arg Ala Tyr Tyr Phe Lys Ser Glu Ile Thr Ser
                85                  90                  95

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

Ala Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln
        115                 120                 125

Ile Thr Gln Gly Asp Lys Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp
    130                 135                 140

Leu Leu Leu Thr Phe Met Glu Ala Val Asn Lys Lys Ala Arg Val Val
145                 150                 155                 160

Lys Asn Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu
                165                 170                 175

Val Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Thr Lys Asn Phe Pro
            180                 185                 190

Asn Lys Phe Asp Ser Asp Asn Lys Val Ile Gln Phe Glu Val Ser Trp
        195                 200                 205

Arg Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe
    210                 215                 220

Asn Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp
225                 230                 235                 240

Leu Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro
                245                 250
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<210> 60
<211> 247
<212> PRT
<213> Trichosanthes kirilowii

<300>
<308> GenBank/AAB22585.1
<309> 1993-05-08
<313> (1)..(247)

<400> 60

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Asp Val Ser Phe Arg Leu Ser Gly Ala Thr Ser Ser Ser Tyr Gly Val
1               5                  10                  15

Phe Ile Ser Asn Leu Arg Lys Ala Leu Pro Asn Glu Arg Lys Leu Tyr
            20                  25                  30

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

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

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

Tyr Phe Phe Asn Glu Ala Ser Ala Thr Glu Ala Ala Lys Tyr Val Phe
                85                  90                  95

Lys Asp Ala Met Arg Lys Val Thr Leu Pro Tyr Ser Gly Asn Tyr Glu
            100                 105                 110

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

Leu Pro Ala Leu Asp Ser Ala Ile Thr Thr Leu Phe Tyr Tyr Asn Ala
    130                 135                 140

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

Ala Ala Arg Tyr Lys Phe Ile Glu Gln Gln Ile Gly Lys Arg Val Asp
                165                 170                 175

Lys Thr Phe Leu Pro Ser Leu Ala Ile Ile Ser Leu Glu Asn Ser Trp
            180                 185                 190

Ser Ala Leu Ser Lys Gln Ile Gln Ile Ala Ser Thr Asn Asn Gly Gln
        195                 200                 205

Phe Glu Ser Pro Val Val Leu Ile Asn Ala Gln Asn Gln Arg Val Thr
    210                 215                 220
```

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

Leu Asn Arg Asn Asn Met Ala
245

<210> 61
<211> 245
<212> PRT
<213> Trichosanthes anguina

<300>
<308> GenBank/AAD02686.1
<309> 1999-03-03
<313> (20)..(264)

<400> 61

Asp Val Ser Phe Asp Leu Ser Thr Ala Thr Lys Lys Ser Tyr Ser Ser
1 5 10 15

Phe Ile Thr Gln Leu Arg Asp Ala Leu Pro Thr Gln Gly Thr Val Cys
20 25 30

Gly Ile Pro Leu Leu Pro Ser Thr Ala Ser Gly Ser Gln Trp Phe Arg
35 40 45

Phe Phe Asn Leu Thr Asn Tyr Asn Asp Glu Thr Val Thr Val Ala Val
50 55 60

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

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

Gly Thr Lys Thr Val Lys Leu Pro Tyr Ser Gly Asn Tyr Asp Lys Leu
100 105 110

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

Ala Leu Ser Ser Ala Ile Thr Asn Met Val Tyr Tyr Asp Tyr Gln Ser
130 135 140

Thr Ala Ala Ala Leu Leu Val Leu Ile Gln Cys Thr Ala Glu Ala Ala
145 150 155 160

Arg Tyr Lys Tyr Ile Glu Gln Gln Val Ser Ser His Ile Ser Ser Asn
165 170 175

```
Phe Tyr Pro Asn Gln Ala Val Ile Ser Leu Glu Asn Lys Trp Gly Ala
            180                 185                 190

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

Glu Asn Pro Val Glu Leu Tyr Asn Pro Asp Gly Thr Arg Phe Ser Val
    210                 215                 220

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

Tyr Tyr Lys Ala Ser
                245
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<210> 62
<211> 249
<212> PRT
<213> Viscum album

<300>
<308> GenBank/AAL87006.1
<309> 2002-03-17
<313> (1)..(249)

<400> 62

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Tyr Glu Arg Leu Arg Leu Arg Val Thr His Gln Thr Thr Gly Glu Glu
1               5                   10                  15

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

Phe Ser Asn Glu Ile Pro Leu Leu Arg Gln Ser Thr Ile Pro Val Ser
        35                  40                  45

Asp Ala Gln Arg Phe Val Leu Val Glu Leu Thr Asn Glu Gly Gly Asp
    50                  55                  60

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

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

Glu Thr His Leu Phe Thr Gly Thr Thr Arg Ser Ser Leu Pro Phe Asn
            100                 105                 110

Gly Ser Tyr Pro Asp Leu Glu Arg Tyr Ala Gly His Arg Asp Gln Ile
        115                 120                 125
```

Pro Leu Gly Ile Asp Gln Leu Ile Gln Ser Val Thr Ala Leu Arg Phe
130 135 140

Pro Gly Gly Ser Thr Arg Thr Gln Ala Arg Ser Ile Leu Ile Leu Ile
145 150 155 160

Gln Met Ile Ser Glu Ala Ala Arg Phe Asn Pro Ile Leu Trp Arg Ala
165 170 175

Arg Gln Tyr Ile Asn Ser Gly Ala Ser Phe Leu Pro Asp Val Tyr Met
180 185 190

Leu Glu Leu Glu Thr Ser Trp Gly Gln Gln Ser Thr Gln Val Gln Gln
195 200 205

Ser Thr Asp Gly Val Phe Asn Asn Pro Ile Arg Leu Ala Ile Pro Pro
210 215 220

Gly Asn Phe Val Thr Leu Thr Asn Val Arg Asp Val Ile Ala Ser Leu
225 230 235 240

Ala Ile Met Leu Phe Val Cys Gly Glu
245

<210> 63
<211> 273
<212> PRT
<213> Sambucus ebulus L

<300>
<308> GenBank/CAC33178.1
<309> 2001-02-17
<313> (26)..(298)

<400> 63

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

Thr Tyr Arg Asp Phe Leu Lys Asn Leu Arg Asp Arg Val Ala Thr Gly
20 25 30

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

Gln Val Lys Asn Arg Phe Val Leu Val Arg Leu Thr Asn Tyr Asn Gly
50 55 60

Asp Thr Val Thr Ser Ala Val Asp Val Thr Asn Leu Tyr Leu Val Ala

65 70 75 80

Phe Ser Ala Asn Gly Asn Ser Tyr Phe Phe Lys Asp Ala Thr Glu Leu
85 90 95

Gln Lys Ser Asn Leu Phe Leu Gly Thr Thr Gln His Thr Leu Ser Phe
100 105 110

Thr Gly Asn Tyr Asp Asn Leu Glu Thr Ala Ala Gly Thr Arg Arg Glu
115 120 125

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

Trp Tyr Asp Gly Gly Val Ala Arg Ser Leu Leu Val Leu Ile Gln Met
145 150 155 160

Val Pro Glu Ala Ala Arg Phe Arg Tyr Ile Glu Gln Glu Val Arg Arg
165 170 175

Ser Leu Gln Gln Leu Thr Ser Phe Thr Pro Asn Ala Leu Met Leu Ser
180 185 190

Met Glu Asn Asn Trp Ser Ser Met Ser Leu Glu Val Gln Leu Ser Gly
195 200 205

Asp Asn Val Ser Pro Phe Ser Gly Thr Val Gln Leu Gln Asn Tyr Asp
210 215 220

His Thr Pro Arg Leu Val Asp Asn Phe Glu Glu Leu Tyr Lys Ile Thr
225 230 235 240

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

Asn Ala Ile Arg Met Pro His Val Leu Val Gly Glu Asp Asn Lys Phe
260 265 270

Asn

<210> 64
<211> 272
<212> PRT
<213> Sambucus nigra

<300>
<308> GenBank/AAB39475.1
<309> 1996-12-13

<313> (26)..(297)

<400> 64

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

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

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

Gln Val Lys Ser Arg Phe Val Leu Val Pro Leu Thr Asn Tyr Asn Gly
    50                  55                  60

Asn Thr Val Thr Leu Ala Val Asp Val Thr Asn Leu Tyr Val Val Ala
65                  70                  75                  80

Phe Ser Gly Asn Ala Asn Ser Tyr Phe Phe Lys Asp Ala Thr Glu Val
                85                  90                  95

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

Thr Gly Asn Tyr Asp Asn Leu Glu Thr Ala Ala Asn Thr Arg Arg Glu
        115                 120                 125

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

Tyr His Gly Asp Ser Val Ala Arg Ser Leu Leu Val Val Ile Gln Met
145                 150                 155                 160

Val Ser Glu Ala Ala Arg Phe Arg Tyr Ile Glu Gln Glu Val Arg Arg
                165                 170                 175

Ser Leu Gln Gln Ala Thr Ser Phe Thr Pro Asn Ala Leu Met Leu Ser
            180                 185                 190

Met Glu Asn Asn Trp Ser Ser Met Ser Leu Glu Ile Gln Gln Ala Gly
        195                 200                 205

Asn Asn Val Ser Pro Phe Phe Gly Thr Val Gln Leu Leu Asn Tyr Asp
    210                 215                 220

His Thr His Arg Leu Val Asp Asn Phe Glu Glu Leu Tyr Lys Ile Thr
225                 230                 235                 240
```

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

Ala Ile Arg Met Pro Leu Asp Leu Ala Gly Glu Asp Asn Lys Tyr Asn
260 265 270

<210> 65
<211> 47
<212> PRT
<213> Luffa cylindrica

<300>
<308> Swiss-Prot/P56568.1
<309> 2011-06-28
<313> (1)..(47)

<400> 65

Pro Arg Gly Ser Pro Arg Thr Glu Tyr Glu Ala Cys Arg Val Arg Cys
1 5 10 15

Gln Val Ala Glu His Gly Val Glu Arg Gln Arg Arg Cys Gln Gln Val
20 25 30

Cys Glu Lys Arg Leu Arg Glu Arg Glu Gly Arg Arg Glu Val Asp
35 40 45

<210> 66
<211> 249
<212> PRT
<213> Adenia volkensii

<300>
<308> GenBank/CAD61022.1
<309> 2005-04-15
<313> (1)..(244)

<400> 66

Val Phe Pro Lys Val Pro Phe Asp Val Pro Lys Ala Thr Val Glu Ser
1 5 10 15

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

Ser Pro Gln Gly Ile Arg Arg Leu Arg Asn Pro Ala Glu Ile Gln Pro
35 40 45

Ser Gln Gly Phe Ile Leu Ile Gln Leu Thr Gly Tyr Val Gly Ser Val
50 55 60

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

```
His Asn Val Leu Tyr His Phe Asn Asp Val Ser Ala Ser Ser Ile Ala
                85                  90                  95

Ser Val Phe Pro Asp Ala Gln Arg Arg Gln Leu Pro Phe Gly Gly Gly
            100                 105                 110

Tyr Pro Ser Met Arg Asn Tyr Ala Pro Glu Arg Asp Gln Ile Asp His
        115                 120                 125

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

Asn Asn Asn Gln Ile Ala Leu Gly Leu Val Ile Cys Ala Gly Met Val
145                 150                 155                 160

Ala Glu Ala Ser Arg Phe Arg Tyr Ile Glu Gly Leu Val Arg Gln Ser
                165                 170                 175

Ile Val Gly Pro Gly Asp Tyr Arg Thr Phe Arg Pro Asp Ala Leu Met
            180                 185                 190

Tyr Ser Ile Val Thr Gln Trp Gln Thr Leu Ser Glu Arg Ile Gln Gly
        195                 200                 205

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

Pro Phe Tyr Trp Asp Asn Val Ala Gln Ala Ile Thr Arg Leu Ser Leu
225                 230                 235                 240

Met Leu Phe Val Ser Arg Ser Thr Asp
                245
```

<210> 67
<211> 246
<212> PRT
<213> Momordica charantia

<300>
<308> GenBank/AAB22586.1
<309> 1993-05-08
<313> (1)..(246)

<400> 67

```
Asp Val Ser Phe Arg Leu Ser Gly Ala Asp Pro Arg Ser Tyr Gly Met
1               5                   10                  15

Phe Ile Lys Asp Leu Arg Asn Ala Leu Pro Phe Arg Glu Lys Val Tyr
```

20 25 30

Asn Ile Pro Leu Leu Leu Pro Ser Val Ser Gly Ala Gly Arg Tyr Leu
35 40 45

Leu Met His Leu Phe Asn Tyr Asp Gly Lys Thr Ile Thr Val Ala Leu
50 55 60

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

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

Arg Asp Ala Arg Arg Lys Ile Thr Leu Pro Tyr Ser Gly Asn Tyr Glu
100 105 110

Arg Leu Gln Ile Ala Ala Gly Lys Pro Arg Glu Lys Ile Pro Ile Gly
115 120 125

Leu Pro Ala Leu Asp Ser Ala Ile Ser Thr Leu Leu His Tyr Asp Ser
130 135 140

Thr Ala Ala Ala Gly Ala Leu Leu Val Leu Ile Gln Thr Thr Ala Glu
145 150 155 160

Ala Ala Arg Phe Lys Tyr Ile Glu Gln Gln Ile Gln Glu Arg Ala Tyr
165 170 175

Arg Asp Glu Val Pro Ser Leu Ala Thr Ile Ser Leu Glu Asn Ser Trp
180 185 190

Ser Gly Leu Ser Lys Gln Ile Gln Leu Ala Gln Gly Asn Asn Gly Ile
195 200 205

Phe Arg Thr Pro Ile Val Leu Val Asp Asn Lys Gly Asn Arg Val Gln
210 215 220

Ile Thr Asn Val Thr Ser Lys Val Val Thr Ser Asn Ile Gln Leu Leu
225 230 235 240

Leu Asn Thr Arg Asn Ile
245

<210> 68
<211> 342
<212> PRT
<213> Pseudomonas aeruginosa

<400> 68

```
Pro Glu Gly Gly Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys His
1               5                  10                  15

Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu
            20                  25                  30

Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr
        35                  40                  45

Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Ala Asn
    50                  55                  60

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

Glu Ser Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu
                85                  90                  95

Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala
            100                 105                 110

Ala Asn Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr
        115                 120                 125

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

Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His
145                 150                 155                 160

Arg Gln Leu Glu Glu Ala Gly Tyr Val Phe Val Gly Tyr His Gly Thr
                165                 170                 175

Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala Arg
            180                 185                 190

Ser Gln Asp Leu Asp Ala Ile Trp Ala Gly Phe Tyr Ile Ala Gly Asp
        195                 200                 205

Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Ala
    210                 215                 220

Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser
225                 230                 235                 240
```

Ser Leu Pro Gly Phe Tyr Ala Thr Ser Leu Thr Leu Ala Ala Pro Glu
245 250 255

Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg
260 265 270

Leu Asp Ala Ile Thr Gly Pro Glu Glu Ser Gly Gly Arg Leu Glu Thr
275 280 285

Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala
290 295 300

Ile Pro Thr Asp Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser Ser
305 310 315 320

Ile Pro Asp Ser Glu Gln Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser
325 330 335

Gln Pro Gly Lys Pro Pro
340

<210> 69
<211> 354
<212> PRT
<213> Pseudomonas aeruginosa

<400> 69

Pro Glu Gly Gly Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys His
1 5 10 15

Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu
20 25 30

Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr
35 40 45

Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn
50 55 60

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

Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu
85 90 95

Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Val Val Ser Leu Thr
100 105 110

```
Cys Pro Val Ala Ala Gly Glu Cys Ala Gly Pro Ala Asp Ser Gly Asp
        115                 120                 125

Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe Leu Gly Asp
    130                 135                 140

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

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

Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile Val
            180                 185                 190

Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile Trp Arg
        195                 200                 205

Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln
    210                 215                 220

Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg Asn Gly Ala Leu Leu
225                 230                 235                 240

Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Arg Thr Ser
                245                 250                 255

Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg Leu Ile
            260                 265                 270

Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu
        275                 280                 285

Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala Glu Arg
    290                 295                 300

Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn Val Gly
305                 310                 315                 320

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

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

Leu Lys
```

<210> 70
<211> 241
<212> PRT
<213> Shigella dysentarie

<300>
<308> GenBank/ABR09970.1
<309> 2007-12-21
<313> (6)..(244)

<400> 70

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Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser
1               5                   10                  15

Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser
            20                  25                  30

Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp Asn
        35                  40                  45

Leu Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe
    50                  55                  60

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

Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser
                85                  90                  95

His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp Ser
            100                 105                 110

Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly Met
        115                 120                 125

Gln Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser
    130                 135                 140

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

Phe Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg
                165                 170                 175

Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val Met
            180                 185                 190

Thr Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg Leu Ser Ser
        195                 200                 205
```

Val Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val Gly Arg Ile
210 215 220

Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala Leu Ile Leu
225 230 235 240

Asn

<210> 71
<211> 149
<212> PRT
<213> Aspergillus restrictus

<300>
<308> GenBank/AAA32707.1
<309> 1993-04-27
<313> (28)..(176)

<400> 71

Ala Thr Trp Thr Cys Ile Asn Gln Gln Leu Asn Pro Lys Thr Asn Lys
1 5 10 15

Trp Glu Asp Lys Arg Leu Leu Tyr Ser Gln Ala Lys Ala Glu Ser Asn
20 25 30

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

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

Arg Thr Pro Ile Lys Phe Gly Lys Ala Asp Cys Asp Arg Pro Pro Lys
65 70 75 80

His Ser Gln Asn Gly Met Gly Lys Asp Asp His Tyr Leu Leu Glu Phe
85 90 95

Pro Thr Phe Pro Asp Gly His Asp Tyr Lys Phe Asp Ser Lys Lys Pro
100 105 110

Lys Glu Asp Pro Gly Pro Ala Arg Val Ile Tyr Thr Tyr Pro Asn Lys
115 120 125

Val Phe Cys Gly Ile Val Ala His Gln Arg Gly Asn Gln Gly Asp Leu
130 135 140

Arg Leu Cys Ser His

<210> 72
<211> 130
<212> PRT
<213> Hirsutella thompsonii var thompsonii

<300>
<308> GenBank/AAB47280.1
<309> 2003-01-15
<313> (35)..(164)

<400> 72

Ala Pro Ile Val Thr Cys Arg Pro Lys Leu Asp Gly Arg Glu Lys Pro
1 5 10 15

Phe Lys Val Asp Val Ala Thr Ala Gln Ala Gln Ala Arg Lys Ala Gly
20 25 30

Leu Thr Thr Gly Lys Ser Gly Asp Pro His Arg Tyr Phe Ala Gly Asp
35 40 45

His Ile Arg Trp Gly Val Asn Asn Cys Asp Lys Ala Asp Ala Ile Leu
50 55 60

Trp Glu Tyr Pro Ile Tyr Trp Val Gly Lys Asn Ala Glu Trp Ala Lys
65 70 75 80

Asp Val Lys Thr Ser Gln Gln Lys Gly Gly Pro Thr Pro Ile Arg Val
85 90 95

Val Tyr Ala Asn Ser Arg Gly Ala Val Gln Tyr Cys Gly Val Met Thr
100 105 110

His Ser Lys Val Asp Lys Asn Asn Gln Gly Lys Glu Phe Phe Glu Lys
115 120 125

Cys Asp
130

<210> 73
<211> 109
<212> PRT
<213> Salmonella typhi

<300>
<308> GenBank/ACJ63596.1
<309> 2010-04-22
<313> (28)..(136)

<400> 73

Glu Arg Gly Glu Ile Trp Leu Val Ser Leu Asp Pro Thr Ala Gly His
1 5 10 15

Glu Gln Gln Gly Thr Arg Pro Val Leu Ile Val Thr Pro Ala Ala Phe
20 25 30

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

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

Ile Arg Thr Thr Gly Val Val Arg Cys Asp Gln Pro Arg Thr Ile Asp
65 70 75 80

Met Lys Ala Arg Gly Gly Lys Arg Leu Glu Arg Val Pro Glu Thr Ile
85 90 95

Met Asn Glu Val Leu Gly Arg Leu Ser Thr Ile Leu Thr
100 105

<210> 74
<211> 100
<212> PRT
<213> Escherichia coli

<300>
<308> GenBank/AAL77580.1
<309> 2005-06-29
<313> (27)..(126)

<400> 74

Gln Phe Lys Val Tyr Thr Tyr Lys Arg Glu Ser Arg Tyr Arg Leu Phe
1 5 10 15

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

Ile Pro Leu Ala Ser Ala Arg Leu Leu Ser Asp Lys Val Ser Arg Glu
35 40 45

Leu Tyr Pro Val Val His Ile Gly Asp Glu Ser Trp Arg Met Met Thr
50 55 60

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

Asp Leu Ser His Arg Glu Asn Asp Ile Lys Asn Ala Ile Asn Leu Met
85 90 95

Phe Trp Gly Ile
100

<210> 75
<211> 47
<212> PRT
<213> Escherichia coli

<300>
<301> Trovatti E, Cotrim CA, Garrido SS, Barros RS, Marchetto R.
<302> Peptides based on CcdB protein as novel inhibitors of bacterial topoisomerases
<303> Bioorg Med Chem Lett.
<304> 18
<305> 23
<306> 6161-6164
<307> 2008-10-07

<400> 75

Gln Phe Lys Val Tyr Thr Tyr Lys Gly Gly Ser Gly Gly Arg Leu Leu
1 5 10 15

Ser Asp Lys Val Ser Arg Glu Leu Gly Gly Ser Gly Gly Ser His Arg
20 25 30

Glu Asn Asp Ile Lys Asn Ala Ile Asn Leu Met Phe Trp Gly Ile
35 40 45

<210> 76
<211> 94
<212> PRT
<213> Escherichia coli

<300>
<308> NCBI Reference Sequence/NP_416081.1
<309> 2011-02-13
<313> (2)..(95)

<400> 76

Ala Tyr Phe Leu Asp Phe Asp Glu Arg Ala Leu Lys Glu Trp Arg Lys
1 5 10 15

Leu Gly Ser Thr Val Arg Glu Gln Leu Lys Lys Lys Leu Val Glu Val
20 25 30

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

Cys Tyr Lys Ile Lys Leu Arg Ser Ser Gly Tyr Arg Leu Val Tyr Gln
50 55 60

Val Ile Asp Glu Lys Val Val Val Phe Val Ile Ser Val Gly Lys Arg

65 70 75 80

Glu Arg Ser Glu Val Tyr Ser Glu Ala Val Lys Arg Ile Leu
85 90

<210> 77
<211> 90
<212> PRT
<213> Paracoccus methylutens

<300>
<308> NCBI Reference Sequence/YP_001429553.1
<309> 2010-11-03
<313> (2)..(91)

<400> 77

Pro Glu Leu Glu Trp Lys Ala Ala Ala Val Ala Asp Leu Leu Ala Ile
1 5 10 15

Val Asp Tyr Ile Ser Asp Asp Asn Pro Asp Ala Ala Phe Ala Leu Met
20 25 30

Glu Glu Ile Gln Asp Lys Val Ala Gln Leu Pro Ala His Pro Lys Arg
35 40 45

Cys Arg Pro Gly Arg Val Glu Gly Thr Arg Glu Leu Val Val Arg Pro
50 55 60

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

Arg Val Leu His Ala Ala Gln Met Trp Pro
85 90

<210> 78
<211> 251
<212> PRT
<213> Gelonium multoflorum

<300>
<301> Veenendaal LM, Jin H, Ran S, Cheung L, Navone N, Marks JW, Waltenberger J,
<302> In vitro and in vivo studies of a VEGF121/rGelonin
<303> Proc Natl Acad Sci U S A.
<304> 99
<305> 12
<306> 7866-71
<307> 2001-06-11

<400> 78

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

```
Tyr Val Asn Phe Leu Asn Glu Leu Arg Val Lys Leu Lys Pro Glu Gly
            20                  25                  30

Asn Ser His Gly Ile Pro Leu Leu Arg Lys Lys Ala Asp Asp Pro Gly
        35                  40                  45

Lys Ala Phe Val Leu Val Ala Leu Ser Asn Asp Asn Gly Gln Leu Ala
    50                  55                  60

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

Arg Asn Arg Ser Tyr Phe Phe Lys Asp Ala Pro Asp Ala Ala Tyr Glu
                85                  90                  95

Gly Leu Phe Lys Asn Thr Ile Lys Thr Arg Leu His Phe Gly Gly Ser
            100                 105                 110

Tyr Pro Ser Leu Glu Gly Glu Lys Ala Tyr Arg Glu Thr Thr Asp Leu
        115                 120                 125

Gly Ile Glu Pro Leu Arg Ile Gly Ile Lys Lys Leu Asp Glu Asn Ala
    130                 135                 140

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

Ile Gln Met Val Ser Glu Ala Ala Arg Phe Thr Phe Ile Glu Asn Gln
                165                 170                 175

Ile Arg Asn Asn Phe Gln Gln Arg Ile Arg Pro Ala Asn Asn Thr Ile
            180                 185                 190

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

Gly Ala Asn Gly Met Phe Ser Glu Ala Val Glu Leu Glu Arg Ala Asn
    210                 215                 220

Gly Lys Lys Tyr Tyr Val Thr Ala Val Asp Gln Val Lys Pro Lys Ile
225                 230                 235                 240

Ala Leu Leu Lys Phe Val Asp Lys Asp Pro Lys
                245                 250
```

<210> 79
<211> 387

<212> PRT
<213> Corynobacterium diptheriae

<300>
<308> GenBank/AAA72359.1
<309> 1993-02-23
<313> (2)..(388)

<400> 79

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Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met Glu Asn
1               5                   10                  15

Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val Asp Ser Ile Gln
            20                  25                  30

Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp Asp
        35                  40                  45

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

Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly Val
65                  70                  75                  80

Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val
                85                  90                  95

Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu
            100                 105                 110

Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe Gly
        115                 120                 125

Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly Ser
    130                 135                 140

Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu Ser
145                 150                 155                 160

Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln Asp
                165                 170                 175

Ala Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn Arg Val Arg
            180                 185                 190

Arg Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val
        195                 200                 205

Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly
```

210 215 220

Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val Ser Glu
225 230 235 240

Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu Glu
245 250 255

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

Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln Val
275 280 285

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

Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala
305 310 315 320

Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser
325 330 335

Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val Asp
340 345 350

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

Gln Val Val His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly His
370 375 380

Lys Thr His
385

<210> 80
<211> 300
<212> PRT
<213> Corynobacterium diptheriae

<300>
<308> GenBank/AAA72359.1
<309> 1993-07-23
<313> (2)..(194)

<400> 80

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

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Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val Asp Ser Ile Gln Lys
            20                  25                  30

Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp Asp Asp
        35                  40                  45

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

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

Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val Asp
                85                  90                  95

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

Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe Gly Asp
        115                 120                 125

Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly Ser Ser
    130                 135                 140

Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu Ser Val
145                 150                 155                 160

Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln Asp Ala
                165                 170                 175

Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn Arg Val Arg Arg
            180                 185                 190

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

Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu
    210                 215                 220

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

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

Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg
            260                 265                 270
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Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu
275 280 285

Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Gly
290 295 300

<210> 81
<211> 297
<212> PRT
<213> Corynobacterium diptheriae

<300>
<308> GenBank/AAA72359.1
<309> 1993-07-23
<313> (2)..(190)

<400> 81

Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met Glu Asn
1 5 10 15

Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val Asp Ser Ile Gln
20 25 30

Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp Asp
35 40 45

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

Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly Val
65 70 75 80

Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val
85 90 95

Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu
100 105 110

Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe Gly
115 120 125

Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly Ser
130 135 140

Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu Ser
145 150 155 160

Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln Asp
165 170 175

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Ala Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn Pro Glu Gly
            180                 185                 190

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

Glu Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu
    210                 215                 220

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

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

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

Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg
        275                 280                 285

Phe Val Arg Gln Gly Thr Gly Asn Gly
    290                 295


<210>  82
<211>  251
<212>  PRT
<213>  Abrus precatorius

<300>
<308>  GenBank/CAA38655.1
<309>  2005-04-18
<313>  (2)..(252)

<400>  82

Glu Asp Arg Pro Ile Lys Phe Ser Thr Glu Gly Ala Thr Ser Gln Ser
1               5                   10                  15

Tyr Lys Gln Phe Ile Glu Ala Leu Arg Glu Arg Leu Arg Gly Gly Leu
            20                  25                  30

Ile His Asp Ile Pro Val Leu Pro Asp Pro Thr Thr Leu Gln Glu Arg
        35                  40                  45

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

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

Gly Thr Gln Ser Tyr Phe Leu Arg Asp Ala Pro Ser Ser Ala Ser Asp
85 90 95

Tyr Leu Phe Thr Gly Thr Asp Gln His Ser Leu Pro Phe Tyr Gly Thr
100 105 110

Tyr Gly Asp Leu Glu Arg Trp Ala His Gln Ser Arg Gln Gln Ile Pro
115 120 125

Leu Gly Leu Gln Ala Leu Thr His Gly Ile Ser Phe Phe Arg Ser Gly
130 135 140

Gly Asn Asp Asn Glu Glu Lys Ala Arg Thr Leu Ile Val Ile Ile Gln
145 150 155 160

Met Val Ala Glu Ala Ala Arg Phe Arg Tyr Ile Ser Asn Arg Val Arg
165 170 175

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

Ser Leu Glu Asn Asn Trp Asp Asn Leu Ser Arg Gly Val Gln Glu Ser
195 200 205

Val Gln Asp Thr Phe Pro Asn Gln Val Thr Leu Thr Asn Ile Arg Asn
210 215 220

Glu Pro Val Ile Val Asp Ser Leu Ser His Pro Thr Val Ala Val Leu
225 230 235 240

Ala Leu Met Leu Phe Val Cys Asn Pro Pro Asn
245 250

<210> 83
<211> 342
<212> PRT
<213> Pseudomonas aeruginosa

<400> 83

Pro Glu Gly Gly Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys His
1 5 10 15

Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu
20 25 30

Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr

35 40 45

Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Ala Asn
50 55 60

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

Glu Ser Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu
85 90 95

Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala
100 105 110

Ala Asn Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr
115 120 125

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

Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His
145 150 155 160

Arg Gln Leu Glu Glu Arg Gly Tyr Val Phe Val Gly Tyr His Gly Thr
165 170 175

Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala Arg
180 185 190

Ser Gln Asp Leu Asp Ala Ile Trp Ala Gly Phe Tyr Ile Ala Gly Asp
195 200 205

Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Ala
210 215 220

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

Ser Leu Pro Gly Phe Tyr Ala Thr Ser Leu Thr Leu Ala Ala Pro Glu
245 250 255

Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg
260 265 270

Leu Asp Ala Ile Thr Gly Pro Glu Glu Ser Gly Gly Arg Leu Glu Thr
275 280 285

Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala
290 295 300

Ile Pro Thr Asp Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser Ser
305 310 315 320

Ile Pro Asp Ser Glu Gln Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser
325 330 335

Gln Pro Gly Lys Pro Pro
340

<210> 84
<211> 342
<212> PRT
<213> Pseudomonas aeruginosa

<400> 84

Pro Glu Gly Gly Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys His
1 5 10 15

Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu
20 25 30

Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr
35 40 45

Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Ala Asn
50 55 60

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

Glu Ser Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu
85 90 95

Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala
100 105 110

Ala Asn Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr
115 120 125

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

Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His
145 150 155 160

Arg Gln Leu Glu Glu Ala Gly Tyr Val Phe Val Gly Tyr His Gly Thr
165 170 175

Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala Arg
180 185 190

Ser Gln Asp Leu Asp Ala Ile Trp Ala Gly Phe Tyr Ile Ala Gly Asp
195 200 205

Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Ala
210 215 220

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

Ser Leu Pro Gly Phe Tyr Ala Thr Ser Leu Thr Leu Ala Ala Pro Glu
245 250 255

Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg
260 265 270

Leu Asp Ala Ile Thr Gly Pro Glu Glu Ser Gly Gly Arg Leu Glu Thr
275 280 285

Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala
290 295 300

Ile Pro Thr Asp Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser Ser
305 310 315 320

Ile Pro Asp Ser Glu Gln Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser
325 330 335

Gln Pro Gly Lys Pro Pro
340

<210> 85
<211> 1290
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 85
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ctgcgtaatg aactggcaaa aggtacaccg gtttgtcagc tgccggttac cctgcagacc 120

attgcagatg ataaacgttt tgttctggtg gatatcacca ccaccagtaa aaaaaccgtt 180

aaagttgcca tcgatgtgac cgatgtttat gttgttggct atcaggataa atgggatggt 240

aaagatcgtg ccgtttttct ggataaagtt ccgaccgttg caaccagcaa actgtttccg 300

ggtgttacca atcgtgttac cctgaccttt gatggtagct atcagaaact ggttaatgca 360

gccaaagtgg atcgtaaaga tctggaactg ggcgtttata aactggaatt cagcattgaa 420

gccatccatg gtaaaaccat taacggccaa gaaatcgcca aatttttcct gattgtgatt 480

cagatggtta gcgaagccgc acgctttaaa tacattgaaa ccgaagttgt ggatcgcggt 540

ctgtatggta gctttaaacc gaactttaaa gtgctgaacc tggaaaataa ctggggtgat 600

attagcgacg caattcataa aagcagtccg cagtgtacca ccattaatcc ggcactgcag 660

ctgattagcc cgagcaatga tccgtgggtt gttaataaag ttagccagat tagtccggac 720

atgggcattc tgaaattcaa aagcggtggt ggtggtagcc gtaaaaaacg tgcaagcggt 780

tgtggtccgg aaggtggtgg cggtagtcgt gttgcagcac atattaccgg cacccgtggt 840

cgtagcaata ccctgagcag cccgaatagc aaaaatgaaa aagccctggg tcgcaaaatt 900

aacagctggg aaagcagccg tagcggtcat agctttctga gcaatctgca tctgcgcaat 960

ggtgaactgg tgattcacga aaaaggcttc tattatatct acagccagac ctatttccgc 1020

ttccaagaag agatcaaaga gaacaccaaa aacgacaaac aaatggtgca gtacatctat 1080

aaatacacca gctatccgga tccgattctg ctgatgaaaa gcgcacgtaa tagctgttgg 1140

agcaaagatg cagaatatgg cctgtatagc atctatcagg gtggcatttt tgaactgaaa 1200

gaaaacgatc gcatctttgt gagcgtgacc aatgaacatc tgattgatat ggatcacgaa 1260

gccagctttt ttggtgcctt tctggttggt 1290

<210> 86
<211> 1359
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 86
cgtgttgcag cacatattac cggcacccgt ggtcgtagca ataccctgag cagcccgaat 60

agcaaaaatg aaaaagcact gggtcgcaaa attaatagct gggaaagcag ccgtagcggt 120

catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttttattata tttatagcca gacctatttt cgctttcagg aagaaattaa agaaaatacc 240

aaaaatgata aacaaatggt gcagtacatc tataaatata ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 360

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 420

accaatgaac atctgattga tatggatcat gaagccagct tttttggtgc atttctggtt 480

ggtggtggtg gcggtagcgc aagcggttgt ggtccggaac gtaaaaaacg cggtggtggt 540

ggtagtgaag ataataatat ttttccgaaa cagtacccga ttattaattt taccaccgca 600

ggcgcaaccg ttcagagcta taccaatttt attcgtgcag ttcgtggtcg tctgacaacc 660

ggtgcggatg ttcgtcatga aattccggtt ctgccgaatc gtgttggtct gccgattaat 720

cagcgtttta ttctggttga actgagcaat catgcagaac tgagcgttac cctggcactg 780

gatgttacca atgcctatgt tgttggttat cgtgcaggta atagcgccta ttttttttcat 840

ccggataatc aggaagatgc agaagcaatt acccacctgt ttaccgatgt gcagaatcgt 900

tataccttttg catttggtgg caattatgat cgtctggaac agctggcagg tagcctgcgt 960

gaaaatattg aactgggtaa tggtccgctg gaagaagcaa ttagcgcact gtattattat 1020

agcaccggtg gcacccagct gccgaccctg gcacgtagct ttattgtttg tattcagatg 1080

attagcgaag cagcccgttt tcagtatatt gaaggtgaaa tgcgtacccg cattcgttat 1140

aatcgtcgta gcgcaccgga tccgagcgtt attaccctgg aaaatagctg gggtcgtctg 1200

agtaccgcaa ttcaggaatc aaatcaggga gcatttgcaa gcccgattca gctgcagcgt 1260

cgtaatggta gcaaatttag cgtttatgat gtgagcattc tgattccgat tattgccctg 1320

atggtttatc gttgtgcacc gcctccgaaa gaagatctg 1359

<210> 87
<211> 1134
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 87
cgtgttgcag cacatattac cggcacccgt ggtcgtagca ataccctgag cagcccgaat 60

agcaaaaatg aaaaagcact gggtcgcaaa attaatagct gggaaagcag ccgtagcggt 120

catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttttattata tttatagcca gacctatttt cgctttcagg aagaaattaa agaaaatacc 240

aaaaatgata aacaaatggt gcagtacatc tataaatata ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 360

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 420

accaatgaac atctgattga tatggatcat gaagccagct tttttggtgc atttctggtt 480

ggtggtggtg gcggtagcgc aagcggttgt ggtccggaac gtaaaaaacg cggtggtggt 540

ggtagtggtc cgggtccgaa acagtacccg attattaatt ttaccaccgc aggcgcaacc 600

gttcagagct ataccaattt tattcgtgca gttcgtggtc gtctgacaac cggtgcggat 660

gttcgtcatg aaattccggt tctgccgaat cgtgttggtc tgccgattaa tcagcgtttt 720

attctggttg aactgagcaa tcatgcagaa ctgagcgtta ccctggcact ggatgttacc 780

aatgcctatg ttgttggtta tcgtgcaggt aatagcgcct atttttttca tccggataat 840

caggaagatg cagaagcaat tacccacctg tttaccgatg tgcagaatcg ttatacctttt 900

gcatttggtg gcaattatga tcgtctggaa cagctggcag gtaatctgcg tgaaaatatt 960

gaactgggta atggtccgct ggaagaagca attagcgcac tgtattatta tagcaccggt 1020

ggcacccagc tgccgaccct ggcacgtagc tttattattt gtattcagat gattagcgaa 1080

gccgcacgct ttcagtatat tgaaggtgaa atgcgtgtgc cgaaagaaga tctg 1134

<210> 88
<211> 1419
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 88
cgtgttgcag cacatattac cggcacccgt ggtcgtagca ataccctgag cagcccgaat 60

agcaaaaatg aaaaagcact gggtcgcaaa attaatagct gggaaagcag ccgtagcggt 120

catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttttattata tttatagcca gacctatttt cgctttcaag aagaaattaa agaaaacacc 240

aaaaatgata aacaaatggt gcagtacatt tataaatata ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 360

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 420

accaatgaac atctgattga tatggatcat gaagccagct tttttggtgc atttctggtt 480

ggtggtggtg gcggtagcgc aagcggttgt ggtccggaag gtggtggtgg tagtgcaatt 540

aataccatta cctttgatgc aggcaatgcc accattaata aatatgccac ctttatggaa 600

agcctgcgta atcaggcaaa agatccgaaa ctgaaatgct atggtattcc gatgctgccg 660

gataccaata gcaccccgaa atatctgctg gttaaactgc agggtgcaaa tctgaaaacc 720

attaccctga tgctgcgtcg taataatctg tatgttatgg gttatagcga tccgtttaat 780

ggtaataaat gccgctatca tatttttaat gatattacca gcaccgaacg caccgatgtt 840

gaaaataccc tgtgtagcag cagcagcagt cgtgttgcaa tgagcattaa ttataatagc 900

ctgtatccga ccatggaaaa aaaagcagaa gtgaatagcc gtaatcaggt tcagctgggt 960

attcagattc tgagcagcga tattggtaaa atcagcggtg ttgatagctt tccggttaaa 1020

accgaagcat tttttctgct ggttgccatt cagatggtta gcgaagcagc acgctttaaa 1080

tatattgaaa atcaggtgaa aaccaatttt aatcgtgcct tttatccgga tccgaaagtg 1140

attaatctgg aagaaaaatg gggcaaaatt agcgaagcca ttcataatgc aaaaaatggt 1200

gcactgccga aaccgctgga actggttgat gcaaaaggca ccaaatggat tgttctgcgt 1260

gtggatgaaa ttaatcgtga tgttgccctg ctgaaatatg ttaatggcac ctgtcagacc 1320

acctatcaga atgcaatgtt tagccaggtg attattagca cctattataa ttatatgagc 1380

aatctgggcg acctgtttga aggctttaaa gatgaactg 1419

<210> 89
<211> 1290
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 89
cgtgttgcag cacatattac cggcacccgt ggtcgtagca ataccctgag cagcccgaat 60

agcaaaaatg aaaaagcact gggtcgcaaa atcaatagct gggaaagcag ccgtagcggt 120

catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttttattata tttatagcca gacctatttt cgctttcaag aagagattaa agaaaatacc 240

aaaaatgata aacaaatggt gcagtacatt tataaatata ccagctatcc ggacccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 360

agcatttatc agggtggcat ctttgagctg aaagaaaatg atcgcatctt tgttagcgtg 420

accaacgaac atctgatcga tatggatcat gaagccagct tttttggtgc atttctggtt 480

ggtggtggtg gcggtagcgc aagcggttgt ggtccggaag gtggtggtgg tagtgttacc 540

agcattaccc tggatctggt taatccgacc gcaggtcagt atagcagctt tgttgataaa 600

attcgcaata acgtgaaaga tccgaatctg aaatatggtg gcaccgatat tgcagttatt 660

ggtccgccta gcaaagataa atttctgcgc attaactttc agagcagccg tggcaccgtt 720

agcctgggtc tgaaacgtga taatctgtat gttgttgcat atctggccat ggataatacc 780

aatgttaacc gtgcctatta ttttaaaagc gaaatcacca gcgcagaact gaccgcactg 840

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atcgaaaaaa atgcccagat tacccagggt gataaaagcc gtaaagaact gggtctgggt 960

attgatctgc tgctgacctt tatggaagcc gttaataaaa aagcccgtgt ggttaaaaac 1020

gaagcacgtt ttctgctgat tgcaattcag atgaccgcag aagttgcacg ttttcgttat 1080

attcagaacc tggtgaccaa aaactttccg aacaaattcg acagcgataa caaagtgatc 1140

cagtttgaag ttagctggcg taaaatttcc accgcaattt atggtgatgc caaaaatggc 1200

gtgtttaaca aagattatga cttcggtttt ggcaaagtgc gtcaggttaa agatctgcag 1260

atgggtctgc tgatgtatct gggtaaaccg 1290

<210> 90
<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 90
gttcgtgaac gtggtccgca gcgtgttgca gcacatatta ccggcacccg tggtcgtagc 60

aataccctga gcagcccgaa tagcaaaaat gaaaaagcac tgggtcgcaa aatcaatagc 120

tgggaaagca gccgtagcgg tcatagcttt ctgagcaatc tgcatctgcg taatggtgaa 180

ctggtgattc atgaaaaagg cttttattat atctatagcc agacctattt tcgctttcaa 240

gaagagatta aagaaaatac caaaaatgat aaacaaatgg tgcagtatat ctataaatat 300

accagctatc cggacccgat tctgctgatg aaaagcgcac gtaatagctg ttggagcaaa 360

gatgcagaat atggtctgta tagcatttat cagggtggca tctttgagct gaaagaaaat 420

gatcgcatct ttgttagcgt gaccaacgaa catctgatcg atatggatca tgaagccagc 480

ttttttggtg catttctggt tggtgcaagc ggttgtggtc cggaaggtgg tggtggtggc 540

agcggtggtg gcggtagccg taaaaaacgt gttaccagca ttaccctgga tctggttaat 600

ccgaccgcag gtcagtatag cagctttgtt gataaaattc gcaataacgt gaaagatccg 660

aatctgaaat atggtggcac cgatattgca gttattggtc cgcctagcaa agataaattt 720

ctgcgcatta actttcagag cagccgtggc accgttagcc tgggtctgaa acgtgataat 780

ctgtatgttg ttgcatatct ggccatggat aataccaatg ttaaccgtgc ctattatttt 840

aaaagcgaaa tcaccagcgc agaactgacc gcactgtttc cggaagcaac caccgcaaat 900

cagaaagcac tggaatatac cgaagattat cagagcatcg aaaaaaatgc ccagattacc 960

cagggtgata aaagccgtaa agaactgggt ctgggtattg atctgctgct gacctttatg 1020

gaagccgtta ataaaaaagc ccgtgtggtt aaaaacgaag cacgttttct gctgattgca 1080

attcagatga ccgcagaagt tgcacgtttt cgttatattc agaacctggt gaccaaaaac 1140

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atttccaccg caatttatgg tgatgccaaa aatggcgtgt ttaacaaaga ttatgacttc 1260

ggttttggca aagtgcgtca ggttaaagat ctgcagatgg gtctgctgat gtatctgggt 1320

aaaccg 1326

<210> 91
<211> 1287
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 91
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<210> 92
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 92
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gcaagcggta gccagtggtt tcgtttttt aatctgacca attataatga tgaaaccgtt 180

accgtggccg ttaatgttac caatgtttat attgttgcct atcgtgcaga tgccgtgagc 240

tatttttttg aagatacacc ggcagaagcc tttaaactga tttttgcagg caccaaaacc 300

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gatatgattg aactgggtat tccggcactg agcagcgcaa ttaccaatat ggtgtattat 420

gattatcaga gcaccgcagc agcactgctg gttctgattc agtgtaccgc agaagcagca 480

cgctataaat atattgaaca gcaggttagc agccatatta gcagcaattt ttatccgaat 540

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<211> 1281
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<213> Artificial Sequence

<220>
<223> none

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ttttttggtg catttctggt t 1281

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<211> 1386
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 94
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gttctgcgtc gtgaaagcga agttcaggtt aaaaatcgtt ttgttctggt gcgcctgacc 180

aattataatg gtgataccgt taccagcgca gttgatgtta ccaatctgta tctggttgca 240

tttagcgcaa atggcaatag ctatttttt aaagatgcca ccgaactgca gaaaagcaac 300

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gttggt 1386

<210> 95
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 95
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gttctgcgtc gtgaaagcga agttcaggtt aaaagccgtt ttgttctggt tccgctgacc 180

aattataatg gtaataccgt taccctggcc gttgatgtta ccaatctgta tgttgttgcc 240

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<211> 663
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 96
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<210> 97
<211> 681
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 97

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accaatgaac atctgattga tatggatcat gaagccagct tttttggtgc atttctggtt 480

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ccgcgtggta gtccgcgtac cgaatatgaa gcatgtcgtg ttcgttgtca ggttgcagaa 600

catggtgttg aacgtcagcg tcgttgtcag caggtttgtg aaaaacgtct gcgtgaacgt 660

gaaggtcgtc gtgaagttga t 681

<210> 98
<211> 762
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 98
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<211> 1314

<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 99
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<210> 100
<211> 1293
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 100
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ttttattata tttatagcca gacctatttt cgctttcaag aagaaattaa agaaaatacc 240

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ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 360

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<211> 1284
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 101
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gttagcggtg caggtcgtta tctgctgatg cacctgttta attatgacgg taaaaccatt 180

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<210> 102
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<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 102
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agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 420

accaatgaac atctgattga tatggatcat gaagccagct tttttggtgc atttctggtt 480

ggtggtggtg gtagcgcaag cggtggtccg gaaggtggta gcctggcagc actgaccgca 540

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gcagcaaatg gtccggcaga tagcggtgat gcactgctgg aacgtaatta tccgaccggt 900

gcagaatttc tgggtgatgg cggtgatgtt agctttagca cccgtggcac ccagaattgg 960

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ccggattatg ccagccagcc tggtaaacct ccgaaagatg aactg 1545

<210> 103
<211> 1578
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 103
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catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

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ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 360

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accaatgaac atctgattga tatggatcat gaagccagct tttttggtgc atttctggtt 480

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ccggaaggtg gtagcctggc agcactgacc gcacatcagg catgtcatct gccgctggaa 600

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attccggata gcgaacaggc aattagcgca ctgccggatt atgcaagcca gcctggtaaa 1560

cctccgaaag atgaactg 1578

<210> 104
<211> 1578
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 104
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catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

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aaaaatgata aacaaatggt gcagtatatc tataaatata ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 360

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 420

accaatgaac atctgattga tatggatcat gaagccagct tttttggtgc atttctggtt 480

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ccggaaggtg gtagtctggc agcactgacc gcacatcagg catgtcatct gccgctggaa 600

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gatgcactgc tggaacgtaa ttatccgacc ggtgcagaat ttctgggtga tggcggtgat 960

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attccggata gcgaacaggc aattagcgca ctgccggatt atgccagcca gcctggtaaa 1560

cctccgaaag atgaactg 1578

<210> 105
<211> 1602
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 105
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catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttctactata tctacagcca gacctatttt cgcttccaag aagagattaa agaaaacacc 240

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ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggcctgtat 360

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<210> 106
<211> 1545
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 106
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catagctttc tgagcaacct gcatctgcgt aacggcgaac tggtgattca tgaaaaaggc 180

ttttattata tttatagcca gaccaacttt aaatttcgtg aagaaattaa agaaaacacc 240

aaaaacgata aacagatggt gcagtatatt tataaatata ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcgcg taacagctgc tggagcaaag atgcggaata tggcctgtat 360

agcatttatc agggcggcat ttttgaactg aaagaaaacg atcgtatttt tgtgagcgtg 420

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gtgggcggcg atctggatcc gagcagcatt ccggatagcg aacaggcgat tagcgcgctg 1500

ccggattatg cgagccagcc gggcaaaccg ccgaaagatg aactg 1545

<210> 107
<211> 1578
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 107
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cattcatttt tatcaaattt acatttaaga aatggagaat tagtgataca tgaaaaggga 180

ttttattata tatattcaca aacatatttt agatttcaag aagaaataaa ggaaaataca 240

aagaatgata agcaaatggt gcaatatata tataagtata catcatatcc agatccaata 300

ttattaatga agtcagcaag aaattcatgt tggtcaaagg atgcagaata tggattatat 360

tcaatatatc aaggaggaat atttgaatta aaggaaaatg atagaatatt tgtgtcagtg 420

acaaatgaac atttaataga tatggatcat gaagcatcat tttttggagc atttttagtg 480

ggaggaggag gatcagcatc aggatgtgga ccagaaagaa agaagagagc atcaggagga 540

ccagaaggag gatcattagc agcattaaca gcacatcaag catgtcattt accattagaa 600

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gaatcaccag aacaagcaag attagcatta acattagcag cagcagaatc agaaagattt 840

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gcacaatcaa tagtgtttgg aggagtgaga gcaagatcac aagatttaga tgcaatatgg 1140

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ccagatgcag caggaagaat aagaaatgga gcattattaa gagtgtatgt gccaagatca 1260

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ataccagatt cagaacaagc aatatcagca ttaccagatt atgcatcaca accaggaaag 1560

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<210> 108
<211> 1578
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 108
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catagctttc tgagcaacct gcatctgcgt aacggcgaac tggtgattca tgaaaaaggc 180

ttttattata tttatagcca gacctatttt cgttttcagg aagaaattaa agaaaacacc 240

aaaaacgata aacagatggt gcagtatatt tataaatata ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcgcg taacagctgc tggagcaaag atgcggaata tggcctgtat 360

agcatttatc agggcggcat ttttgaactg aaagaaaacg atcgtatttt tgtgagcgtg 420

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ccgccgaaag atgaactg 1578

<210> 109
<211> 1269
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 109
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attgatagcg gcaccggtga taacctgttt gcagttgatg tgcgtggtat tgatccggaa 180

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ccgggtacaa ccgcagttac cctgagcggt gatagcagct ataccaccct gcagcgtgtt 360

gcaggtatta gccgtaccgg tatgcagatt aatcgtcata gcctgaccac ctcttatctg 420

gatctgatga gccatagcgg tacaagcctg acccagagcg ttgcacgtgc aatgctgcgt 480

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gttggtcgta ttagctttgg tagcattaat gcaattctgg gtagcgttgc actgattctg 720

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ccgcagcgtg tggcagcaca tattaccggc acccgtggtc gtagcaatac cctgagcagc 840

ccgaatagca aaaatgaaaa agccctgggt cgcaaaatta atagctggga aagcagccgt 900

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ctgtatagca tttatcaggg tggcattttt gaactgaaag aaaatgatcg cattttgtg 1200

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<210> 110
<211> 1296
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 110
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ggcttttatt atatttatag ccagacctat tttcgctttc aggaagaaat taaagaaaat 240

accaaaaatg ataaacaaat ggtgcagtac atctataaat ataccagcta tccggatccg 300

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tatagcattt atcagggtgg cattttgaa ctgaaagaaa atgatcgcat ttttgtgagc 420

gtgaccaatg aacatctgat tgatatggat catgaagcca gctttttgg tgcatttctg 480

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ctgatgattg atagcggcac cggtgataac ctgtttgcag ttgatgttcg tggtattgat 720

ccggaagaag gtcgttttaa taatctgcgt ctgattgtgg aacgcaataa tctgtatgtt 780

accggttttg tgaatcgcac caataatgtg ttttatcgct ttgccgattt tagccatgtt 840

acctttccgg gtacaaccgc agttaccctg agcggtgata gcagctatac caccctgcag 900

cgtgtggcag gtattagccg taccggtatg cagattaatc gtcatagcct gaccaccagt 960

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<210> 111
<211> 1076
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 111
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gttatttata cctatccgaa taaagtgttc tgcggtattg ttgcacatca gcgtggtaat 420

cagggtgatc tgcgtctgtg tagccatggt ggtggtggta gcggtggtgg tggcagccgt 480

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gcacatatta ccggcacccg tggtcgtagc aataccctga gcagcccgaa tagcaaaaat 600

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atttatagcc agacctattt tcgctttcaa gaagagatta aagaaaatac caaaaatgat 780

aaacaaatgg tgcagtacat ctataaatat accagctatc cggacccgat tctgctgatg 840

aaaagcgcac gtaatagctg ttggagcaaa gatgcagaat atggtctgta tagcatttat 900

cagggtggca tctttgagct gaaagaaaat gatcgcatct ttgttagcgt gaccaacgaa 960

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<210> 112
<211> 1005
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 112
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catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttttattata tttatagcca gacctatttt cgctttcaag aagagattaa agaaaatacc 240

aaaaatgata aacaaatggt gcagtacatc tataaatata ccagctatcc ggacccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 360

agcatttatc agggtggcat ctttgagctg aaagaaaatg atcgcatctt tgttagcgtg 420

accaacgaac atctgatcga tatggatcat gaagccagct tttttggtgc atttctggtt 480

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ggtagtgcaa cctggacctg tattaatcag cagctgaatc cgaaaaccaa caaatgggaa 600

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ggcaaactga ttaaaggtcg taccccgatt aaatttggta aagcagattg tgatcgccct 780

ccgaaacatt cacagaatgg tatgggtaaa gatgatcact atctgctgga atttccgacc 840

tttccggatg gtcacgatta taaatttgat agcaaaaaac cgaaagagga tccgggtccg 900

gcacgtgtta tttataccta tccgaataaa gtgttctgcg gtattgttgc acatcagcgt 960

ggtaatcagg gtgatctgcg tctgtgtagc cataaagaag atctg 1005

<210> 113
<211> 957
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 113
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gttgcaaccg cacaggcaca ggcacgtaaa gcaggtctga ccaccggtaa aagcggtgat 120

ccgcatcgtt attttgccgg tgatcatatt cgttggggtg ttaataattg cgataaagca 180

gatgccatcc tgtgggaata tccgatttat tgggttggta aaaatgccga atgggccaaa 240

gatgttaaaa ccagccagca gaaaggtggt ccgaccccga ttcgtgttgt ttatgcaaat 300

agccgtggtg cagttcagta ttgtggtgtt atgacccata gcaaagtgga taaaaacaac 360

cagggcaaag aatttttga aaaatgtgat ggtggtggtg gtagcggtgg tggtggcagc 420

cgtaaaaaac gtgcaagcgg ttgtggtccg gaagttcgtg aacgtggtcc gcagcgtgtt 480

gcagcacata ttaccggcac ccgtggtcgt agcaataccc tgagcagccc gaatagcaaa 540

aatgaaaaag cactgggtcg caaaatcaat agctgggaaa gcagccgtag cggtcatagc 600

tttctgagca atctgcatct gcgtaatggt gaactggtga ttcatgaaaa aggcttttat 660

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gataaacaaa tggtgcagta catctataaa tataccagct atccggaccc gattctgctg 780

atgaaaagcg cacgtaatag ctgttggagc aaagatgcag aatatggtct gtatagcatt 840

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gaacatctga tcgatatgga tcatgaagcc agctttttg gtgcatttct ggtgggt 957

<210> 114
<211> 870
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 114
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agcaaaaatg aaaaagcact gggtcgcaaa attaatagct gggaaagcag ccgtagcggt 120

catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttttattata tttatagcca gacctatttt cgctttcaag aagaaatcaa agaaaatacc 240

aaaaatgata aacaaatggt gcagtatatt tacaaatata ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 360

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 420

accaatgaac atctgattga tatggatcat gaagccagct tttttggtgc atttctggtt 480

ggtggtggtg gcggtagcgc aagcggttgt ggtccggaac gtaaaaaacg tgaacgtggt 540

gaaatttggc tggttagcct ggatccgacc gcaggtcatg aacagcaggg cacccgtccg 600

gttctgattg ttacaccggc agcatttaat cgtgttaccc gtctgccggt tgttgttccg 660

gttaccagcg gtggtaattt tgcacgtacc gcaggttttg cagtgagcct ggatggtgtt 720

ggtattcgta ccaccggtgt tgttcgttgt gatcagcctc gtaccattga tatgaaagca 780

cgtggtggta aacgtctgga acgtgttccg gaaaccatta tgaatgaagt tctgggtcgt 840

ctgagcacca ttctgaccaa agaagatctg 870

<210> 115
<211> 831
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 115
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catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttttattata tttatagcca gacctatttt cgctttcaag aagaaatcaa agaaaatacc 240

aaaaatgata aacaaatggt gcagtatatt tacaaatata ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 360

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 420

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ggtggtggtg gcggtagcgc aagcggttgt ggtccggaac gtaaaaaacg tcagtttaaa 540

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attgatacac cgggtcgtcg tatggttatt ccgctggcaa gcgcacgtct gctgagcgat 660

aaagttagcc gtgaactgta tccggttgtt catattggtg atgaaagctg gcgtatgatg 720

accaccgata tggcaagcgt tccggttagc gttattggtg aagaagttgc agatctgagc 780

catcgtgaaa atgatattaa aaatgccatt aatctgatgt tttggggcat t 831

<210> 116
<211> 684
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 116
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agcaaaaatg aaaaagcact gggtcgcaaa attaatagct gggaaagcag ccgtagcggt 120

catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttttattata tttatagcca gacctatttt cgctttcaag aagaaatcaa agaaaatacc 240

aaaaatgata aacaaatggt gcagtatatt tacaaatata ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 360

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 420

accaatgaac atctgattga tatggatcat gaagccagct tttttggtgc atttctggtt 480

ggtggtggtg gcggtagcgc aagcggttgt ggtccggaac gtaaaaaacg tcagtttaaa 540

gtgtatacct ataaaggtgg tagcggtggt cgtctgctga gcgataaagt tagccgtgaa 600

ctgggtggta gtggaggtag ccatcgtgaa aatgatatta aaaatgccat taatctgatg 660

ttttggggca ttaaagaaga tctg 684

<210> 117
<211> 825
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 117
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ttttattata tttatagcca gacctatttt cgctttcaag aagaaatcaa agaaaatacc 240

aaaaatgata aacaaatggt gcagtatatc tataaatata ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 360

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 420

accaatgaac atctgattga tatggatcat gaagccagct tttttggtgc atttctggtt 480

ggtggtggtg gcggtagcgc aagcggttgt ggtccggaac gtaaaaaacg tgcatatttt 540

ctggattttg atgaacgtgc cctgaaagaa tggcgtaaac tgggtagcac cgttcgtgaa 600

cagctgaaaa aaaaactggt tgaagttctg gaaagtccgc gtattgaagc aaataaactg 660

cgtggtatgc cggattgcta taaaattaaa ctgcgtagca gcggctatcg tctggtttat 720

caggttattg atgaaaaagt ggtggtgttt gtgattagcg ttggtaaacg tgaacgtagc 780

gaagtttata gcgaagcagt taaacgcatt ctgaaagaag atctg 825

<210> 118
<211> 813
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 118
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agcaaaaatg aaaaagcact gggtcgcaaa attaatagct gggaaagcag ccgtagcggt 120

catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttttattata tttatagcca gacctatttt cgctttcaag aagaaatcaa agaaaatacc 240

aaaaatgata aacaaatggt gcagtatatt tacaaatata ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 360

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 420

accaatgaac atctgattga tatggatcat gaagccagct tttttggtgc atttctggtt 480

ggtggtggtg gcggtagcgc aagcggttgt ggtccggaac gtaaaaaacg tccggaactg 540

gaatggaaag cagcagcagt tgcagatctg ctggcaattg ttgattatat tagtgatgat 600

aatccggatg cagcatttgc actgatggaa gaaattcagg ataaagttgc acagctgcct 660

gcacatccga aacgttgtcg tccgggtcgt gttgaaggca cccgtgaact ggttgttcgt 720

ccgaattatc tggttgttta tgcagaaaca ccggcagttg ttaccattct gcgtgttctg 780

catgcagcac agatgtggcc gaaagaagat ctg 813

<210> 119
<211> 1287
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 119
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ctgaatgaac tgcgcgttaa actgaaaccg gaaggtaata gccatggtat tccgctgctg 120

cgtaaaaaag cagatgatcc gggtaaagca tttgttctgg ttgcactgag caatgataat 180

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cgtaatcgca gctatttttt taaagatgca ccggatgcag cctatgaagg cctgtttaaa 300

aataccatta aaacccgtct gcattttggt ggtagctatc cgagcctgga aggtgaaaaa 360

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gatgaaaatg ccattgataa ttataaaccg accgaaattg cctctagcct gctggttgtt 480

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tttcagcagc gtattcgtcc ggcaaataat accattagcc tggaaaataa atggggcaaa 600

ctgagctttc agattcgtac cagcggtgca aatggtatgt ttagcgaagc cgttgaactg 660

gaacgtgcca atggcaaaaa atactatgtg accgcagtgg atcaggttaa accgaaaatt 720

gccctgctga aatttgttga taaagatccg aaaggtggtg gtggtagcgg tggcggtggc 780

tctgttcgtg aacgtggtcc gcagcgtgtt gcagcacata ttaccggcac ccgtggtcgt 840

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gaactggtga ttcatgaaaa aggcttttat tatatttata gccagaccta ttttcgcttt 1020

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aatgatcgca tttttgtgag cgtgaccaat gaacatctga ttgatatgga tcatgaagcc 1260

agctttttg gtgcatttct ggtgggc 1287

<210> 120
<211> 1302
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 120
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ctgaatgaac tgcgcgttaa actgaaaccg gaaggtaata gccatggtat tccgctgctg 120

cgtaaaaaag cagatgatcc gggtaaagca tttgttctgg ttgcactgag caatgataat 180

ggtcagctgg ccgaaattgc aattgatgtg accagcgttt atgtggttgg ttatcaggtt 240

cgtaatcgca gctatttttt taaagatgca ccggatgcag cctatgaagg cctgtttaaa 300

aataccatta aaacccgtct gcattttggt ggtagctatc cgagcctgga aggtgaaaaa 360

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gatgaaaatg ccattgataa ttataaaccg accgaaattg cctctagcct gctggttgtt 480

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ctgagctttc agattcgtac cagcggtgca aatggtatgt ttagcgaagc cgttgaactg 660

gaacgtgcca atggcaaaaa atactatgtg accgcagtgg atcaggttaa accgaaaatt 720

gccctgctga aatttgttga taaagatccg aaaggtggtg gtggcagccg taaaaaacgt 780

gcaagcggtt gtggtccgga aggtggtggt ggtagccagc gtgttgcagc acatattacc 840

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tttgaactga aagaaaatga tcgcattttt gtgagcgtga ccaatgaaca tctgattgat 1260

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<210> 121
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 121
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agcaaaaatg aaaaagcact gggtcgcaaa attaatagct gggaaagcag ccgtagcggt 120

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aaaaatgata aacaaatggt gcagtacatt tataaatata ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 360

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 420

accaatgaac atctgattga tatggatcat gaagccagct tttttggtgc atttctggtt 480

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gcaaataata ccattagcct ggaaaataaa tggggcaaac tgagctttca gattcgtacc 1140

agcggtgcaa atggtatgtt tagcgaagcc gttgaactgg aacgtgccaa tggcaaaaaa 1200

tactatgtta ccgcagtgga tcaggtgaaa ccgaaaattg cactgctgaa atttgtggat 1260

aaagatccga aagatgaact g 1281

<210> 122
<211> 1299
<212> DNA

<213> Artificial Sequence

<220>
<223> none

<400> 122
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cgtaaaaaag cagatgatcc gggtaaagca tttgttctgg ttgcactgag caatgataat 180

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gcatatcgtg aaaccaccga tctgggtatt gaaccgctgc gtattggtat taaaaaactg 420

gatgaaaatg ccattgataa ttataaaccg accgaaattg caagcagcct gctggttgtt 480

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ctgagctttc agattcgtac cagcggtgca aatggtatgt ttagcgaagc cgttgaactg 660

gaacgtgcca atggcaaaaa gtattatgtt accgcagtgg atcaggtaaa accgaaaatt 720

gcactgctga aatttgtgga taaagatccg aaaggtggtg gtggtagccg taaaaaacgt 780

gcaagcggtt gtggtccgga aggtggtggc ggttcacgtg ttgcagcaca tattaccggc 840

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cgcaaaatta atagctggga aagcagccgt agcggtcata gctttctgag caatctgcat 960

ctgcgtaatg gtgaactggt gattcatgaa aaaggctttt attatattta tagccagacc 1020

tattttcgct ttcaggaaga aattaaagaa aataccaaaa atgataaaca aatggtgcag 1080

tatatctata aatataccag ctatccggat ccgattctgc tgatgaaaag cgcacgtaat 1140

agctgttgga gcaaagatgc agaatatggt ctgtatagca tttatcaggg tggcattttt 1200

gaactgaaag aaaatgatcg cattttgtg agcgtgacca atgaacatct gattgatatg 1260

gatcatgaag ccagcttttt tggtgcattt ctggttggt 1299

<210> 123
<211> 1674
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 123
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ggcacccagg gtaattatga tgatgattgg aaaggctttt atagcaccga taataaatat 180

gatgccgcag gctatagcgt tgataatgaa aatccgctgt ctggtaaagc cggtggtgtt 240

gttaaagtta cctatccggg tctgaccaaa gttctggcac tgaaagttga taatgccgaa 300

accattaaaa aagaactggg tctgtctctg accgaaccgc tgatggaaca ggttggcacc 360

gaagaattta ttaaacgctt tggtgatggt gcaagccgtg ttgttctgag cctgccgttt 420

gcagaaggta gcagcagcgt tgaatatatt aataattggg aacaggccaa agcactgagc 480

gttgaactgg aaattaattt tgaaacccgt ggcaaacgtg gtcaggatgc catgtatgaa 540

tatatggcac aggcatgtgc aggcaatcgt gttcgtcgta gcgttggtag cagcctgagc 600

tgtattaatc tggattggga tgtgattcgc gataaaacca aaaccaaaat tgaaagcctg 660

aaagaacatg gtccgattaa aaataaaatg agcgaaagcc cgaataaaac cgtgagcgaa 720

gaaaaagcaa aacagtatct ggaagaattt catcagaccg cactggaaca tccggaactg 780

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tctccgggtc ataaaaccca tggtggtggt ggtagcggtg gtggtggcag ccgtgttgca 1200

gcacatatta ccggcacccg tggtcgtagc aataccctga gcagcccgaa tagcaaaaat 1260

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aaaagcgcac gtaatagctg ttggagcaaa gatgcagaat atggcctgta tagcatttat 1560

cagggtggca tttttgaact gaaagaaaat gatcgcattt ttgtgagcgt gaccaatgaa 1620

catctgattg atatggatca tgaagccagc ttttttggtg catttctggt gggt 1674

<210> 124
<211> 1443
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 124

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catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttctactata tctatagcca gacctatttc cgcttccaag aagaaatcaa agaaaatacc 240

aaaaacgata aacaaatggt gcagtatatc tataaataca ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 360

agcatttatc agggtggcat ctttgagctg aaagaaaatg atcgcatctt tgttagcgtg 420

accaacgaac atctgatcga tatggatcat gaagccagct tttttggtgc atttctggtt 480

ggtggtggtg gtagcggtgg tggtggcagc cgtaaaaaac gtccggaagg tggtagcctg 540

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gataacaaat atgatgcagc cggttatagc gtggataatg aaaatccgct gagcggtaaa 1080

gccggtggtg ttgttaaagt tacctatccg ggtctgacca aagttctggc actgaaagtt 1140

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caggttggca ccgaagaatt tatcaaacgt tttggtgatg gtgcaagccg tgttgttctg 1260

agtctgccgt ttgcagaagg tagcagcagc gttgaatata tcaataattg ggaacaggca 1320

aaagccctga gcgttgaact ggaaatcaat tttgaaaccc gtggtaaacg tggtcaggat 1380

gcaatgtatg aatatatggc acaggcatgt gcaggcaatc gtgttcgtcg taaagaagat 1440

ctg 1443

<210> 125
<211> 1443
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 125
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catggcacca aaccgggcta tgtggatagc attcagaaag gcattcagaa accgaaaagc 120

ggcacccagg gcaactatga tgatgattgg aaaggctttt atagcaccga taacaaatat 180

gatgcggcgg gctatagcgt ggataacgaa aacccgctga gcggcaaagc gggcggcgtg 240

gtgaaagtga cctatccggg cctgaccaaa gtgctggcgc tgaaagtgga taacgcggaa 300

accattaaaa aagaactggg cctgagcctg accgaaccgc tgatggaaca ggtgggcacc 360

gaagaattta ttaaacgctt tggcgatggc gcgagccgcg tggtgctgag cctgccgttt 420

gcggaaggca gcagcagcgt ggaatatatt aacaactggg aacaggcgaa agcgctgagc 480

gtggaactgg aaattaactt tgaaacccgc ggcaaacgcg gccaggatgc gatgtatgaa 540

tatatggcgc aggcgtgcgc gggcaaccgc aaaaaacgcg gcggcggcgg cagcccggaa 600

ggcggcagcc tggcggcgct gaccgcgcat caggcgtgcc atctgccgct ggaaaccttt 660

acccgccatc gccagccgcg cggctgggaa cagctggaac agtgcggcta tccggtgcag 720

cgcctggtgg cgctgtatct ggcggcgcgc ctgagctgga accaggtgga tcaggtgatt 780

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cagggcaccg gcaacggccg caaaaaacgc ggcggcggcg gcagcggcgg cggcggcagc 960

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aaaaacgata aacagatggt gcagtatatt tataaatata ccagctatcc ggatccgatt 1260

ctgctgatga aaagcgcgcg caacagctgc tggagcaaag atgcggaata tggcctgtat 1320

agcatttatc agggcggcat ttttgaactg aaagaaaacg atcgcatttt tgtgagcgtg 1380

accaacgaac atctgattga tatggatcat gaagcgagct tttttggcgc gtttctggtg 1440

ggc 1443

<210> 126
<211> 1104
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 126
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tataaacagt ttattgaagc gctgcgtgaa cgtctgcgtg gcggtctgat tcatgatatt 120

ccggttctgc cggatccgac aactctgcag gaacgcaatc gttatattac cgtggaactg 180

agtaattccg atacagaatc tattgaagtg ggcattgtga cgcatggtat ttctttttt 240

cgtagtggcg gtaatgataa tgaagaaaaa gcgcgtaccc tgattgttat tattcagatg 300

gttgctgaag ccgctcgctt tcgttatatt tccaatcgtg tgcgtgtgtc tattcagact 360

ggtactgcct ttcagccgga tgcagctatg atttccctgg aaaataattg ggataatctg 420

tctcgtggtg ttcaggaatc cgttcaggat acctttccga atcaggttac cctgaccaat 480

attcgtaatg aaccggttat tgttgatagc ctgtctcatc cgaccgttgc tgttctggcc 540

ctgatgctgt ttgtttgcaa tcctccgaat ggtggtggtg gttctggtgg cggtggttca 600

gtgcgtgaac gtggtccgca gcgtgttgcc gctcatatta ccggtactcg tggtcgttct 660

aataccctgt ctagcccgaa tagtaaaaat gaaaaagccc tgggtcgcaa aattaatagt 720

tgggaatcta gtcgtagtgg ccattctttt ctgagcaatc tgcatctgcg taatggtgaa 780

ctggtgattc atgaaaaagg tttttattat atctattccc agacttattt tcgttttcag 840

gaagaaatta aagaaaacac gaaaaatgat aaacagatgg tgcagtatat ctataaatat 900

acctcttatc cggatccgat tctgctgatg aaaagtgccc gtaattcttg ttggagtaaa 960

gatgcggaat atggcctgta ttctatttat cagggtggta tttttgaact gaaagaaaat 1020

gatcgcattt ttgtgtctgt gaccaatgaa catctgattg atatggatca tgaagcatct 1080

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<210> 127
<211> 1359
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 127
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tataaacagt ttattgaagc actgcgtgaa cgtctgcgtg gtggtctgat tcatgatatt 120

ccggttctgc cggatccgac caccctgcag gaacgtaatc gttatattac cgttgaactg 180

agcaatagcg ataccgaaag cattgaagtt ggtattgatg tgaccaatgc ctatgttgtt 240

gcatatcgtg caggcaccca gagctatttt ctgcgtgatg caccgagcag cgcaagcgat 300

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gaacgttggg cacatcagag ccgtcagcag attccgctgg gtctgcaggc actgacccat 420

ggtattagct tttttcgtag cggtggcaat gataatgaag aaaaagcacg taccctgatt 480

gtgattattc agatggttgc agaagcagca cgctttcgtt atatttcaaa tcgtgttcgt 540

gtgagcattc agaccggcac cgcatttcag ccggatgcag caatgattag cctggaaaat 600

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gttaccctga ccaatattcg taatgaaccg gttattgttg atagcctgag ccatccgacc 720

gttgcagttc tggcactgat gctgtttgtt tgtaatcctc cgaatgttcg tgaacgtggt 780

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actcgtggtc gttctaatac cctgtctagc ccgaatagta aaaatgaaaa agccctgggt 960

cgcaaaatta atagttggga atctagtcgt agtggccatt cttttctgag caatctgcat 1020

ctgcgtaatg gtgaactggt gattcatgaa aaaggttttt attatatcta ttcccagact 1080

tattttcgtt ttcaggaaga aattaaagaa aacacgaaaa atgataaaca gatggtgcag 1140

tatatctata aatatacctc ttatccggat ccgattctgc tgatgaaaag tgcccgtaat 1200

tcttgttgga gtaaagatgc ggaatatggc ctgtattcta tttatcaggg tggtattttt 1260

gaactgaaag aaaatgatcg cattttgtg tctgtgacca atgaacatct gattgatatg 1320

gatcatgaag catctttttt tggtgccttt ctggtgggc 1359

<210> 128
<211> 1302
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 128
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tttattgaag cgctgcgtga acgtctgcgt ggcggtctga ttcatgatat tccggttctg 120

ccggatccga caactctgca ggaacgcaat cgttatatta ccgtggaact gagtaattcc 180

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gctggcaccc agagttattt tctgcgtgat gctccgtcat ctgccagtga ttacctgttt 300

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gctcatcagt ctcgtcagca gattccgctg ggtctgcagg ctctgacgca tggtatttct 420

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cagatggttg ctgaagccgc tcgctttcgt tatatttcca atcgtgtgcg tgtgtctatt 540

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cagtatatct ataaatatac ctcttatccg gatccgattc tgctgatgaa aagtgcccgt 1140

aattcttgtt ggagtaaaga tgcggaatat ggcctgtatt ctatttatca gggtggtatt 1200

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<210> 129
<211> 1320
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 129
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attgaagcgc tgcgtgaacg tctgcgtggc ggtctgattc atgatattcc ggttctgccg 120

gatccgacaa ctctgcagga acgcaatcgt tatattaccg tggaactgag taattccgat 180

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aatattcgta atgaaccggt tattgttgat agcctgtctc atccgaccgt tgctgttctg 720

gccctgatgc tgtttgtttg caatcctccg aatcgtcgtc gtcgtcgccg tcgtcgtaag 780

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<210> 130
<211> 1671
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 130
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tgggaatcta gtcgtagtgg ccattctttt ctgagcaatc tgcatctgcg taatggtgaa 180

ctggtgattc atgaaaaagg tttttattat atctattccc agacttattt tcgttttcag 240

gaagaaatta aagaaaacac gaaaaatgat aaacagatgg tgcagtatat ctataaatat 300

acctcttatc cggatccgat tctgctgatg aaaagtgccc gtaattcttg ttggagtaaa 360

gatgcggaat atggcctgta ttctatttat cagggtggta tttttgaact gaaagaaaat 420

gatcgcattt ttgtgtctgt gaccaatgaa catctgattg atatggatca tgaagcatct 480

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tctcgtggtg ttcaggaatc cgttcaggat acctttccga atcaggttac cctgaccaat 1560

attcgtaatg aaccggttat tgttgatagc ctgtctcatc cgaccgttgc tgttctggcc 1620

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<210> 131
<211> 1377
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 131
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gatccgacca ccctgcaaga acgtaatcgt tatattaccg tggaactgag caatagcgat 180

accgaaagca ttgaagttgg tattgatgtg accaatgcct atgttgttgc atatcgtgca 240

ggcacccaga gctattttct gcgtgatgca ccgagcagcg caagcgatta cctgtttacc 300

ggcaccgatc agcatagcct gccgttttat ggcacctatg gtgatctgga acgttgggca 360

catcagagcc gtcagcagat tccgctgggt ctgcaggcac tgacccatgg tattagcttt 420

tttcgtagcg gtggcaatga caatgaagaa aaagcacgta ccctgattgt gattattcag 480

atggttgcag aagcagcacg ctttcgttat atttcaaatc gtgttcgtgt gagcattcag 540

accggaaccg catttcagcc ggatgcagca atgattagcc tggaaaataa ttgggataat 600

ctgagccgtg gtgttcaaga aagcgttcag gataccttтc cgaatcaggt taccctgacc 660

aatattcgta atgaaccggt tattgttgat agcctgagcc atccgaccgt tgcagttctg 720

gcactgatgc tgtttgtttg taatccgcct aatggtggtg gtggtagcgg tggtggtggc 780

agccgtaaaa aacgtgcaag cggttgtggt ccggaaacca gcgaagaaac cattagcacc 840

gttcaagaaa aacagcagaa tattagtccg ctggttcgtg aacgtggtcc gcagcgtgtt 900

gcagcacata ttaccggaac ccgtggtcgt agcaataccc tgagcagccc gaatagcaaa 960

aatgaaaaag cactgggtcg caaaatcaat agctgggaaa gcagccgtag cggtcatagc 1020

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gataaacaaa tggtgcagta tatctataaa tataccagct atccggatcc gatcctgctg 1200

atgaaaagcg cacgtaatag ctgttggagc aaagatgcag aatatggtct gtatagcatt 1260

tatcagggtg gcatctttga gctgaaagaa aatgatcgca tctttgttag cgtgaccaac 1320

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<213> Artificial Sequence

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catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttttattata tttatagcca gacctatttt cgctttcagg aagaaattaa agaaaatacc 240

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ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 360

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 420

accaatgaac atctgattga tatggatcat gaagccagct tttttggtgc atttctggtt 480

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<212> DNA

<213> Artificial Sequence

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<223> none

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catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttttattata tttatagcca gacctatttt cgctttcagg aagaaattaa agaaaatacc 240

aaaaatgata aacaaatggt gcagtatatc tataaatata ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 360

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 420

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<213> Artificial Sequence

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aaaaatgata aacaaatggt gcagtatatc tataaataca ccagctatcc ggatccgatt 1140

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 1200

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 1260

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ggt 1323

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<213> Artificial Sequence

<220>
<223> none

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catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttttattata tttatagcca gacctatttt cgctttcagg aagaaattaa agaaaacacc 240

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ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggcctgtat 360

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 420

accaatgaac atctgattga tatggatcat gaagccagct tttttggtgc atttctggtt 480

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<212> DNA
<213> Artificial Sequence

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<211> 1557
<212> DNA
<213> Artificial Sequence

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<212> DNA
<213> Artificial Sequence

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<210> 139
<211> 108
<212> PRT
<213> Pseudomonas aeruginosa

<400> 139

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Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr
35 40 45

Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn
50 55 60

Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg
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Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Gly
100 105

<210> 140
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<213> Artificial Sequence

<220>
<223> none

<300>
<301> Wang H, Yan Z, Shi J, Han W, Zhang Y.
<302> Expression, purification, and characterization of a neovasculature targeted rmhTNF-alpha in Escherichia coli
<303> Protein Expr Purif.
<304> 45
<305> 1
<306> 60-5
<307> 2005-07-21

<400> 140

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<211> 281
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<213> Homo sapiens

<400> 141

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35 40 45

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

Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val
65 70 75 80

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

Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
    130                 135                 140

Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
145                 150                 155                 160

His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
                165                 170                 175

His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
            180                 185                 190

Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
        195                 200                 205

Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
    210                 215                 220

Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
225                 230                 235                 240

Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
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<311> 2008-11-21
<312> 2009-05-28

<400> 142

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Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
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Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
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Pro His Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
115 120 125

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Gly

<210> 143
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<300>
<301> Gasparian ME,
<302> DR4-selective tumor necrosis factor-related apoptosis-inducing ligand(TRAIL) variants obtained by structure-based design

<303> J Biol Chem
<304> 283
<305> 29
<306> 20560-8
<307> 2008-07-18

<400> 143

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Asn Phe Lys Phe Arg Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
115 120 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu Arg
130 135 140

Leu Arg Asp Met His His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145 150 155 160

Gly

<210> 144
<211> 433
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 144

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

1 5 10 15

Tyr Lys Gln Phe Ile Glu Ala Leu Arg Glu Arg Leu Arg Gly Gly Leu
20 25 30

Ile His Asp Ile Pro Val Leu Pro Asp Pro Thr Thr Leu Gln Glu Arg
35 40 45

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

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

Gly Thr Gln Ser Tyr Phe Leu Arg Asp Ala Pro Ser Ser Ala Ser Asp
85 90 95

Tyr Leu Phe Thr Gly Thr Asp Gln His Ser Leu Pro Phe Tyr Gly Thr
100 105 110

Tyr Ala Asp Leu Glu Arg Trp Ala His Gln Ser Arg Gln Gln Ile Pro
115 120 125

Leu Gly Leu Gln Ala Leu Thr His Gly Ile Ser Phe Phe Arg Ser Gly
130 135 140

Gly Asn Asp Asn Glu Glu Lys Ala Arg Thr Leu Ile Val Ile Ile Gln
145 150 155 160

Met Val Ala Glu Ala Ala Arg Phe Arg Tyr Ile Ser Asn Arg Val Arg
165 170 175

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

Ser Leu Glu Asn Asn Trp Asp Asn Leu Ser Arg Gly Val Gln Glu Ser
195 200 205

Val Gln Asp Thr Phe Pro Asn Gln Val Thr Leu Thr Asn Ile Arg Asn
210 215 220

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

Ala Leu Met Leu Phe Val Cys Asn Pro Pro Asn Gly Gly Gly Gly Ser
245 250 255

Gly Gly Gly Gly Ser Arg Lys Lys Arg Val Arg Glu Arg Gly Pro Gln
260 265 270

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
275 280 285

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
290 295 300

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
305 310 315 320

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
325 330 335

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
340 345 350

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
355 360 365

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
370 375 380

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
385 390 395 400

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
405 410 415

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
420 425 430

Gly

<210> 145
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 145

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn

20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
115 120 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
130 135 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145 150 155 160

Gly Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Arg Lys Lys
165 170 175

Arg Gly Gly Gly Gly Ser Glu Asp Asn Asn Ile Phe Pro Lys Gln Tyr
180 185 190

Pro Ile Ile Asn Phe Thr Thr Ala Gly Ala Thr Val Gln Ser Tyr Thr
195 200 205

Asn Phe Ile Arg Ala Val Arg Gly Arg Leu Thr Thr Gly Ala Asp Val
210 215 220

Arg His Glu Ile Pro Val Leu Pro Asn Arg Val Gly Leu Pro Ile Asn
225 230 235 240

Gln Arg Phe Ile Leu Val Glu Leu Ser Asn His Ala Glu Leu Ser Val
245 250 255

Thr Leu Ala Thr Asn Ala Tyr Val Val Gly Tyr Arg Ala Gly Asn Ser
260 265 270

Ala Tyr Phe Phe His Pro Asp Asn Gln Glu Asp Ala Glu Ala Ile Thr
275 280 285

His Leu Phe Thr Asp Val Gln Asn Arg Tyr Thr Phe Ala Phe Gly Gly
290 295 300

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

Glu Leu Gly Asn Gly Pro Leu Glu Glu Ala Ile Ser Ala Leu Tyr Tyr
325 330 335

Tyr Ser Thr Gly Gly Thr Gln Leu Pro Thr Leu Ala Arg Ser Phe Ile
340 345 350

Val Cys Ile Gln Met Ile Ser Glu Ala Ala Arg Phe Gln Tyr Ile Glu
355 360 365

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

Pro Ser Val Ile Thr Leu Glu Asn Ser Trp Gly Arg Leu Ser Thr Ala
385 390 395 400

Ile Gln Glu Ser Asn Gln Gly Ala Phe Ala Ser Pro Ile Gln Leu Gln
405 410 415

Arg Arg Asn Gly Ser Lys Phe Ser Val Tyr Asp Val Ser Ile Leu Ile
420 425 430

Pro Ile Ile Ala Leu Met Val Tyr Arg Cys Ala Pro Pro Pro Lys Glu
435 440 445

Asp Leu
450

<210> 146
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 146

Gly Ala Asp Asp Val Ala Asp Ser Ser Lys Ser Phe Val Met Glu Asn
1 5 10 15

Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Ala Asp Ser Ile Gln

20 25 30

Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp Asp
35 40 45

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

Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly Val
65 70 75 80

Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val
85 90 95

Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu
100 105 110

Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe Gly
115 120 125

Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly Ser
130 135 140

Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu Ser
145 150 155 160

Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln Asp
165 170 175

Ala Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn Arg Lys Lys
180 185 190

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

Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr Arg His Arg
210 215 220

Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln
225 230 235 240

Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val
245 250 255

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

Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu
275 280 285

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

Asn Gly Arg Lys Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
305 310 315 320

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
325 330 335

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
340 345 350

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
355 360 365

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
370 375 380

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
385 390 395 400

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
405 410 415

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
420 425 430

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
435 440 445

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
450 455 460

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
465 470 475 480

Gly

<210> 147
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 147

```
Gly Ala Asp Asp Val Ser Lys Ser Phe Val Met Glu Asn Phe Ser Ser
1               5                  10                  15

Tyr His Gly Thr Lys Pro Gly Tyr Ala Asp Ser Ile Gln Lys Gly Ile
            20                  25                  30

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

Gly Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala Gly Tyr Ser Val
    50                  55                  60

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

Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val Asp Asn Ala
                85                  90                  95

Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu Pro Leu Met
            100                 105                 110

Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe Gly Asp Gly Ala
        115                 120                 125

Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly Ser Ser Ser Val
    130                 135                 140

Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu Ser Val Glu Leu
145                 150                 155                 160

Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln Asp Ala Met Tyr
                165                 170                 175

Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn Arg Lys Lys Arg Gly Gly
            180                 185                 190

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

Ala Cys His Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg
    210                 215                 220

Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val
225                 230                 235                 240
```

```
Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val
                245                 250                 255

Ile Arg Asn Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu
            260                 265                 270

Ala Ile Arg Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala
        275                 280                 285

Ala Ala Glu Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Gly Arg
    290                 295                 300

Lys Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Val Ala
305                 310                 315                 320

Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro
                325                 330                 335

Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu
            340                 345                 350

Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn
        355                 360                 365

Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln
    370                 375                 380

Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp
385                 390                 395                 400

Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro
                405                 410                 415

Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala
            420                 425                 430

Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys
        435                 440                 445

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

Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
465                 470                 475
```

<210> 148
<211> 433
<212> PRT

<213> Artificial Sequence

<220>
<223> fusion protein

<400> 148

```
Gly Leu Asp Thr Val Ser Phe Ser Thr Lys Gly Ala Thr Tyr Ile Thr
1               5                   10                  15

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

Asn Ser His Gly Ile Pro Leu Leu Arg Lys Lys Ala Asp Asp Pro Gly
        35                  40                  45

Lys Ala Phe Val Leu Val Ala Leu Ser Asn Asp Asn Gly Gln Leu Ala
    50                  55                  60

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

Arg Asn Arg Ser Tyr Phe Phe Lys Asp Ala Pro Asp Ala Ala Tyr Glu
                85                  90                  95

Gly Leu Phe Lys Asn Thr Ile Lys Thr Arg Leu His Phe Gly Gly Ser
            100                 105                 110

Tyr Pro Ser Leu Glu Gly Glu Lys Ala Tyr Arg Glu Thr Thr Asp Leu
        115                 120                 125

Gly Ile Glu Pro Leu Arg Ile Gly Ile Lys Lys Leu Asp Glu Asn Ala
    130                 135                 140

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

Ile Gln Met Val Ser Glu Ala Ala Arg Phe Thr Phe Ile Glu Asn Gln
                165                 170                 175

Ile Arg Asn Asn Phe Gln Gln Arg Ile Arg Pro Ala Asn Asn Thr Ile
            180                 185                 190

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

Gly Ala Asn Gly Met Phe Ser Glu Ala Val Glu Leu Glu Arg Ala Asn
    210                 215                 220
```

Gly Lys Lys Tyr Tyr Val Thr Ala Val Asp Gln Val Lys Pro Lys Ile
225 230 235 240

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

Arg Lys Lys Arg Ala Ser Gly Cys Gly Pro Glu Gly Gly Gly Gly Ser
260 265 270

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
275 280 285

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
290 295 300

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
305 310 315 320

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
325 330 335

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
340 345 350

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
355 360 365

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
370 375 380

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
385 390 395 400

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
405 410 415

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
420 425 430

Gly

<210> 149
<211> 258
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 149

```
Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile
1               5                  10                  15

Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile
            20                  25                  30

Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys
        35                  40                  45

Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg
    50                  55                  60

Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu
65                  70                  75                  80

Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe
                85                  90                  95

Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met
            100                 105                 110

Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu
        115                 120                 125

Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly
    130                 135                 140

Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp
145                 150                 155                 160

Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His
                165                 170                 175

Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Gly Gly Gly Ser
            180                 185                 190

Gly Gly Gly Cys Ala Ala Ala Cys Ala Ala Cys Arg Lys Lys Arg Pro
        195                 200                 205

Arg Gly Ser Pro Arg Thr Glu Tyr Glu Ala Cys Arg Val Arg Cys Gln
    210                 215                 220

Val Ala Glu His Gly Val Glu Arg Gln Arg Arg Cys Gln Gln Val Cys
225                 230                 235                 240
```

Glu Lys Arg Leu Arg Glu Arg Glu Gly Arg Arg Glu Val Asp Lys Asp
245 250 255

Glu Leu

<210> 150
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 150

Pro Arg Gly Ser Pro Arg Thr Glu Tyr Glu Ala Cys Arg Val Arg Cys
1 5 10 15

Gln Val Ala Glu His Gly Val Glu Arg Gln Arg Arg Cys Gln Gln Val
20 25 30

Cys Glu Lys Arg Leu Arg Glu Arg Glu Gly Arg Arg Glu Val Asp Lys
35 40 45

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

Ala Cys Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln
65 70 75 80

Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala
85 90 95

His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn
100 105 110

Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser
115 120 125

Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly
130 135 140

Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr
145 150 155 160

Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys
165 170 175

Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile

180 185 190

Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu
195 200 205

Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu
210 215 220

Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met
225 230 235 240

Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
245 250

<210> 151
<211> 539
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 151

Asp Val Ser Phe Arg Leu Ser Gly Ala Thr Ser Ser Ser Tyr Gly Val
1 5 10 15

Phe Ile Ser Asn Leu Arg Lys Ala Leu Pro Asn Glu Arg Lys Leu Tyr
20 25 30

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

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

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

Ala Cys Ser Asn Glu Ala Ser Ala Thr Glu Ala Ala Lys Tyr Val Phe
85 90 95

Lys Asp Ala Met Arg Lys Val Thr Leu Pro Tyr Ser Gly Asn Tyr Glu
100 105 110

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

Leu Pro Ala Leu Asp Ser Ala Ile Thr Thr Leu Phe Tyr Tyr Asn Ala
130 135 140

```
Asn Ser Ala Ala Ser Ala Leu Met Val Leu Ile Gln Ser Thr Ser Glu
145                 150                 155                 160

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

Lys Thr Phe Leu Pro Ser Leu Ala Ile Ile Ser Leu Glu Asn Ser Trp
            180                 185                 190

Ser Ala Leu Ser Lys Gln Ile Gln Ile Ala Ser Thr Asn Asn Gly Gln
        195                 200                 205

Phe Glu Ser Pro Val Val Leu Ile Asn Ala Gln Asn Gln Arg Val Thr
    210                 215                 220

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

Leu Asn Arg Asn Asn Met Ala Arg Lys Lys Arg Gly Gly Gly Gly Ser
                245                 250                 255

Pro Glu Gly Gly Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys His
            260                 265                 270

Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu
        275                 280                 285

Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr
    290                 295                 300

Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn
305                 310                 315                 320

Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg
                325                 330                 335

Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu
            340                 345                 350

Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Gly Arg Lys Lys Arg
        355                 360                 365

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Val Ala Ala His Ile
    370                 375                 380

Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys
```

385 390 395 400

Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg
405 410 415

Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu
420 425 430

Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe
435 440 445

Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met
450 455 460

Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu
465 470 475 480

Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly
485 490 495

Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp
500 505 510

Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His
515 520 525

Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
530 535

<210> 152
<211> 429
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 152

Asp Ala Ser Phe Arg Leu Ser Gly Ala Thr Ser Ser Ser Tyr Gly Val
1 5 10 15

Phe Ile Ser Asn Leu Arg Lys Ala Leu Pro Asn Glu Arg Lys Leu Tyr
20 25 30

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

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

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

Ala Cys Ser Asn Glu Ala Ser Ala Thr Glu Ala Ala Lys Tyr Val Phe
85 90 95

Lys Asp Ala Met Arg Lys Val Thr Leu Pro Tyr Ser Gly Asn Tyr Glu
100 105 110

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

Leu Pro Ala Gly Asp Ser Ala Ile Thr Thr Leu Phe Tyr Tyr Asn Ala
130 135 140

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

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

Lys Thr Phe Leu Pro Ser Leu Ala Ile Ile Ser Leu Glu Asn Ser Trp
180 185 190

Ser Ala Leu Ser Lys Gln Ile Gln Ile Ala Ser Thr Asn Asn Gly Gln
195 200 205

Phe Glu Ser Pro Val Val Leu Ile Asn Ala Gln Asn Gln Arg Val Thr
210 215 220

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

Leu Asn Arg Asn Asn Met Ala Gly Gly Gly Gly Ser Arg Lys Lys Arg
245 250 255

Ala Ser Gly Cys Gly Pro Glu Gly Gly Gly Gly Ser Arg Val Ala Ala
260 265 270

His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn
275 280 285

Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser
290 295 300

Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly

305 310 315 320

Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr
325 330 335

Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys
340 345 350

Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile
355 360 365

Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu
370 375 380

Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu
385 390 395 400

Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met
405 410 415

Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
420 425

<210> 153
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 153

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

```
Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Ser Ala Ser Gly Gly Pro Glu Gly Gly Ser Leu Ala
                165                 170                 175

Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr
            180                 185                 190

Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr
        195                 200                 205

Pro Val Gln Lys Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp
    210                 215                 220

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

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

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

Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Gly Pro Ala Asp Ser
        275                 280                 285

Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe Leu
    290                 295                 300

Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Gln Trp
305                 310                 315                 320

Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Ala Gly
                325                 330                 335

Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser
```

340 345 350

Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile
355 360 365

Trp Ala Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr
370 375 380

Ala Gln Asp Gln Glu Pro Asp Ala Ala Gly Arg Ile Arg Asn Gly Ala
385 390 395 400

Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Ala
405 410 415

Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg
420 425 430

Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro
435 440 445

Glu Glu Ser Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala
450 455 460

Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Lys Asn
465 470 475 480

Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Ser Glu Gln Ala
485 490 495

Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Lys
500 505 510

Asp Glu Leu
515

<210> 154
<211> 402
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 154

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

```
Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
        35                  40                  45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
    50                  55                  60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65                  70                  75                  80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
                85                  90                  95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Arg Lys Lys Arg Arg His Arg
                165                 170                 175

Gln Pro Arg Gly Trp Glu Gln Leu Pro Thr Gly Ala Glu Phe Leu Gly
            180                 185                 190

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

Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Ala Gly Tyr
    210                 215                 220

Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile
225                 230                 235                 240

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

Ala Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr Ala
            260                 265                 270

Gln Asp Gln Glu Pro Asp Ala Ala Gly Arg Ile Arg Asn Gly Ala Leu
```

275 280 285

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

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

Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu
325 330 335

Glu Ser Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala Glu
340 345 350

Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn Val
355 360 365

Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Ser Glu Gln Ala Ile
370 375 380

Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Lys Glu
385 390 395 400

Asp Leu

<210> 155
<211> 403
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 155

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

```
Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
                85                  90                  95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Arg Lys Lys Arg Arg His Arg
                165                 170                 175

Gln Pro Arg Gly Trp Glu Gln Leu Tyr Pro Thr Gly Ala Glu Phe Leu
            180                 185                 190

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

Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Gly Gly
    210                 215                 220

Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser
225                 230                 235                 240

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

Trp Ala Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr
            260                 265                 270

Ala Gln Asp Gln Glu Pro Asp Ala Ala Gly Arg Ile Arg Asn Gly Ala
        275                 280                 285

Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Ala
    290                 295                 300

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

Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro
```

325 330 335

Glu Glu Ala Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala
340 345 350

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

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

Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Lys
385 390 395 400

Glu Asp Leu

<210> 156
<211> 470
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 156

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
115 120 125

```
Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Ser Ala Ser Gly Cys Gly Pro Glu Arg Lys Lys Arg
                165                 170                 175

Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Ser Gly Tyr
            180                 185                 190

Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp
        195                 200                 205

Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly Ser
    210                 215                 220

Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala Arg
225                 230                 235                 240

Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Tyr Pro Thr Gly Ala
                245                 250                 255

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

Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu
        275                 280                 285

Glu Gly Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala
    290                 295                 300

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

Asp Ala Ile Trp Ala Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala
                325                 330                 335

Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Ala Gly Arg Ile Arg
            340                 345                 350

Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly
        355                 360                 365

Phe Tyr Ala Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu
```

370 375 380

Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile
385 390 395 400

Thr Gly Pro Glu Glu Ala Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp
405 410 415

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

Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Ala
435 440 445

Glu Ala Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys
450 455 460

Pro Pro Lys Glu Asp Leu
465 470

<210> 157
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 157

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
100 105 110

```
Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Lys Lys Arg Arg His
                165                 170                 175

Arg Gln Pro Arg Gly Trp Glu Gln Leu Gly Gly Gly Gly Ser Gly Gly
            180                 185                 190

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

Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg
    210                 215                 220

Asn Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile
225                 230                 235                 240

Arg Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala
                245                 250                 255

Glu Ser Glu Tyr Pro Thr Gly Ala Glu Phe Leu Gly Asp Gly Gly Ala
            260                 265                 270

Val Ser Phe Ser Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu
        275                 280                 285

Leu Gln Ala His Arg Gln Leu Glu Glu Gly Gly Tyr Val Phe Val Gly
    290                 295                 300

Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly
305                 310                 315                 320

Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile Trp Ala Gly Phe Tyr
                325                 330                 335

Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu
            340                 345                 350

Pro Asp Ala Ala Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr
```

355 360 365

Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Ala Thr Ser Leu Thr Leu
370 375 380

Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro
385 390 395 400

Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Ala Gly Gly
405 410 415

Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val
420 425 430

Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn Val Gly Gly Asp Leu
435 440 445

Asp Pro Ser Ser Ile Pro Asp Ala Glu Ala Ala Ile Ser Ala Leu Pro
450 455 460

Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Lys Glu Asp Leu
465 470 475

<210> 158
<211> 402
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 158

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

```
Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Arg Lys Lys Arg Arg His Arg
                165                 170                 175

Gln Pro Arg Gly Trp Glu Gln Leu Pro Thr Gly Ala Glu Phe Leu Gly
            180                 185                 190

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

Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg Gly Tyr
    210                 215                 220

Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile
225                 230                 235                 240

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

Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr Ala
            260                 265                 270

Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg Asn Gly Ala Leu
        275                 280                 285

Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Arg Thr
    290                 295                 300

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

Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu
                325                 330                 335

Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala Glu
```

340 345 350

Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn Val
355 360 365

Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln Ala Ile
370 375 380

Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Lys Glu
385 390 395 400

Asp Leu

<210> 159
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 159

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
115 120 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
130 135 140

```
Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Lys Lys Arg Gly Gly
                165                 170                 175

Gly Gly Ser Gly Gly Gly Gly Ser Glu Gln Ser Gly Tyr Pro Val Gln
            180                 185                 190

Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val
        195                 200                 205

Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp
    210                 215                 220

Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu
225                 230                 235                 240

Thr Leu Ala Ala Ala Glu Ser Glu Tyr Pro Thr Gly Ala Glu Phe Leu
                245                 250                 255

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

Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Gly Gly
        275                 280                 285

Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser
    290                 295                 300

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

Trp Ala Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr
                325                 330                 335

Ala Gln Asp Gln Glu Pro Asp Ala Ala Gly Arg Ile Arg Asn Gly Ala
            340                 345                 350

Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Ala
        355                 360                 365

Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg
    370                 375                 380

Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro
```

385 390 395 400

Glu Glu Ala Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala
405 410 415

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

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

Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Lys
450 455 460

Glu Asp Leu
465

<210> 160
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 160

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
115 120 125

```
Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg His Arg Gln Pro Arg
                165                 170                 175

Gly Trp Glu Gln Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
            180                 185                 190

Gln Ser Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala
        195                 200                 205

Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala
    210                 215                 220

Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro
225                 230                 235                 240

Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Tyr
                245                 250                 255

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

Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His
        275                 280                 285

Arg Gln Leu Glu Glu Gly Gly Tyr Val Phe Val Gly Tyr His Gly Thr
    290                 295                 300

Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala Arg
305                 310                 315                 320

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

Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Ala
            340                 345                 350

Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser
        355                 360                 365

Ser Leu Pro Gly Phe Tyr Ala Thr Ser Leu Thr Leu Ala Ala Pro Glu
```

370 375 380

Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg
385 390 395 400

Leu Asp Ala Ile Thr Gly Pro Glu Glu Ala Gly Gly Arg Leu Glu Thr
405 410 415

Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala
420 425 430

Ile Pro Thr Asp Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser Ser
435 440 445

Ile Pro Asp Ala Glu Ala Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser
450 455 460

Gln Pro Gly Lys Pro Pro Lys Glu Asp Leu
465 470

<210> 161
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 161

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
100 105 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
115 120 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
130 135 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145 150 155 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg His Arg Gln Pro Arg
165 170 175

Gly Trp Glu Gln Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
180 185 190

Gln Ser Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala
195 200 205

Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala
210 215 220

Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro
225 230 235 240

Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Tyr
245 250 255

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

Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His
275 280 285

Arg Gln Leu Glu Glu Gly Gly Tyr Val Phe Val Gly Tyr His Gly Thr
290 295 300

Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala Arg
305 310 315 320

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

Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Ala
340 345 350

Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser

355 360 365

Ser Leu Pro Gly Phe Tyr Ala Thr Ser Leu Thr Leu Ala Ala Pro Glu
370 375 380

Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg
385 390 395 400

Leu Asp Ala Ile Thr Gly Pro Glu Glu Ala Gly Gly Arg Leu Glu Thr
405 410 415

Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala
420 425 430

Ile Pro Thr Asp Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser Ser
435 440 445

Ile Pro Asp Ala Glu Ala Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser
450 455 460

Gln Pro Gly Lys Pro Pro Lys Asp Glu Leu
465 470

<210> 162
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 162

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

```
Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg His Arg Gln Pro Arg
                165                 170                 175

Gly Trp Glu Gln Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
            180                 185                 190

Gln Ser Gly Tyr Pro Val Gln Lys Leu Val Ala Leu Tyr Leu Ala Ala
        195                 200                 205

Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala
    210                 215                 220

Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro
225                 230                 235                 240

Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Tyr
                245                 250                 255

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

Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His
        275                 280                 285

Arg Gln Leu Glu Glu Gly Gly Tyr Val Phe Val Gly Tyr His Gly Thr
    290                 295                 300

Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala Arg
305                 310                 315                 320

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

Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Ala
```

340 345 350

Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser
355 360 365

Ser Leu Pro Gly Phe Tyr Ala Thr Ser Leu Thr Leu Ala Ala Pro Glu
370 375 380

Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg
385 390 395 400

Leu Asp Ala Ile Thr Gly Pro Glu Glu Ala Gly Gly Arg Leu Glu Thr
405 410 415

Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala
420 425 430

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

Ile Pro Asp Ala Glu Ala Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser
450 455 460

Gln Pro Gly Lys Pro Pro Lys Asp Glu Leu
465 470

<210> 163
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 163

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

```
Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
                85                  90                  95

Pro His Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Ser Ala Ser Gly Gly Pro Glu Gly Gly Ser Leu Ala
                165                 170                 175

Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr
            180                 185                 190

Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr
        195                 200                 205

Pro Val Gln Lys Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp
    210                 215                 220

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

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

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

Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Gly Pro Ala Asp Ser
        275                 280                 285

Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe Leu
    290                 295                 300

Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Gln Trp
305                 310                 315                 320

Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Ala Gly
```

325 330 335

Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser
340 345 350

Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile
355 360 365

Trp Ala Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr
370 375 380

Ala Gln Asp Gln Glu Pro Asp Ala Ala Gly Arg Ile Arg Asn Gly Ala
385 390 395 400

Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Ala
405 410 415

Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg
420 425 430

Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro
435 440 445

Glu Glu Ser Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala
450 455 460

Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Lys Asn
465 470 475 480

Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Ser Glu Gln Ala
485 490 495

Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Lys
500 505 510

Asp Glu Leu
515

<210> 164
<211> 475
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 164

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

```
Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
            20                  25                  30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
        35                  40                  45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
    50                  55                  60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65                  70                  75                  80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
                85                  90                  95

Pro His Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg His Arg Gln Pro
                165                 170                 175

Arg Gly Trp Glu Gln Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            180                 185                 190

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

Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu
    210                 215                 220

Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln
225                 230                 235                 240

Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu
                245                 250                 255

Tyr Pro Thr Gly Ala Glu Phe Leu Gly Asp Gly Gly Ala Val Ser Phe
```

260 265 270

Ser Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala
275 280 285

His Arg Gln Leu Glu Glu Gly Gly Tyr Val Phe Val Gly Tyr His Gly
290 295 300

Thr Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala
305 310 315 320

Arg Ser Gln Asp Leu Asp Ala Ile Trp Ala Gly Phe Tyr Ile Ala Gly
325 330 335

Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala
340 345 350

Ala Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg
355 360 365

Ser Ser Leu Pro Gly Phe Tyr Ala Thr Ser Leu Thr Leu Ala Ala Pro
370 375 380

Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu
385 390 395 400

Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Ala Gly Gly Arg Leu Glu
405 410 415

Thr Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser
420 425 430

Ala Ile Pro Thr Asp Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser
435 440 445

Ser Ile Pro Asp Ala Glu Ala Ala Ile Ser Ala Leu Pro Asp Tyr Ala
450 455 460

Ser Gln Pro Gly Lys Pro Pro Lys Asp Glu Leu
465 470 475

<210> 165
<211> 463
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 165

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

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
            20                  25                  30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
        35                  40                  45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
    50                  55                  60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65                  70                  75                  80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
                85                  90                  95

Pro His Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Ser Arg His Arg Gln Pro Arg Gly
                165                 170                 175

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

Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile
        195                 200                 205

Arg Asn Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala
    210                 215                 220

Ile Arg Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala
225                 230                 235                 240

Ala Glu Ser Glu Tyr Pro Thr Gly Ala Glu Phe Leu Gly Asp Gly Gly
```

245 250 255

Ala Val Ser Phe Ser Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg
260 265 270

Leu Leu Gln Ala His Arg Gln Leu Glu Glu Gly Gly Tyr Val Phe Val
275 280 285

Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly
290 295 300

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

Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln
325 330 335

Glu Pro Asp Ala Ala Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val
340 345 350

Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Ala Thr Ser Leu Thr
355 360 365

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

Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Ala Gly
385 390 395 400

Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val
405 410 415

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

Leu Asp Pro Ser Ser Ile Pro Asp Ala Glu Ala Ala Ile Ser Ala Leu
435 440 445

Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Lys Asp Glu Leu
450 455 460

<210> 166
<211> 475
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 166

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

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
            20                  25                  30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
        35                  40                  45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
    50                  55                  60

Tyr Ser Gln Thr Asn Phe Lys Phe Arg Glu Glu Ile Lys Glu Asn Thr
65                  70                  75                  80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
                85                  90                  95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu Arg
    130                 135                 140

Leu Arg Asp Met His His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg His Arg Gln Pro
                165                 170                 175

Arg Gly Trp Glu Gln Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            180                 185                 190

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

Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu
    210                 215                 220

Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln
225                 230                 235                 240

Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu
```

245 250 255

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

Ser Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala
275 280 285

His Arg Gln Leu Glu Glu Gly Gly Tyr Val Phe Val Gly Tyr His Gly
290 295 300

Thr Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala
305 310 315 320

Arg Ser Gln Asp Leu Asp Ala Ile Trp Ala Gly Phe Tyr Ile Ala Gly
325 330 335

Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala
340 345 350

Ala Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg
355 360 365

Ser Ser Leu Pro Gly Phe Tyr Ala Thr Ser Leu Thr Leu Ala Ala Pro
370 375 380

Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu
385 390 395 400

Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Ala Gly Gly Arg Leu Glu
405 410 415

Thr Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser
420 425 430

Ala Ile Pro Thr Asp Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser
435 440 445

Ser Ile Pro Asp Ala Glu Ala Ala Ile Ser Ala Leu Pro Asp Tyr Ala
450 455 460

Ser Gln Pro Gly Lys Pro Pro Lys Asp Glu Leu
465 470 475

<210> 167
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 167

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Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1               5                  10                  15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
            20                  25                  30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
        35                  40                  45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
    50                  55                  60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65                  70                  75                  80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
                85                  90                  95

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
            100                 105                 110

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
        115                 120                 125

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
    130                 135                 140

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg His Arg Gln Pro Arg
                165                 170                 175

Gly Trp Glu Gln Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
            180                 185                 190

Gln Ser Gly Tyr Pro Val Gln Lys Leu Val Ala Leu Tyr Leu Ala Ala
        195                 200                 205

Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala
    210                 215                 220

Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro
```

225 230 235 240

Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Tyr
245 250 255

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

Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His
275 280 285

Arg Gln Leu Glu Glu Gly Gly Tyr Val Phe Val Gly Tyr His Gly Thr
290 295 300

Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala Arg
305 310 315 320

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

Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Ala
340 345 350

Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser
355 360 365

Ser Leu Pro Gly Phe Tyr Ala Thr Ser Leu Thr Leu Ala Ala Pro Glu
370 375 380

Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg
385 390 395 400

Leu Asp Ala Ile Thr Gly Pro Glu Glu Ala Gly Gly Arg Leu Glu Thr
405 410 415

Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala
420 425 430

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

Ile Pro Asp Ala Glu Ala Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser
450 455 460

Gln Pro Gly Lys Pro Pro Lys Glu Asp Leu
465 470

<210> 168
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 168

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Lys Leu Pro Arg Ser Ser Leu Val Trp Cys Val Leu Ile Val Cys Leu
1               5                   10                  15

Thr Leu Leu Ile Phe Thr Tyr Leu Thr Arg Lys Ser Leu Cys Glu Ile
            20                  25                  30

Arg Tyr Arg Asp Gly His Arg Glu Val Ala Ala Phe Met Ala Tyr Glu
        35                  40                  45

Ser Gly Lys Gly Gly Gly Gly Ser Arg Val Val Arg Pro Leu Gly Leu
    50                  55                  60

Ala Gly Gly Gly Gly Gly Ser Arg Val Ala Ala His Ile Thr Gly Thr
65                  70                  75                  80

Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys
                85                  90                  95

Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His
            100                 105                 110

Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His
        115                 120                 125

Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln
    130                 135                 140

Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr
145                 150                 155                 160

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

Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser
            180                 185                 190

Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe
        195                 200                 205

Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser
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210 215 220

Phe Phe Gly Ala Phe Leu Val Gly
225 230

<210> 169
<211> 1299
<212> DNA
<213> Artificial Sequence

<220>
<223> -

<400> 169
gaagatcgtc cgatcaaatt tagcaccgaa ggtgcaacca gccagagcta taaacagttt 60

attgaagcac tgcgtgaacg tctgcgtggt ggtctgattc atgatattcc ggttctgccg 120

gatccgacca ccctgcaaga acgtaatcgt tatattaccg ttgaactgag caatagcgat 180

accgaaagca ttgaagttgg tattgatgca accaatgcct atgttgttgc atatcgtgca 240

ggtacacaga gctattttct gcgtgatgca ccgagcagcg caagcgatta cctgtttacc 300

ggcaccgatc agcatagcct gccgttttat ggcacctatg cagatctgga acgttgggca 360

catcagagcc gtcagcagat tccgctgggt ctgcaggcac tgacccatgg tattagcttt 420

tttcgtagcg gtggcaatga taacgaagaa aaagcacgta ccctgattgt gattattcag 480

atggttgcag aagcagcccg ttttcgctat atttcaaatc gtgttcgtgt tagcattcag 540

accggtacag catttcagcc ggatgcagca atgattagcc tggaaaataa ctgggataat 600

ctgagccgtg gtgttcaaga aagcgttcag gataccttc cgaatcaggt taccctgacc 660

aatattcgta atgaaccggt tattgttgat cagctgagcc atccgaccgt tgcagttctg 720

gcactgatgc tgtttgtttg taatccgcct aatggtggtg gtggcagcgg tggtggcggt 780

agccgtaaaa aacgcgttcg tgaacgtggt ccgcagcgtg ttgcagcaca tattaccggt 840

acacgtggtc gtagcaatac cctgagcagc ccgaatagca aaaatgaaaa agccctgggt 900

cgtaaaatca atagctggga aagcagccgt agcggtcata gctttctgag caatctgcat 960

ctgcgtaatg gtgaactggt tattcatgag aaaggcttct actatatcta cagccagacc 1020

tattttcgct tccaagaaga gattaaagaa aacaccaaaa acgataaaca aatggtgcag 1080

tacatctata aatacaccag ctatccggat cctatcctgc tgatgaaaag cgcacgtaat 1140

agctgttgga gcaaagatgc agaatatggc ctgtatagca tttatcaggg tggcatcttt 1200

gaactgaaag aaaacgatcg tattttcgtg agcgtgacca atgaacatct gatcgatatg 1260

gatcatgaag ccagcttttt tggtgcattt ctggtgggt 1299

<210> 170
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> -

<400> 170
cgtgttgcag cacatattac cggcacccgt ggtcgtagca ataccctgag cagcccgaat 60

agcaaaaatg aaaaagcact gggtcgcaaa attaacagct gggaaagcag ccgtagcggt 120

catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttctactata tctacagcca gacctatttt cgcttccaag aagagattaa agaaaacacc 240

aaaaacgata aacaaatggt gcagtacatc tataaataca ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggcctgtat 360

agcatttatc agggtggcat ctttgaactg aaagaaaacg atcgtatttt cgtgagcgtg 420

accaatgaac atctgatcga tatggatcat gaagccagct tttttggtgc atttctggtg 480

ggtggtggtg gcggtagcgc aagcggttgt ggtccggaac gtaaaaaacg tggcggtggt 540

ggtagtgaag ataataacat ttttccgaaa cagtacccga tcatcaattt taccaccgca 600

ggcgcaaccg ttcagagcta taccaacttt attcgtgcag ttcgtggtcg tctgaccacc 660

ggtgcagatg ttcgtcatga aattccggtt ctgccgaatc gtgttggtct gccgattaat 720

cagcgtttta ttctggttga actgagcaac catgcagaac tgagcgttac cctggcaacc 780

aatgcctatg tggttggtta tcgtgcaggt aatagcgcct atttttttcca tccggataat 840

caagaagatg ccgaagcaat tacccacctg tttaccgatg ttcagaatcg ttataccttt 900

gcctttggtg gtaattatga tcgtctggaa cagctggcag gtagcctgcg tgaaaatatt 960

gaactgggta atggtccgct ggaagaagcc attagcgcac tgtattatta cagtaccggt 1020

ggcacccagc tgccgaccct ggcacgtagc tttattgttt gtattcagat gattagcgaa 1080

gccgcacgct ttcagtatat tgaaggtgaa atgcgtaccc gcattcgtta taatcgtcgt 1140

agcgcaccgg atccgtcagt tattaccctg gaaaatagct ggggtcgtct gtcaaccgca 1200

attcaagaaa gcaatcaggg tgcatttgca agcccgattc agctgcagcg tcgtaatggt 1260

agcaaattta gcgtttatga tgtgagcatt ctgatcccga ttattgccct gatggtgtat 1320

cgttgtgcac cgcctccgaa agaagatctg 1350

<210> 171
<211> 1443
<212> DNA
<213> Artificial Sequence

<220>
<223> -

<400> 171

ggtgcagatg atgttgcaga tagcagcaaa agctttgtga tggaaaactt tagcagctat 60

catggcacca aaccgggtta tgccgatagc attcagaaag gtattcagaa accgaaaagc 120

ggcacccagg gtaattatga tgatgattgg aaaggcttct atagcaccga taacaaatat 180

gatgcagccg gttatagcgt ggataatgaa aatccgctga gcggtaaagc cggtggtgtt 240

gttaaagtta cctatccggg tctgaccaaa gttctggcac tgaaagttga taatgccgaa 300

accatcaaaa aagaactggg tctgagcctg accgaaccgc tgatggaaca ggttggcacc 360

gaagaattta tcaaacgttt tggtgatggt gcaagccgtg ttgtgctgag cctgccgttt 420

gcagaaggta gcagcagcgt tgaatatatc aataattggg aacaggcaaa agccctgagc 480

gttgaactgg aaatcaattt tgaaacccgt ggtaaacgtg gtcaggatgc aatgtatgaa 540

tacatggcac aggcatgtgc aggtaatcgt aaaaaacgcg gtggtggtgg tagtccggaa 600

ggtggtagcc tggcagcact gaccgcacat caggcatgtc atctgccgct ggaaaccttt 660

acccgtcatc gtcagcctcg tggctgggaa cagctggaac agtgtggtta tccggttcag 720

cgtctggttg cactgtatct ggcagcccgt ctgagctgga atcaggttga tcaggttatt 780

cgtaatgcac tggcaagtcc gggtagcggt ggtgatctgg gtgaagcaat tcgtgaacag 840

cctgaacagg cacgtctggc cctgaccctg gcagccgcag aaagcgaacg ttttgttcgt 900

cagggcaccg gtaatggtcg caaaaaacgt ggcggtggcg gttcaggggg tggtggttca 960

cgtgttgcag cacatattac cggcacccgt ggtcgtagca ataccctgag cagcccgaat 1020

agcaaaaatg aaaaagcgct gggtcgtaaa atcaatagct gggaaagcag ccgtagcggt 1080

catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgagaaaggc 1140

ttttattata tctatagcca gacctacttt cgcttccaag aagagattaa agaaaacacc 1200

aaaaacgata aacaaatggt gcagtacatc tataaataca ccagctatcc ggatccgatt 1260

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggcctgtat 1320

agcatttatc agggtggcat ctttgaactg aaagaaaacg atcgtatttt cgtgagcgtg 1380

accaatgaac atctgatcga tatggatcat gaagccagct tttttggtgc atttctggtg 1440

ggt 1443

<210> 172
<211> 1434
<212> DNA
<213> Artificial Sequence

<220>
<223> -

<400> 172
ggtgcagatg atgtgagcaa aagctttgtg atggaaaact ttagcagcta tcatggcacc 60

aaaccgggtt atgcagatag cattcagaaa ggtattcaga aaccgaaaag cggcacccag 120

ggtaattatg atgatgattg gaaaggcttc tatagcaccg ataacaaata tgatgcagcc 180

ggttatagcg tggataatga aaatccgctg agcggtaaag ccggtggtgt tgttaaagtt 240

acctatccgg gtctgaccaa agttctggca ctgaaagttg ataatgccga aaccatcaaa 300

aaagaactgg gtctgagcct gaccgaaccg ctgatggaac aggttggcac cgaagaattt 360

atcaaacgtt ttggtgatgg tgcaagccgt gttgtgctga gcctgccgtt tgcagaaggt 420

agcagcagcg ttgaatatat caataattgg gaacaggcaa aagccctgag cgttgaactg 480

gaaatcaatt ttgaaacccg tggtaaacgt ggtcaggatg caatgtatga atacatggca 540

caggcatgtg caggtaatcg taaaaaacgc ggtggtggtg gtagtccgga aggtggtagc 600

ctggcagcac tgaccgcaca tcaggcatgt catctgccgc tggaaacctt tacccgtcat 660

cgtcagcctc gtggctggga acagctggaa cagtgtggtt atccggttca gcgtctggtt 720

gcactgtatc tggcagcccg tctgagctgg aatcaggttg atcaggttat tcgtaatgca 780

ctggcaagtc cgggtagcgg tggtgatctg ggtgaagcaa ttcgtgaaca gcctgaacag 840

gcacgtctgg ccctgaccct ggcagccgca gaaagcgaac gttttgttcg tcagggcacc 900

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gcacatatta ccggcacccg tggtcgtagc aataccctga gcagcccgaa tagcaaaaat 1020

gaaaaagcgc tgggtcgtaa aatcaatagc tgggaaagca gccgtagcgg tcatagcttt 1080

ctgagcaatc tgcatctgcg taatggtgaa ctggtgattc atgagaaagg cttttattat 1140

atctatagcc agacctactt tcgcttccaa gaagagatta aagaaaacac caaaaacgat 1200

aaacaaatgg tgcagtacat ctataaatac accagctatc cggatccgat tctgctgatg 1260

aaaagcgcac gtaatagctg ttggagcaaa gatgcagaat atggcctgta tagcatttat 1320

cagggtggca tctttgaact gaaagaaaac gatcgtattt tcgtgagcgt gaccaatgaa 1380

catctgatcg atatggatca tgaagccagc ttttttggtg catttctggt gggt 1434

<210> 173
<211> 1299
<212> DNA
<213> Artificial Sequence

<220>
<223> -

<400> 173
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cgtaaaaaag cagatgatcc gggtaaagca tttgttctgg ttgcactgag caatgataat 180

ggtcagctgg cagaaattgc cattgatgca accagcgttt atgttgttgg ttatcaggtt 240

cgtaatcgca gctatttctt caaagatgca ccggatgcag cctatgaagg tctgtttaaa 300

aacaccatta aaacccgtct gcatttcggt ggtagctatc cgagcctgga aggtgaaaaa 360

gcatatcgtg aaaccaccga tctgggtatt gaaccgctgc gtattggtat caaaaaactg 420

gatgaaaacg ccatcgataa ctataaaccg accgaaattg caagcagcct gctggttgtt 480

attcagatgg ttagcgaagc agcacgcttt acctttattg aaaatcagat ccgcaacaac 540

tttcagcagc gtattcgtcc ggcaaataat accattagcc tggaaaacaa atggggcaaa 600

ctgagctttc agattcgtac cagcggtgca aatggtatgt ttagtgaagc agttgaactg 660

gaacgtgcca atggcaaaaa atactatgtt accgcagttg atcaggtgaa accgaaaatt 720

gcactgctga aattcgttga caaagatccg aaaggtggtg gtggtagccg taaaaaacgt 780

gcaagcggtt gtggtccgga aggcggtggc ggtagtcgtg ttgcagcaca tattaccggc 840

acccgtggtc gtagcaatac cctgagcagc ccgaatagca aaaatgaaaa agccctgggt 900

cgtaaaatca atagctggga aagcagccgt agcggtcata gctttctgag caatctgcat 960

ctgcgtaatg gtgaactggt gattcatgaa aaaggcttct actatatcta cagccagacc 1020

tattttcgct tccaagaaga gattaaagaa aacaccaaaa acgataaaca aatggtgcag 1080

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agctgttgga gcaaagatgc cgaatatggt ctgtatagca tttatcaggg tggcatcttc 1200

gaactgaaag aaaacgatcg tatttttgtg agcgtgacca acgaacatct gatcgatatg 1260

gatcatgaag ccagcttttt tggtgcattt ctggttggc 1299

<210> 174
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> -

<400> 174
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catggtgttg aacgtcagcg tcgttgccag caggtttgtg aaaaacgtct gcgtgaacgt 120

gaaggtcgtc gtgaagttga taaagatgaa ctgcgtaaaa aacgtggtgg tggttgtgca 180

gcagcatgtg cagcctgtac cagcgaagaa accattagca ccgttcaaga aaaacagcag 240

aatattagtc cgctggttcg tgaacgcggt ccgcagcgtg ttgcagcaca tattaccggc 300

acccgtggtc gtagcaatac cctgagcagc ccgaatagca aaaatgaaaa agcactgggt 360

cgcaaaatta acagctggga aagcagccgt agcggtcata gctttctgag caatctgcat 420

ctgcgtaatg gtgaactggt gattcatgaa aaaggcttct actatatcta cagccagacc 480

tattttcgct tccaagaaga gattaaagaa aacaccaaaa acgataaaca aatggtgcag 540

tacatctata aatacaccag ctatccggat ccgattctgc tgatgaaaag cgcacgtaat 600

agctgttgga gcaaagatgc agaatatggc ctgtatagca tttatcaggg tggcatcttt 660

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gatcatgaag ccagcttttt tggtgcattt ctggtgggt 759

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<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> -

<400> 175
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catggtgttg aacgtcagcg tcgttgccag caggtttgtg aaaaacgtct gcgtgaacgt 120

gaaggtcgtc gtgaagttga taaagatgaa ctgcgtaaaa aacgtggtgg tggttgtgca 180

gcagcatgtg cagcctgtac cagcgaagaa accattagca ccgttcaaga aaaacagcag 240

aatattagtc cgctggttcg tgaacgcggt ccgcagcgtg ttgcagcaca tattaccggc 300

acccgtggtc gtagcaatac cctgagcagc ccgaatagca aaaatgaaaa agcactgggt 360

cgcaaaatta acagctggga aagcagccgt agcggtcata gctttctgag caatctgcat 420

ctgcgtaatg gtgaactggt gattcatgaa aaaggcttct actatatcta cagccagacc 480

tattttcgct tccaagaaga gattaaagaa aacaccaaaa acgataaaca aatggtgcag 540

tacatctata aatacaccag ctatccggat ccgattctgc tgatgaaaag cgcacgtaat 600

agctgttgga gcaaagatgc agaatatggc ctgtatagca tttatcaggg tggcatcttt 660

gaactgaaag aaaacgatcg tattttcgtg agcgtgacca atgaacatct gatcgatatg 720

gatcatgaag ccagcttttt tggtgcattt ctggtgggt 759

<210> 176
<211> 1617
<212> DNA
<213> Artificial Sequence

<220>
<223> -

<400> 176
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gcatgtagca atgaagcaag cgcaaccgaa gcagcaaaat atgttttaa agatgccatg 300

cgcaaagtga ccctgccgta tagcggtaat tatgaacgcc tgcagaccgc agcaggtaaa 360

attcgtgaaa acattccgct gggtctgcct gcactggata gcgcaattac caccctgttt 420

tattacaatg caaatagcgc agccagcgca ctgatggttc tgattcagag caccagcgaa 480

gcagctcgct ataaattcat tgaacagcag attggttgcg gtgtggataa aacctttctg 540

ccgagcctgg caattattag cctggaaaat agctggtcag cactgagcaa acaaattcag 600

attgcaagca ccaataacgg ccagtttgaa agtccggttg ttctgattaa tgcacagaat 660

cagcgtgtga ccattaccaa tgttgatgcc ggtgttgtta ccagtaatat tgcactgctg 720

ctgaatcgca ataatatggc acgtaaaaaa cgcggtggtg gtggtagtcc ggaaggtggt 780

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gcagcacata ttaccggcac ccgtggtcgt agcaataccc tgagcagccc gaatagcaaa 1200

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gataaacaaa tggtgcagta catctataaa tacaccagct atccggatcc gattctgctg 1440

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tatcagggtg gcatttttga gctgaaagaa aacgatcgta ttttcgtgag cgtgaccaat 1560

gaacatctga tcgatatgga tcatgaagcc agctttttg gtgcatttct ggtgggt 1617

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<211> 1287
<212> DNA
<213> Artificial Sequence

<220>
<223> -

<400> 177
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ctgcgtaaag cactgccgaa tgaacgtaaa ctgtatgata ttccgctgct gcgtagcagc 120

ctgcctggta gccagcgtta tgcactgatt catctgacca attatgccga tgaaaccatt 180

agcgttgcaa ttgatgcaac caacgtgtat atcatgggtt atcgtgccgg tgataccagc 240

gcatgtagca atgaagcaag cgcaaccgaa gcagcaaaat atgttttaa agatgccatg 300

cgcaaagtga ccctgccgta tagcggtaat tatgaacgcc tgcagaccgc agcaggtaaa 360

attcgtgaaa acattccgct gggtctgcct gcgggtgata gcgcaattac caccctgttt 420

tattacaatg caaatagcgc agccagcgca ctgatggttc tgattcagag caccagcgaa 480

gcagctcgct ataaattcat tgaacagcag attggttgcg gtgtggataa aacctttctg 540

ccgagcctgg caattattag cctggaaaat agctggtcag cactgagcaa acaaattcag 600

attgcaagca ccaataacgg ccagtttgaa agtccggttg ttctgattaa tgcacagaat 660

cagcgtgtga ccattaccaa tgttgatgcc ggtgttgtta ccagtaatat tgcactgctg 720

ctgaatcgca ataatatggc aggcggtggt ggtagccgta aaaaacgtgc aagcggttgt 780

ggtccggaag gtggtggtgg ttcacgtgtt gcagcacata ttaccggcac ccgtggtcgt 840

agcaataccc tgagcagccc gaatagcaaa aatgaaaaag cactgggtcg caaaattaac 900

agctgggaaa gcagccgtag cggtcatagc tttctgagta atctgcatct gcgcaatggt 960

gaactggtga ttcatgaaaa aggcttctac tatatctaca gccagaccta ttttcgcttc 1020

caagaagaga ttaaagaaaa caccaaaaac gataaacaaa tggtgcagta catctataaa 1080

tacaccagct atccggatcc gattctgctg atgaaaagcg cacgtaatag ctgttggagc 1140

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aacgatcgta ttttcgtgag cgtgaccaat gaacatctga tcgatatgga tcatgaagcc 1260

agctttttg gtgcatttct ggtgggt 1287

<210> 178
<211> 1545
<212> DNA
<213> Artificial Sequence

<220>
<223> -

<400> 178
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agcaaaaatg aaaaagcact gggtcgcaaa attaacagct gggaaagcag ccgtagcggt 120

catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttctactata tctacagcca gacctatttt cgcttccaag aagagattaa agaaaacacc 240

aaaaacgata aacaaatggt gcagtacatc tataaataca ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggcctgtat 360

agcatttatc agggtggcat ctttgaactg aaagaaaacg atcgtatttt cgtgagcgtg 420

accaatgaac atctgatcga tatggatcat gaagccagct tttttggtgc atttctggtg 480

ggtggtggtg gtagcgcaag cggtggtccg gaaggtggta gcctggcagc actgaccgca 540

catcaggcat gtcatctgcc gctggaaacc tttacccgtc atcgtcagcc tcgtggttgg 600

gaacagctgg aacagtgtgg ttatccggtt cagaaactgg ttgcactgta tctggcagcc 660

cgtctgagct ggaatcaggt tgatcaggtt attgcaaatg cactggcaag tccgggtagc 720

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ctggcagccg cagaaagcga acgttttgtt cgtcagggca ccggtaatga tgaagccggt 840

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gttggtggcg atctggatcc gagcagcatt ccggatagtg aacaggcaat tagcgcactg 1500

ccggattatg ccagccagcc tggtaaaccg cctaaagatg aactg 1545

<210> 179
<211> 1206
<212> DNA
<213> Artificial Sequence

<220>
<223> -

<400> 179
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agcaaaaatg aaaaagcact gggtcgcaaa attaacagct gggaaagcag ccgtagcggt 120

catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttctactata tctacagcca gacctatttt cgcttccaag aagagattaa agaaaacacc 240

aaaaacgata aacaaatggt gcagtacatc tataaataca ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggcctgtat 360

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accaatgaac atctgatcga tatggatcat gaagccagct tttttggtgc atttctggtg 480

ggtggtggtg gtagcggtgg tggcggtcgt aaaaaacgtc gtcatcgtca gcctcgtggt 540

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acccgtggca cccagaattg gaccgttgaa cgtctgctgc aggcacaccg tcagctggaa 660

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<210> 180
<211> 1209
<212> DNA
<213> Artificial Sequence

<220>
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<400> 180
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tgcttcggca tccggaatgc tgctcggatc cagatcacca ccaacattac gcggatcggt 120

cggaattgcg ctcggaataa caacggtacg ttctgccaga ggccaaccca gaatggtttc 180

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ataaaaacca ggcaggctgc tacgcggaac ataaacacgc agcagtgcac cattgcgaat 360

acgacctgct gcatccggtt cttgatcctg tgcataacca taggccagtg ccggatcacc 420

ggcaatatag aaacctgccc aaattgcatc cagatcctgg ctacgtgcac gaacaccacc 480

aaacacaatg ctctgtgctg cttccagaaa ggtgccatga taaccaacaa aaacataacc 540

accctcttcc agctgacggt gtgcctgcag cagacgttca acggtccaat tctgggtgcc 600

acgggtacta aagctaactg cgccaccatc acccagaaat tctgcaccgg tcggatacag 660

ctgttcccaa ccacgaggct gacgatgacg acgtttttta cgaccgccac caccgctacc 720

accaccaccc accagaaatg caccaaaaaa gctggcttca tgatccatat cgatcagatg 780

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tgcaacacg 1209

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<211> 1410
<212> DNA
<213> Artificial Sequence

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<223> -

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cggaattgcg ctcggaataa caacggtacg ttctgccaga ggccaaccca gaatggtttc 180

cagacgaccg cctgcttctt ccggaccggt aatggcatcc agacgcagcg gcagcggatg 240

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ggcaatatag aaacctgccc aaattgcatc cagatcctgg ctacgtgcac gaacaccacc 480

aaacacaatg ctctgtgctg cttccagaaa ggtgccatga taaccaacaa aaacataacc 540

accctcttcc agctgacggt gtgcctgcag cagacgttca acggtccaat tctgggtgcc 600

acgggtacta aagctaactg cgccaccatc acccagaaat tctgcaccgg tcggatattc 660

gctttctgct gctgccaggg tcagtgccag acgtgcctgt tcaggctgtt cacgaattgc 720

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accacaaccg cttgcgctac caccaccacc caccagaaat gcaccaaaaa agctggcttc 960

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cagttcaaag atgccaccct gataaatgct atacaggcca tattctgcat ctttgctcca 1080

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gatgtactgc accatttgtt tatcgttttt ggtgttttct ttaatctctt cttggaagcg 1200

aaaataggtc tggctgtaga tatagtagaa gccttttca tgaatcacca gttcaccatt 1260

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<210> 182
<211> 1434
<212> DNA
<213> Artificial Sequence

<220>
<223> -

<400> 182
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cggaattgcg ctcggaataa caacggtacg ttctgccaga ggccaaccca gaatggtttc 180

cagacgaccg cctgcttctt ccggaccggt aatggcatcc agacgcagcg gcagcggatg 240

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ataaaaacca ggcaggctgc tacgcggaac ataaacacgc agcagtgcac cattgcgaat 360

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acgggtacta aagctaactg cgccaccatc acccagaaat tctgcaccgg tcggatattc 660

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ttcacccaga tcaccaccac tacccggact tgccagtgca ttacgaataa cctgatcaac 780

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accaatgaac atctgatcga tatggatcat gaagccagct tttttggtgc atttctggtg 480

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cgtctgagct ggaatcaggt tgatcaggtt attgcaaatg cactggcaag tccgggtagc 720

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agcatttatc agggtggcat ctttgaactg aaagaaaacg atcgtatttt cgtgagcgtg 420

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ggttatcatg gcacctttct ggaagcagca cagagcattg tgtttggtgg tgttcgtgca 960

cgtagccagg atctggatgc aatttgggca ggtttctata ttgccggtga tccggcactg 1020

gcctatggtt atgcacagga tcaagaaccg gatgcagcag gtcgtattcg caatggtgca 1080

ctgctgcgtg tttatgttcc gcgtagcagc ctgcctggtt tttatgcaac cagcctgaca 1140

ctggctgcac cggaagcagc cggtgaagtg gaacgtctga ttggtcatcc gctgccgctg 1200

cgtctggatg ccattaccgg tccggaagaa gcaggcggtc gtctggaaac cattctgggt 1260

tggcctctgg cagaacgtac cgttgttatt ccgagcgcaa ttccgaccga tccgcgtaat 1320

gttggtggcg atctggatcc gagcagcatt ccggatgccg aagcagcaat tagcgcactg 1380

ccggattatg ccagccagcc tggtaaaccg cctaaagatg aactg 1425

<210> 192
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> -

<400> 192
cgtgttgcag cacatattac cggcacccgt ggtcgtagca ataccctgag cagcccgaat 60

agcaaaaatg aaaaagcact gggtcgcaaa attaacagct gggaaagcag ccgtagcggt 120

catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttctactata tctacagcca gacctatttt cgcttccaag aagagattaa agaaaacacc 240

aaaaacgata aacaaatggt gcagtacatc tataaataca ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggcctgtat 360

agcatttatc agggtggcat ctttgaactg aaagaaaacg atcgtatttt cgtgagcgtg 420

accaatgaac atctgatcga tatggatcat gaagccagct tttttggtgc atttctggtg 480

ggtggtggtg gtagcggtgg tggcggttca cgtcatcgtc agcctcgtgg ttgggagcag 540

ctgggtggcg gtggctcagg tgggggtggt tcagaacaga gcggttatcc ggttcagaaa 600

ctggttgcac tgtatctggc agcacgtctg agctggaatc aggttgatca ggttattcgt 660

aatgcactgg caagtccggg tagtggtggt gatctgggtg aagcaattcg tgaacagccg 720

gaacaggcac gtctggcact gaccctggca gcagcagaaa gcgaatatcc gaccggtgca 780

gaatttctgg gtgatggtgg cgcagttagc tttagtaccc gtggcaccca gaattggacc 840

gttgaacgtc tgctgcaggc acaccgtcag ctggaagagg gtggttatgt ttttgttggt 900

tatcatggca cctttctgga agcagcacag agcattgtgt ttggtggtgt tcgtgcacgt 960

agccaggatc tggatgcaat ttgggcaggt ttctatattg ccggtgatcc ggcactggcc 1020

tatggttatg cacaggatca agaaccggat gcagcaggtc gtattcgcaa tggtgcactg 1080

ctgcgtgttt atgttccgcg tagcagcctg cctggttttt atgcaaccag cctgacactg 1140

gctgcaccgg aagcagccgg tgaagtggaa cgtctgattg gtcatccgct gccgctgcgt 1200

ctggatgcca ttaccggtcc ggaagaagca ggcggtcgtc tggaaaccat tctgggttgg 1260

cctctggcag aacgtaccgt tgttattccg agcgcaattc cgaccgatcc gaaaaatgtt 1320

ggcggagatc tggatccgag cagcattccg gatgccgaag cagcaattag cgcactgccg 1380

gattatgcca gccagcctgg taaaccgcct aaagaagatc tg 1422

<210> 193
<211> 696
<212> DNA
<213> Artificial Sequence

<220>
<223> -

<400> 193
aaactgcctc gtagcagcct ggtttggtgt gttctgattg tttgtctgac cctgctgatt 60

tttacctatc tgacccgtaa aagcctgtgc gaaattcgtt atcgtgatgg tcatcgtgaa 120

gttgcagcat ttatggccta tgaaagcggt aaaggtggtg gtggtagccg tgttgttcgt 180

ccgctgggtc tggcaggcgg tggtggcggt tcacgtgttg cagcacatat taccggcacc 240

cgtggtcgta gcaataccct gagcagcccg aatagcaaaa atgaaaaagc actgggtcgc 300

aaaattaaca gctgggaaag cagccgtagc ggtcatagct ttctgagcaa tctgcatctg 360

cgtaatggtg aactggtgat tcatgaaaaa ggcttctact atatctacag ccagacctat 420

tttcgcttcc aagaagagat taaagaaaac accaaaaacg ataaacaaat ggtgcagtac 480

atctataaat acaccagcta tccggatccg attctgctga tgaaaagcgc acgtaatagc 540

tgttggagca aagatgcaga atatggcctg tatagcattt atcagggtgg catctttgaa 600

ctgaaagaaa acgatcgtat tttcgtgagc gtgaccaatg aacatctgat cgatatggat 660

catgaagcca gctttttgg tgcatttctg gtgggt 696

<210> 194
<211> 251
<212> PRT
<213> Abrus precatorius

<300>
<308> genbank/CAA38655.1
<309> 2005-04-18
<313> (2)..(251)

<400> 194

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

1 5 10 15

Tyr Lys Gln Phe Ile Glu Ala Leu Arg Glu Arg Leu Arg Gly Gly Leu
20 25 30

Ile His Asp Ile Pro Val Leu Pro Asp Pro Thr Thr Leu Gln Glu Arg
35 40 45

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

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

Gly Thr Gln Ser Tyr Phe Leu Arg Asp Ala Pro Ser Ser Ala Ser Asp
85 90 95

Tyr Leu Phe Thr Gly Thr Asp Gln His Ser Leu Pro Phe Tyr Gly Thr
100 105 110

Tyr Ala Asp Leu Glu Arg Trp Ala His Gln Ser Arg Gln Gln Ile Pro
115 120 125

Leu Gly Leu Gln Ala Leu Thr His Gly Ile Ser Phe Phe Arg Ser Gly
130 135 140

Gly Asn Asp Asn Glu Glu Lys Ala Arg Thr Leu Ile Val Ile Ile Gln
145 150 155 160

Met Val Ala Glu Ala Ala Arg Phe Arg Tyr Ile Ser Asn Arg Val Arg
165 170 175

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

Ser Leu Glu Asn Asn Trp Asp Asn Leu Ser Arg Gly Val Gln Glu Ser
195 200 205

Val Gln Asp Thr Phe Pro Asn Gln Val Thr Leu Thr Asn Ile Arg Asn
210 215 220

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

Ala Leu Met Leu Phe Val Cys Asn Pro Pro Asn
245 250

<210> 195
<211> 264
<212> PRT
<213> Ricinus communis

<300>
<301> Baluna et al.
<302> -
<303> Proc. Natl. Acad. Sci. USA
<304> 96
<306> 3957-3962
<307> 1999-03-01

<400> 195

Glu Asp Asn Asn Ile Phe Pro Lys Gln Tyr Pro Ile Ile Asn Phe Thr
1 5 10 15

Thr Ala Gly Ala Thr Val Gln Ser Tyr Thr Asn Phe Ile Arg Ala Val
20 25 30

Arg Gly Arg Leu Thr Thr Gly Ala Asp Val Arg His Glu Ile Pro Val
35 40 45

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

Glu Leu Ser Asn His Ala Glu Leu Ser Val Thr Leu Ala Thr Asn Ala
65 70 75 80

Tyr Val Val Gly Tyr Arg Ala Gly Asn Ser Ala Tyr Phe Phe His Pro
85 90 95

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

Gln Asn Arg Tyr Thr Phe Ala Phe Gly Gly Asn Tyr Asp Arg Leu Glu
115 120 125

Gln Leu Ala Gly Ser Leu Arg Glu Asn Ile Glu Leu Gly Asn Gly Pro
130 135 140

Leu Glu Glu Ala Ile Ser Ala Leu Tyr Tyr Tyr Ser Thr Gly Gly Thr
145 150 155 160

Gln Leu Pro Thr Leu Ala Arg Ser Phe Ile Val Cys Ile Gln Met Ile
165 170 175

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

Ile Arg Tyr Asn Arg Arg Ser Ala Pro Asp Pro Ser Val Ile Thr Leu
195 200 205

Glu Asn Ser Trp Gly Arg Leu Ser Thr Ala Ile Gln Glu Ser Asn Gln
210 215 220

Gly Ala Phe Ala Ser Pro Ile Gln Leu Gln Arg Arg Asn Gly Ser Lys
225 230 235 240

Phe Ser Val Tyr Asp Val Ser Ile Leu Ile Pro Ile Ile Ala Leu Met
245 250 255

Val Tyr Arg Cys Ala Pro Pro Pro
260

<210> 196
<211> 189
<212> PRT
<213> Corynebacterium diphtheriae

<400> 196

Gly Ala Asp Asp Val Ala Asp Ser Ser Lys Ser Phe Val Met Glu Asn
1 5 10 15

Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Ala Asp Ser Ile Gln
20 25 30

Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp Asp
35 40 45

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

Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly Val
65 70 75 80

Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val
85 90 95

Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu
100 105 110

Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe Gly
115 120 125

Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly Ser
130 135 140

Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu Ser
145 150 155 160

Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln Asp
165 170 175

Ala Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn
180 185

<210> 197
<211> 186
<212> PRT
<213> Corynebacterium diphtheriae

<300>
<301> Baluna et al.
<302> -
<303> Proc. Natl. Acad. Sci. USA
<304> 96
<306> 3957-3962
<307> 1999-03-01

<400> 197

Gly Ala Asp Asp Val Ser Lys Ser Phe Val Met Glu Asn Phe Ser Ser
1 5 10 15

Tyr His Gly Thr Lys Pro Gly Tyr Ala Asp Ser Ile Gln Lys Gly Ile
20 25 30

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

Gly Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala Gly Tyr Ser Val
50 55 60

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

Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val Asp Asn Ala
85 90 95

Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu Pro Leu Met
100 105 110

Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe Gly Asp Gly Ala
115 120 125

Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly Ser Ser Ser Val
130 135 140

Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu Ser Val Glu Leu
145 150 155 160

Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln Asp Ala Met Tyr
165 170 175

Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn
180 185

<210> 198
<211> 251
<212> PRT
<213> Gelonium multiflorum

<300>
<301> Baluna et al.
<303> Proc. Natl. Acad. Sci. USA
<304> 96
<306> 3957-3962
<307> 1999-03-01

<400> 198

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

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

Asn Ser His Gly Ile Pro Leu Leu Arg Lys Lys Ala Asp Asp Pro Gly
35 40 45

Lys Ala Phe Val Leu Val Ala Leu Ser Asn Asp Asn Gly Gln Leu Ala
50 55 60

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

Arg Asn Arg Ser Tyr Phe Phe Lys Asp Ala Pro Asp Ala Ala Tyr Glu
85 90 95

Gly Leu Phe Lys Asn Thr Ile Lys Thr Arg Leu His Phe Gly Gly Ser
100 105 110

Tyr Pro Ser Leu Glu Gly Glu Lys Ala Tyr Arg Glu Thr Thr Asp Leu
115 120 125

Gly Ile Glu Pro Leu Arg Ile Gly Ile Lys Lys Leu Asp Glu Asn Ala
130 135 140

Ile Asp Asn Tyr Lys Pro Thr Glu Ile Ala Ser Ser Leu Leu Val Val

145 150 155 160

Ile Gln Met Val Ser Glu Ala Ala Arg Phe Thr Phe Ile Glu Asn Gln
165 170 175

Ile Arg Asn Asn Phe Gln Gln Arg Ile Arg Pro Ala Asn Asn Thr Ile
180 185 190

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

Gly Ala Asn Gly Met Phe Ser Glu Ala Val Glu Leu Glu Arg Ala Asn
210 215 220

Gly Lys Lys Tyr Tyr Val Thr Ala Val Asp Gln Val Lys Pro Lys Ile
225 230 235 240

Ala Leu Leu Lys Phe Val Asp Lys Asp Pro Lys
245 250

<210> 199
<211> 247
<212> PRT
<213> Trichosanthes kirilowii

<300>
<301> An Q, et a
<302> -
<303> J Biomed Sci.
<304> 13
<305> 5
<306> 637-43
<307> 2005-09-01

<400> 199

Asp Val Ser Phe Arg Leu Ser Gly Ala Thr Ser Ser Ser Tyr Gly Val
1 5 10 15

Phe Ile Ser Asn Leu Arg Lys Ala Leu Pro Asn Glu Arg Lys Leu Tyr
20 25 30

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

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

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

Ala Cys Ser Asn Glu Ala Ser Ala Thr Glu Ala Ala Lys Tyr Val Phe
85 90 95

Lys Asp Ala Met Arg Lys Val Thr Leu Pro Tyr Ser Gly Asn Tyr Glu
100 105 110

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

Leu Pro Ala Leu Asp Ser Ala Ile Thr Thr Leu Phe Tyr Tyr Asn Ala
130 135 140

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

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

Lys Thr Phe Leu Pro Ser Leu Ala Ile Ile Ser Leu Glu Asn Ser Trp
180 185 190

Ser Ala Leu Ser Lys Gln Ile Gln Ile Ala Ser Thr Asn Asn Gly Gln
195 200 205

Phe Glu Ser Pro Val Val Leu Ile Asn Ala Gln Asn Gln Arg Val Thr
210 215 220

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

Leu Asn Arg Asn Asn Met Ala
245

<210> 200
<211> 247
<212> PRT
<213> Trichosanthes kirilowii

<400> 200

Asp Ala Ser Phe Arg Leu Ser Gly Ala Thr Ser Ser Ser Tyr Gly Val
1 5 10 15

Phe Ile Ser Asn Leu Arg Lys Ala Leu Pro Asn Glu Arg Lys Leu Tyr
20 25 30

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

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

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

Ala Cys Ser Asn Glu Ala Ser Ala Thr Glu Ala Ala Lys Tyr Val Phe
85 90 95

Lys Asp Ala Met Arg Lys Val Thr Leu Pro Tyr Ser Gly Asn Tyr Glu
100 105 110

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

Leu Pro Ala Gly Asp Ser Ala Ile Thr Thr Leu Phe Tyr Tyr Asn Ala
130 135 140

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

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

Lys Thr Phe Leu Pro Ser Leu Ala Ile Ile Ser Leu Glu Asn Ser Trp
180 185 190

Ser Ala Leu Ser Lys Gln Ile Gln Ile Ala Ser Thr Asn Asn Gly Gln
195 200 205

Phe Glu Ser Pro Val Val Leu Ile Asn Ala Gln Asn Gln Arg Val Thr
210 215 220

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

Leu Asn Arg Asn Asn Met Ala
245

<210> 201
<211> 342
<212> PRT
<213> Pseudomonas aeruginosa

<400> 201

Pro Glu Gly Gly Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys His
1 5 10 15

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Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu
            20                  25                  30

Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Lys Leu Val Ala Leu Tyr
        35                  40                  45

Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Ala Asn
    50                  55                  60

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

Glu Ser Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu
                85                  90                  95

Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala
            100                 105                 110

Ala Asn Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr
        115                 120                 125

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

Thr Arg Gly Thr Gln Gln Trp Thr Val Glu Arg Leu Leu Gln Ala His
145                 150                 155                 160

Arg Gln Leu Glu Glu Ala Gly Tyr Val Phe Val Gly Tyr His Gly Thr
                165                 170                 175

Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala Arg
            180                 185                 190

Ser Gln Asp Leu Asp Ala Ile Trp Ala Gly Phe Tyr Ile Ala Gly Asp
        195                 200                 205

Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Ala
    210                 215                 220

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

Ser Leu Pro Gly Phe Tyr Ala Thr Ser Leu Thr Leu Ala Ala Pro Glu
                245                 250                 255

Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg
            260                 265                 270
```

```
Leu Asp Ala Ile Thr Gly Pro Glu Glu Ser Gly Gly Arg Leu Glu Thr
        275                 280                 285

Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala
    290                 295                 300

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

Ile Pro Asp Ser Glu Gln Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser
                325                 330                 335

Gln Pro Gly Lys Pro Pro
            340
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<210> 202
<211> 225
<212> PRT
<213> Pseudomonas aeruginosa

<400> 202

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Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Pro Thr Gly Ala Glu
1               5                   10                  15

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

Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu
        35                  40                  45

Ala Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala
    50                  55                  60

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

Ala Ile Trp Ala Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr
                85                  90                  95

Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Ala Gly Arg Ile Arg Asn
            100                 105                 110

Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe
        115                 120                 125

Tyr Ala Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val
    130                 135                 140
```

Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr
145 150 155 160

Gly Pro Glu Glu Ser Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro
165 170 175

Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro
180 185 190

Arg Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Ser Glu
195 200 205

Gln Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro
210 215 220

Pro
225

<210> 203
<211> 226
<212> PRT
<213> Pseudomonas aeruginosa

<300>
<301> Onda M et al.
<302> -
<303> Proc Natl Acad Sci U S A.
<304> 108
<305> 14
<306> 5742-7
<307> 2011-04-05

<400> 203

Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Tyr Pro Thr Gly Ala
1 5 10 15

Glu Phe Leu Gly Asp Gly Gly Ala Val Ser Phe Ser Thr Arg Gly Thr
20 25 30

Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu
35 40 45

Glu Gly Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala
50 55 60

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

Asp Ala Ile Trp Ala Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala
85 90 95

```
Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Ala Gly Arg Ile Arg
            100                 105                 110

Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly
        115                 120                 125

Phe Tyr Ala Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu
    130                 135                 140

Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile
145                 150                 155                 160

Thr Gly Pro Glu Glu Ala Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp
                165                 170                 175

Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp
            180                 185                 190

Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Ala
        195                 200                 205

Glu Ala Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys
    210                 215                 220

Pro Pro
225
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<210> 204
<211> 279
<212> PRT
<213> Pseudomonas aeruginosa

<400> 204

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Glu Gln Ser Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala
1               5                   10                  15

Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu
            20                  25                  30

Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln
        35                  40                  45

Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu
    50                  55                  60

Tyr Pro Thr Gly Ala Glu Phe Leu Gly Asp Gly Gly Ala Val Ser Phe
65                  70                  75                  80
```

```
Ser Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala
                85                  90                  95

His Arg Gln Leu Glu Glu Gly Gly Tyr Val Phe Val Gly Tyr His Gly
            100                 105                 110

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

Arg Ser Gln Asp Leu Asp Ala Ile Trp Ala Gly Phe Tyr Ile Ala Gly
    130                 135                 140

Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala
145                 150                 155                 160

Ala Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg
                165                 170                 175

Ser Ser Leu Pro Gly Phe Tyr Ala Thr Ser Leu Thr Leu Ala Ala Pro
            180                 185                 190

Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu
        195                 200                 205

Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Ala Gly Gly Arg Leu Glu
    210                 215                 220

Thr Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser
225                 230                 235                 240

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

Ser Ile Pro Asp Ala Glu Ala Ala Ile Ser Ala Leu Pro Asp Tyr Ala
            260                 265                 270

Ser Gln Pro Gly Lys Pro Pro
        275


<210>  205
<211>  279
<212>  PRT
<213>  Pseudomonas aeruginosa

<400>  205

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

```
Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu
            20                  25                  30

Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln
        35                  40                  45

Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu
    50                  55                  60

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

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

His Arg Gln Leu Glu Glu Gly Gly Tyr Val Phe Val Gly Tyr His Gly
            100                 105                 110

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

Arg Ser Gln Asp Leu Asp Ala Ile Trp Ala Gly Phe Tyr Ile Ala Gly
    130                 135                 140

Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala
145                 150                 155                 160

Ala Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg
                165                 170                 175

Ser Ser Leu Pro Gly Phe Tyr Ala Thr Ser Leu Thr Leu Ala Ala Pro
            180                 185                 190

Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu
        195                 200                 205

Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Ala Gly Gly Arg Leu Glu
    210                 215                 220

Thr Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser
225                 230                 235                 240

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

Ser Ile Pro Asp Ala Glu Ala Ala Ile Ser Ala Leu Pro Asp Tyr Ala
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260 265 270

Ser Gln Pro Gly Lys Pro Pro
275

<210> 206
<211> 214
<212> PRT
<213> Pseudomonas aeruginosa

<300>
<301> Weldon JE et al.
<303> Blood
<304> 113
<305> 16
<306> 3792-3800
<307> 2009-04-16

<400> 206

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

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

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

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

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

Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg
85 90 95

Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser
100 105 110

Ser Leu Pro Gly Phe Tyr Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu
115 120 125

Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg
130 135 140

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

Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala

165 170 175

Ile Pro Thr Asp Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser Ser
180 185 190

Ile Pro Asp Lys Glu Gln Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser
195 200 205

Gln Pro Gly Lys Pro Pro
210

<210> 207
<211> 279
<212> PRT
<213> Pseudomonas aeruginosa

<400> 207

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

Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu
20 25 30

Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln
35 40 45

Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu
50 55 60

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

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

His Arg Gln Leu Glu Glu Gly Gly Tyr Val Phe Val Gly Tyr His Gly
100 105 110

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

Arg Ser Gln Asp Leu Asp Ala Ile Trp Ala Gly Phe Tyr Ile Ala Gly
130 135 140

Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala
145 150 155 160

Ala Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg

165 170 175

Ser Ser Leu Pro Gly Phe Tyr Ala Thr Ser Leu Thr Leu Ala Ala Pro
180 185 190

Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu
195 200 205

Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Ala Gly Gly Arg Leu Glu
210 215 220

Thr Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser
225 230 235 240

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

Ser Ile Pro Asp Ala Glu Ala Ala Ile Ser Ala Leu Pro Asp Tyr Ala
260 265 270

Ser Gln Pro Gly Lys Pro Pro
275

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<212> PRT
<213> Salmonella typhi

<300>
<308> GenBank/1209200A
<309> 1996-10-01
<313> (2)..(52)

<400> 208

Lys Leu Pro Arg Ser Ser Leu Val Trp Cys Val Leu Ile Val Cys Leu
1 5 10 15

Thr Leu Leu Ile Phe Thr Tyr Leu Thr Arg Lys Ser Leu Cys Glu Ile
20 25 30

Arg Tyr Arg Asp Gly His Arg Glu Val Ala Ala Phe Met Ala Tyr Glu
35 40 45

Ser Gly Lys
50