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SEQUENCE LISTING

<110> ADAMED
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<120> ANTICANCER FUSION PROTEIN

<130> P070 02 PL

<160> 132

<170> PatentIn version 3.5

<210> 1
<211> 258
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 1

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

Arg Asp Tyr Arg Thr Cys Leu Thr Ile Val Gln Lys Leu Lys Lys Met
180 185 190

Val Asp Lys Pro Thr Gln Arg Ser Val Ser Asn Ala Ala Thr Arg Val
195 200 205

Cys Arg Thr Gly Arg Ser Arg Trp Arg Asp Val Cys Arg Asn Phe Met
210 215 220

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

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

Pro Leu

<210> 2
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 2

Gly Arg Asp Tyr Arg Thr Cys Leu Thr Ile Val Gln Lys Leu Lys Lys
1 5 10 15

Met Val Asp Lys Pro Thr Gln Arg Ser Val Ser Asn Ala Ala Thr Arg
20 25 30

Val Cys Arg Thr Gly Arg Ser Arg Trp Arg Asp Val Cys Arg Asn Phe
35 40 45

Met Arg Arg Tyr Gln Ser Arg Val Thr Gln Gly Leu Val Ala Gly Glu
50 55 60

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

Gly Pro Leu Arg Val Val Arg Pro Leu Gly Leu Ala Gly Gly Gly Gly
85 90 95

```
Gly Ser Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg
            100                 105                 110

Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly
        115                 120                 125

Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu
    130                 135                 140

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

Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile
                165                 170                 175

Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys
            180                 185                 190

Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn
        195                 200                 205

Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln
    210                 215                 220

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

Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly
                245                 250                 255

Ala Phe Leu Val Gly
            260
```

<210> 3
<211> 186
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<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 Pro Leu Gly Leu Ala Gly Arg Val Val Arg Lys Leu Leu Leu Arg
                165                 170                 175

Leu Leu Lys Lys Leu Leu Arg Leu Leu Lys
            180                 185
```

<210> 4
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 4

```
Gly Leu Gly Ser Val Phe Gly Arg Leu Ala Arg Ile Leu Gly Arg Val
1               5                   10                  15

Ile Pro Lys Val Ala Lys Lys Leu Gly Pro Lys Val Ala Lys Val Leu
            20                  25                  30

Pro Lys Val Met Lys Glu Ala Ile Pro Met Ala Val Glu Met Ala Lys
        35                  40                  45
```

Ser Gln Glu Glu Gln Gln Pro Gln Arg Val Val Arg Pro Leu Gly Leu
50 55 60

Ala Gly Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn
65 70 75 80

Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys
85 90 95

Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn
100 105 110

Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr
115 120 125

Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu
130 135 140

Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr
145 150 155 160

Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys
165 170 175

Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly
180 185 190

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

Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe
210 215 220

Leu Val Gly
225

<210> 5
<211> 264
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 5

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 Cys Ala Ala Cys Ala
            180                 185                 190

Ala Ala Cys Gly Gly Gly Pro Leu Gly Leu Ala Gly Arg Val Val Arg
        195                 200                 205

Gly Leu Gly Ser Val Phe Gly Arg Leu Ala Arg Ile Leu Gly Arg Val
    210                 215                 220

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

Pro Lys Val Met Lys Glu Ala Ile Pro Met Ala Val Glu Met Ala Lys
                245                 250                 255

Ser Gln Glu Glu Gln Gln Pro Gln
            260
```

<210> 6
<211> 299
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 6

```
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 Ser Gly Cys Ala
            180                 185                 190

Ala Cys Ala Ala Ala Cys Pro Leu Gly Leu Ala Gly Arg Val Val Arg
        195                 200                 205

Gly Lys Leu Ser Cys Leu Ser Leu Ala Leu Ala Ile Ile Leu Ile Leu
```

210 215 220

Ala Ile Val His Ser Pro Asn Met Glu Val Lys Ala Leu Ala Asp Pro
225 230 235 240

Glu Ala Asp Ala Phe Gly Glu Ala Asn Ala Phe Gly Glu Ala Asp Ala
245 250 255

Phe Ala Glu Ala Asn Ala Asp Val Lys Gly Met Lys Lys Ala Ile Lys
260 265 270

Glu Ile Leu Asp Cys Val Ile Glu Lys Gly Tyr Asp Lys Leu Ala Ala
275 280 285

Lys Leu Lys Lys Val Ile Gln Gln Leu Trp Glu
290 295

<210> 7
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 7

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 Cys Ala Ala Cys Ala
            180                 185                 190

Ala Ala Cys Gly Gly Pro Leu Gly Leu Ala Gly Arg Val Val Arg Lys
        195                 200                 205

Trp Cys Phe Arg Val Cys Tyr Arg Gly Ile Cys Tyr Arg Arg Cys Arg
    210                 215                 220
```

<210> 8
<211> 202
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 8

```
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 Pro Leu Gly Leu Ala Gly Arg Val
                165                 170                 175

Val Arg Arg Arg Arg Arg Arg Arg Arg Lys Trp Cys Phe Arg Val Cys
            180                 185                 190

Tyr Arg Gly Ile Cys Tyr Arg Arg Cys Arg
        195                 200
```

<210> 9
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 9

```
Gly Ile Gly Lys Phe Leu His Ser Ala Lys Lys Phe Gly Lys Ala Phe
1               5                   10                  15

Val Gly Glu Ile Met Asn Ser Gly Gly Gln Arg Leu Gly Asn Gln Trp
            20                  25                  30

Ala Val Gly His Leu Met Arg Val Val Arg Pro Leu Gly Leu Ala Gly
        35                  40                  45

Cys Ala Ala Ala Cys Ala Ala Cys Thr Ser Glu Glu Thr Ile Ser Thr
    50                  55                  60

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

Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn
                85                  90                  95

Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys
            100                 105                 110
```

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Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn
115 120 125

Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr
130 135 140

Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu
145 150 155 160

Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr
165 170 175

Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys
180 185 190

Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly
195 200 205

Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn
210 215 220

Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe
225 230 235 240

Leu Val Gly

<210> 10
<211> 196
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 10

Gly Ile Gly Lys Phe Leu His Ser Ala Lys Lys Phe Gly Lys Ala Phe
1 5 10 15

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

Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser
35 40 45

Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg
50 55 60

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

65 70 75 80

Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe
85 90 95

Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys
100 105 110

Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr
115 120 125

Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser
130 135 140

Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly
145 150 155 160

Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr
165 170 175

Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala
180 185 190

Phe Leu Val Gly
195

<210> 11
<211> 202
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 11

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 Gly Gly Gly Gly Arg Val Val Arg Pro Leu
                165                 170                 175

Gly Leu Ala Gly Arg Arg Arg Arg Arg Arg Arg Arg Lys Leu Ala Lys
            180                 185                 190

Leu Ala Lys Lys Leu Ala Lys Leu Ala Lys
        195                 200
```

<210> 12
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

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

Gly Leu Ala Gly Arg Val Val Arg Arg Arg Arg Arg Arg Arg Arg Lys
            180                 185                 190

Leu Ala Lys Leu Ala Lys Lys Leu Ala Lys Leu Ala Lys
        195                 200                 205
```

<210> 13
<211> 228
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 13

```
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 Gly Arg Val Val Arg Pro Leu Gly Leu Ala Gly Arg Arg
195 200 205

Arg Arg Arg Arg Arg Arg Lys Leu Ala Lys Leu Ala Lys Lys Leu Ala
210 215 220

Lys Leu Ala Lys
225

<210> 14
<211> 192
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 14

His His His His His His Lys Leu Ala Lys Leu Ala Lys Lys Leu Ala
1 5 10 15

Lys Leu Ala Lys Cys Arg Val Val Arg Pro Leu Gly Leu Ala Gly Arg
20 25 30

Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser
35 40 45

Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser

50 55 60

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

Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr
85 90 95

Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys
100 105 110

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

Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys
130 135 140

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

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

Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
180 185 190

<210> 15
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 15

His His His His His His Lys Leu Ala Lys Leu Ala Lys Lys Leu Ala
1 5 10 15

Lys Leu Ala Lys Cys Arg Arg Arg Arg Arg Arg Arg Arg Arg Val Val
20 25 30

Arg Pro Leu Gly Leu Ala Gly Arg Val Ala Ala His Ile Thr Gly Thr
35 40 45

Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys
50 55 60

Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His
65 70 75 80

```
Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His
                85                  90                  95

Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln
            100                 105                 110

Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr
        115                 120                 125

Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser
    130                 135                 140

Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser
145                 150                 155                 160

Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe
                165                 170                 175

Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser
            180                 185                 190

Phe Phe Gly Ala Phe Leu Val Gly
        195                 200
```

<210> 16
<211> 202
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<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 Gly Gly Gly Gly Pro Leu Gly Leu Ala Gly
                165                 170                 175

Arg Val Val Arg Arg Arg Arg Arg Arg Arg Arg Arg Lys Leu Ala Lys
            180                 185                 190

Leu Ala Lys Lys Leu Ala Lys Leu Ala Lys
        195                 200
```

<210> 17
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 17

```
Lys Trp Lys Leu Phe Lys Lys Ile Gly Ile Gly Ala Val Leu Lys Val
1               5                   10                  15

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

Gly Leu Ala Gly Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr
        35                  40                  45

Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn
    50                  55                  60

Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser
65                  70                  75                  80
```

Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val
85 90 95

Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg
100 105 110

Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val
115 120 125

Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met
130 135 140

Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu
145 150 155 160

Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg
165 170 175

Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu
180 185 190

Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Pro Leu Gly Leu Ala Gly
195 200 205

<210> 18
<211> 203
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 18

Phe Arg Lys Ser Lys Glu Lys Ile Gly Lys Phe Phe Lys Arg Ile Val
1 5 10 15

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

Leu Gly Leu Ala Gly Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile
35 40 45

Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys
50 55 60

Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg
65 70 75 80

Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu

85 90 95

Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe
100 105 110

Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met
115 120 125

Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu
130 135 140

Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly
145 150 155 160

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

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

Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
195 200

<210> 19
<211> 203
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 19

Gly Gly Leu Arg Ser Leu Gly Arg Lys Ile Leu Arg Ala Trp Lys Lys
1 5 10 15

Tyr Gly Pro Ile Ile Val Pro Ile Ile Arg Ile Arg Val Val Arg Pro
20 25 30

Leu Gly Leu Ala Gly Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile
35 40 45

Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys
50 55 60

Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg
65 70 75 80

Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu
85 90 95

Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe
100 105 110

Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met
115 120 125

Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu
130 135 140

Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly
145 150 155 160

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

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

Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
195 200

<210> 20
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<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 Ser Gly Gly Pro Leu Gly Leu Ala Gly Arg Val Val Arg
                165                 170                 175

Gly Leu Val Glu Thr Leu Thr Lys Ile Val Ser Tyr Gly Ile Asp Lys
            180                 185                 190

Leu Ile Glu Lys Ile Leu Glu Gly
        195                 200
```

<210> 21
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<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 Ser Gly Gly Pro Leu Gly Leu Ala Gly Arg Val Val Arg
165 170 175

Gly Phe Ile Ala Thr Leu Thr Lys Val Leu Asp Phe Gly Ile Asp Lys
180 185 190

Leu Ile Gln Leu Ile Glu Asp Lys
195 200

<210> 22
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<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 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 Ser Gly Gly Pro Leu Gly Leu Ala Gly Arg Val Val Arg
165 170 175

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

Leu Val Lys Leu Ile Glu Asn His
195 200

<210> 23
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 23

Gly Leu Leu Glu Ala Leu Ala Glu Leu Leu Glu Gly Arg Arg Arg Arg
1 5 10 15

Arg Arg Arg Arg Val Val Arg Pro Leu Gly Leu Ala Gly Arg Val Ala
20 25 30

Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro
35 40 45

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

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

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

Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp
100 105 110

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

Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala
    130                 135                 140

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

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

Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
            180                 185                 190
```

<210> 24
<211> 429
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 24

```
Trp Asp Gly Lys Ile Asp Gly Thr Gly Thr His Ala Met Ile Val Thr
1               5                   10                  15

Gln Gly Val Ser Ile Leu Glu Asn Asp Met Ser Lys Asn Glu Pro Glu
            20                  25                  30

Ser Val Arg Lys Asn Leu Glu Ile Leu Lys Asp Asn Met His Glu Leu
        35                  40                  45

Gln Leu Gly Ser Thr Tyr Pro Asp Tyr Asp Lys Asn Ala Tyr Asp Leu
    50                  55                  60

Tyr Gln Asp His Phe Trp Asp Pro Asp Thr Asn Asn Asn Phe Ser Lys
65                  70                  75                  80

Asp Asn Ser Trp Tyr Leu Ala Tyr Ser Ile Pro Asp Thr Gly Glu Ser
                85                  90                  95

Gln Ile Arg Lys Phe Ser Ala Leu Ala Arg Tyr Glu Trp Gln Arg Gly
            100                 105                 110

Asn Tyr Lys Gln Ala Thr Phe Tyr Leu Gly Glu Ala Met His Tyr Phe
        115                 120                 125
```

```
Gly Asp Ile Asp Thr Pro Tyr His Pro Ala Asn Val Thr Ala Val Asp
    130                 135                 140

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

Gln Tyr Lys Ile Asn Thr Val Gly Cys Lys Thr Asn Glu Asp Phe Tyr
                165                 170                 175

Ala Asp Ile Leu Lys Asn Lys Asp Phe Asn Ala Trp Ser Lys Glu Tyr
            180                 185                 190

Ala Arg Gly Phe Ala Lys Thr Gly Lys Ser Ile Tyr Tyr Ser His Ala
        195                 200                 205

Ser Met Ser His Ser Trp Asp Asp Trp Asp Tyr Ala Ala Lys Val Thr
    210                 215                 220

Leu Ala Asn Ser Gln Lys Gly Thr Ala Gly Tyr Ile Tyr Arg Phe Leu
225                 230                 235                 240

His Asp Val Ser Glu Gly Asn Gly Gly Gly Gly Gly Gly Ser Ala Ser
                245                 250                 255

Gly Cys Gly Pro Glu Gly Gly 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> 25
<211> 658
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 25

```
His Ala Asp Glu Ile Asp Lys Tyr Ile Gln Gly Leu Asp Tyr Asn Lys
1               5                   10                  15

Asn Asn Val Leu Val Tyr His Gly Asp Ala Val Thr Asn Val Pro Pro
            20                  25                  30

Arg Lys Gly Tyr Lys Asp Gly Asn Glu Tyr Ile Val Val Glu Lys Lys
        35                  40                  45

Lys Lys Ser Ile Asn Gln Asn Asn Ala Asp Ile Gln Val Val Asn Ala
    50                  55                  60

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

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

Thr Leu Ser Ile Asp Leu Pro Gly Met Thr Asn Gln Asp Asn Lys Ile
            100                 105                 110

Val Val Lys Asn Ala Thr Lys Ser Asn Val Asn Asn Ala Val Asn Thr
        115                 120                 125

Leu Val Glu Arg Trp Asn Glu Lys Tyr Ala Gln Ala Tyr Pro Asn Val
    130                 135                 140

Ser Ala Lys Ile Asp Tyr Asp Asp Glu Met Ala Tyr Ser Glu Ser Gln
145                 150                 155                 160
```

```
Leu Ile Ala Lys Phe Gly Thr Ala Phe Lys Ala Val Asn Asn Ser Leu
                165                 170                 175

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

Ile Ser Phe Lys Gln Ile Tyr Tyr Asn Val Asn Val Asn Glu Pro Thr
        195                 200                 205

Arg Pro Ser Arg Phe Phe Gly Lys Ala Val Thr Lys Glu Gln Leu Gln
    210                 215                 220

Ala Leu Gly Val Asn Ala Glu Asn Pro Pro Ala Tyr Ile Ser Ser Val
225                 230                 235                 240

Ala Tyr Gly Arg Gln Val Tyr Leu Lys Leu Ser Thr Asn Ser His Ser
                245                 250                 255

Thr Lys Val Lys Ala Ala Phe Asp Ala Ala Val Ser Gly Lys Ser Val
            260                 265                 270

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

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

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

Asn Arg Glu Thr Pro Gly Val Pro Ile Ala Tyr Thr Thr Asn Phe Leu
                325                 330                 335

Lys Asp Asn Glu Leu Ala Val Ile Lys Asn Asn Ser Glu Tyr Ile Glu
            340                 345                 350

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

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

Asp Pro Glu Gly Asn Glu Ile Val Gln His Lys Asn Trp Ser Glu Asn
385                 390                 395                 400

Asn Lys Ser Lys Leu Ala His Phe Thr Ser Ser Ile Tyr Leu Pro Gly
                405                 410                 415
```

Asn Ala Arg Asn Ile Asn Val Tyr Ala Lys Glu Cys Thr Gly Leu Ala
420 425 430

Trp Glu Trp Trp Arg Thr Val Ile Asp Asp Arg Asn Leu Pro Leu Val
435 440 445

Lys Asn Arg Asn Ile Ser Ile Trp Gly Thr Thr Leu Tyr Pro Lys Tyr
450 455 460

Ser Asn Ser Val Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Arg
465 470 475 480

Lys Lys Arg Ala Ser Gly Cys Gly Pro Glu Gly Gly Gly Gly Gly Gly
485 490 495

Ser Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr
500 505 510

Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile
515 520 525

Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu
530 535 540

His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr
545 550 555 560

Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn
565 570 575

Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser
580 585 590

Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp
595 600 605

Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile
610 615 620

Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu
625 630 635 640

His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu
645 650 655

Val Gly

<210> 26
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 26

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

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

Lys Pro Pro Ala Ala Pro His Asp Ile Asp Ser Lys Leu Pro His Lys
        35                  40                  45

Leu Ser Trp Ser Ala Asp Asn Pro Thr Asn Thr Asp Val Asn Thr His
    50                  55                  60

Tyr Trp Leu Phe Lys Gln Ala Glu Lys Ile Leu Ala Lys Asp Val Asp
65                  70                  75                  80

His Met Arg Ala Asn Leu Met Asn Glu Leu Lys Asn Phe Asp Lys Gln
                85                  90                  95

Ile Ala Gln Gly Ile Tyr Asp Ala Asp His Lys Asn Pro Tyr Tyr Asp
            100                 105                 110

Thr Ser Thr Phe Leu Ser His Phe Tyr Asn Pro Asp Lys Asp Asn Thr
        115                 120                 125

Tyr Leu Pro Gly Phe Ala Asn Ala Lys Ile Thr Gly Ala Lys Tyr Phe
    130                 135                 140

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

Tyr Lys Leu Gly Leu Ala Ile His Tyr Tyr Thr Asp Ile Ser Gln Pro
                165                 170                 175

Met His Ala Asn Asn Phe Thr Ala Ile Ser Tyr Pro Pro Gly Tyr His
            180                 185                 190

Cys Ala Tyr Glu Asn Tyr Val Asp Thr Ile Lys His Asn Tyr Gln Ala
        195                 200                 205
```

Thr Glu Asp Met Val Val Gln Arg Phe Cys Ser Asn Asp Val Lys Glu
210 215 220

Trp Leu Tyr Glu Asn Ala Lys Arg Ala Lys Ala Asp Tyr Pro Lys Ile
225 230 235 240

Val Asn Ala Lys Thr Lys Lys Ser Tyr Leu Val Gly Asn Ser Glu Trp
245 250 255

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

Gln Thr Leu Ala Gly Phe Leu Glu Phe Trp Ser Lys Lys Thr Asn Glu
275 280 285

Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Arg Lys Lys Arg Ala
290 295 300

Ser Gly Cys Gly Pro Glu Gly Gly 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> 27
<211> 361
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 27

Ser Ala Asp Val Ala Gly Ala Val Ile Asp Gly Ala Ser Leu Ser Phe
1 5 10 15

Asp Ile Leu Lys Thr Val Leu Glu Ala Leu Gly Asn Val Lys Arg Lys
20 25 30

Ile Ala Val Gly Val Asp Asn Glu Ser Gly Lys Thr Trp Thr Ala Leu
35 40 45

Asn Thr Tyr Phe Arg Ser Gly Thr Ser Asp Ile Val Leu Pro His Lys
50 55 60

Val Pro His Gly Lys Ala Leu Leu Tyr Asn Gly Gln Lys Asp Arg Gly
65 70 75 80

Pro Val Ala Thr Gly Ala Val Gly Val Leu Ala Tyr Leu Met Ser Asp
85 90 95

Gly Asn Thr Leu Ala Val Leu Phe Ser Val Pro Tyr Asp Tyr Asn Trp
100 105 110

Tyr Ser Asn Trp Trp Asn Val Arg Ile Tyr Lys Gly Lys Arg Arg Ala
115 120 125

Asp Gln Arg Met Tyr Glu Glu Leu Tyr Tyr Asn Leu Ser Pro Phe Arg
130 135 140

Gly Asp Asn Gly Trp His Thr Arg Asn Leu Gly Tyr Gly Leu Lys Ser
145 150 155 160

Arg Gly Phe Met Asn Ser Ser Gly His Ala Ile Leu Glu Ile His Val
165 170 175

Thr Lys Ala Gly Gly Gly Gly Ser Arg Lys Lys Arg Ala Ser Gly Cys
180 185 190

```
Gly Pro Glu Gly Gly Gly Gly Ser Arg Val Ala Ala His Ile Thr Gly
        195                 200                 205

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

Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
225                 230                 235                 240

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

His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
            260                 265                 270

Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
        275                 280                 285

Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
    290                 295                 300

Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
305                 310                 315                 320

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

Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
            340                 345                 350

Ser Phe Phe Gly Ala Phe Leu Val Gly
        355                 360
```

<210> 28
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 28

```
Lys Ser Cys Cys Pro Asn Thr Thr Gly Arg Asn Ile Tyr Asn Ala Cys
1               5                   10                  15

Arg Leu Thr Gly Ala Pro Arg Pro Thr Cys Ala Lys Leu Ser Gly Cys
            20                  25                  30
```

```
Lys Ile Ile Ser Gly Ser Thr Cys Pro Ser Asp Tyr Pro Lys Pro Leu
        35                  40                  45

Gly Leu Ala Gly Arg Val Val Arg Gly Gly Ser Gly Gly Glu Arg Gly
    50                  55                  60

Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn
65                  70                  75                  80

Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys
                85                  90                  95

Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn
            100                 105                 110

Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr
        115                 120                 125

Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu
    130                 135                 140

Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr
145                 150                 155                 160

Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys
                165                 170                 175

Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly
            180                 185                 190

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

Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe
    210                 215                 220

Leu Val Gly
225
```

<210> 29
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 29

```
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 Pro Leu Gly Leu Ala Gly Arg Val
                165                 170                 175

Val Arg Lys Ser Cys Cys Pro Asn Thr Thr Gly Arg Asn Ile Tyr Asn
            180                 185                 190

Ala Cys Arg Leu Thr Gly Ala Pro Arg Pro Thr Cys Ala Lys Leu Ser
        195                 200                 205

Gly Cys Lys Ile Ile Ser Gly Ser Thr Cys Pro Ser Asp Tyr Pro Lys
    210                 215                 220
```

<210> 30
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<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 Gly Ala Pro Cys His Thr Ala Ala Arg Ser
                165                 170                 175

Glu Cys Lys Arg Ser His Lys Phe Val Pro Gly Ala Trp Leu Ala Gly
            180                 185                 190

Glu Gly Val Asp Val Thr Ser Leu
        195                 200
```

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

<220>
<223> Fusion Peptide

<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 Gly Arg Val Val Arg Pro Leu Gly Leu Ala
165 170 175

Gly Ala Pro Cys His Thr Ala Ala Arg Ser Glu Cys Lys Arg Ser His
180 185 190

Lys Phe Val Pro Gly Ala Trp Leu Ala Gly Glu Gly Val Asp Val Thr
195 200 205

Ser Leu
210

<210> 32
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 32

```
Asp Val Ile Arg Glu Tyr Leu Met Phe Asn Glu Leu Ser Ala Leu Ser
1               5                  10                  15

Ser Ser Pro Glu Ser Val Arg Ser Arg Phe Ser Ser Ile Tyr Gly Thr
            20                  25                  30

Asn Pro Asp Gly Ile Ala Leu Asn Asn Glu Thr Tyr Phe Asn Ala Val
        35                  40                  45

Lys Pro Pro Ile Thr Ala Gln Tyr Gly Tyr Tyr Cys Tyr Lys Asn Val
    50                  55                  60

Gly Thr Val Gln Tyr Val Asn Arg Pro Thr Asp Ile Asn Pro Asn Val
65                  70                  75                  80

Ile Leu Ala Gln Asp Thr Leu Thr Asn Asn Thr Asn Glu Pro Phe Thr
                85                  90                  95

Thr Thr Ile Thr Ile Thr Gly Ser Phe Thr Asn Thr Ser Thr Val Thr
            100                 105                 110

Ser Ser Thr Thr Thr Gly Phe Lys Phe Thr Ser Lys Leu Ser Ile Lys
        115                 120                 125

Lys Val Phe Glu Ile Gly Gly Glu Val Ser Phe Ser Thr Thr Ile Gly
    130                 135                 140

Thr Ser Glu Thr Thr Thr Glu Thr Ile Thr Val Ser Lys Ser Val Thr
145                 150                 155                 160

Val Thr Val Pro Ala Gln Ser Arg Arg Thr Ile Gln Leu Thr Ala Lys
                165                 170                 175

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

Tyr Phe Gly Ala Asn Phe Pro Lys Arg Val Gly Pro Gly Gly His Tyr
        195                 200                 205

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

Leu Arg Gly Thr Val Thr Asn Val Ser Ser Phe Asp Phe Gln Thr Ile
225                 230                 235                 240
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Val Gln Pro Ala Arg Ser Leu Leu Asp Glu Gln Arg Val Val Arg Pro
                245                 250                 255

Leu Gly Leu Ala Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Glu Arg
            260                 265                 270

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

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

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

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

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

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

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

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

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

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

Phe Leu Val Gly
        435
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<400> 33

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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 Cys Ala Ala Cys Ala Ala Ala Cys Gly Gly Gly Pro Leu Gly
                165                 170                 175

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

Asn Val Ile Gly Gly Gly Lys Leu Leu Leu Lys Leu Leu Lys Lys Leu
        195                 200                 205

Leu Lys Leu Leu Lys Lys Lys
    210                 215
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<211> 83
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Gly Arg Asp Tyr Arg Thr Cys Leu Thr Ile Val Gln Lys Leu Lys Lys
1 5 10 15

Met Val Asp Lys Pro Thr Gln Arg Ser Val Ser Asn Ala Ala Thr Arg
20 25 30

Val Cys Arg Thr Gly Arg Ser Arg Trp Arg Asp Val Cys Arg Asn Phe
35 40 45

Met Arg Arg Tyr Gln Ser Arg Val Thr Gln Gly Leu Val Ala Gly Glu
50 55 60

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

Gly Pro Leu

<210> 35
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> effector

<300>
<301> Papo N, Shahar M, Eisenbach L, Shai Y.
<302> A novel lytic peptide composed of DL-amino acids selectively kills cancer cells in culture and in mice.
<303> J. Biol. Chem.
<304> 278
<305> 3
<306> 21018-23
<307> 2003-06-06

<400> 35

Lys Leu Leu Leu Arg Leu Leu Lys Lys Leu Leu Arg Leu Leu Lys
1 5 10 15

<210> 36
<211> 56
<212> PRT
<213> Artificial Sequence

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<300>
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<309> 2011-01-11
<313> (57)..(112)

<400> 36

Gly Leu Gly Ser Val Phe Gly Arg Leu Ala Arg Ile Leu Gly Arg Val
1 5 10 15

Ile Pro Lys Val Ala Lys Lys Leu Gly Pro Lys Val Ala Lys Val Leu
20 25 30

Pro Lys Val Met Lys Glu Ala Ile Pro Met Ala Val Glu Met Ala Lys
35 40 45

Ser Gln Glu Glu Gln Gln Pro Gln
50 55

<210> 37
<211> 90
<212> PRT
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<300>
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<309> 2008-08-04
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<400> 37

Lys Leu Ser Cys Leu Ser Leu Ala Leu Ala Ile Ile Leu Ile Leu Ala
1 5 10 15

Ile Val His Ser Pro Asn Met Glu Val Lys Ala Leu Ala Asp Pro Glu
20 25 30

Ala Asp Ala Phe Gly Glu Ala Asn Ala Phe Gly Glu Ala Asp Ala Phe
35 40 45

Ala Glu Ala Asn Ala Asp Val Lys Gly Met Lys Lys Ala Ile Lys Glu
50 55 60

Ile Leu Asp Cys Val Ile Glu Lys Gly Tyr Asp Lys Leu Ala Ala Lys
65 70 75 80

Leu Lys Lys Val Ile Gln Gln Leu Trp Glu
85 90

<210> 38
<211> 17
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<300>
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<400> 38

Lys Trp Cys Phe Arg Val Cys Tyr Arg Gly Ile Cys Tyr Arg Arg Cys
1 5 10 15

Arg

<210> 39
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> effector

<300>
<301> Liu S, Yang H, Wan L, Cai HW, Li SF, Li YP, Cheng JQ, Lu XF.
<302> Enhancement of cytotoxicity of antimicrobial peptide magainin II in tumor cells by bombesin-targeted delivery
<303> Acta Pharmacol. Sin.
<304> 32
<305> 1
<306> 79-88
<307> 2011-01-01

<400> 39

Gly Ile Gly Lys Phe Leu His Ser Ala Lys Lys Phe Gly Lys Ala Phe
1 5 10 15

Val Gly Glu Ile Met Asn Ser Gly Gly Gln Arg Leu Gly Asn Gln Trp
20 25 30

Ala Val Gly His Leu Met
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<210> 40
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<309> 2010-11-30
<313> (83)..(105)

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Gly Ile Gly Lys Phe Leu His Ser Ala Lys Lys Phe Gly Lys Ala Phe
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Val Gly Glu Ile Met Asn Ser
20

<210> 41
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> effector

<300>
<301> avadpour MM, Juban MM, Lo WC, Bishop SM, Alberty JB, Cowell SM, Becker CL, McLaughlin ML
<302> De novo antimicrobial Peptides with low mammalian cell toxicity
<303> J. Med. Chem.
<304> 39
<305> 16
<306> 3107-13
<307> 1996-08-02

<400> 41

Lys Leu Ala Lys Leu Ala Lys Lys Leu Ala Lys Leu Ala Lys
1 5 10

<210> 42
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> effector

<300>
<301> M., Velasco, M., J., Diaz-Guerra, P., Diaz-Achirica, D., Andreu, L., Rivas and L., Bosca,
<302> Macrophage triggering with cecropin A and melittin-derived peptides induces type II nitric oxide synthase expression
<303> The Journal of Immunology
<304> 158
<305> 9
<306> 4437-4443
<307> 1997-09-13

<400> 42

Lys Trp Lys Leu Phe Lys Lys Ile Gly Ile Gly Ala Val Leu Lys Val
1 5 10 15

Leu Thr Thr Gly Leu Pro Ala Leu Ile Ser
20 25

<210> 43
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> effector

<300>
<301> Isogai E.
<302> Antimicrobial and Lipopolysaccharide-Binding Activities of C-Terminal Domain of Human CAP18 Peptides to Genus Leptospira
<303> The Journal of Applied Research
<304> 4
<305> 1
<306> 180-185
<307> 2004-12-01

<400> 43

Phe Arg Lys Ser Lys Glu Lys Ile Gly Lys Phe Phe Lys Arg Ile Val
1 5 10 15

Gln Arg Ile Phe Asp Phe Leu Arg Asn Leu Val
20 25

<210> 44
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> effector

<300>
<301> Risso A, Braidot E, Sordano MC, Vianello A, Macr? F, Skerlavaj B, Zanetti M, Gennaro R, Bernardi P.
<302> MAP-28, an antibiotic oeptide of innate immunity, induces cell death through opening of the mitochondrial permeability transition pore.
<303> Mol. Cell. Biol.
<304> 22
<305> 6
<306> 1926-35
<307> 2002-03

<400> 44

Gly Gly Leu Arg Ser Leu Gly Arg Lys Ile Leu Arg Ala Trp Lys Lys
1 5 10 15

Tyr Gly Pro Ile Ile Val Pro Ile Ile Arg Ile
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<210> 45
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<212> PRT
<213> Artificial Sequence

<220>
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<300>
<301> Andrä J, Berninghausen O, Wülfken J, Leippe M.
<302> Shortened amoebapore analogs with enhanced antibacterial and cytolytic activity.
<303> FEBS Lett.
<304> 385
<305> 12
<306> 96-100
<307> 1996-04-29

<400> 45

Gly Leu Val Glu Thr Leu Thr Lys Ile Val Ser Tyr Gly Ile Asp Lys
1 5 10 15

Leu Ile Glu Lys Ile Leu Glu Gly
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<213> Artificial Sequence

<220>
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<300>
<301> Andrä J, Berninghausen O, Wülfken J, Leippe M.
<302> Shortened amoebapore analogs with enhanced antibacterial and cytolytic activity.
<303> FEBS Lett.
<304> 385
<305> 1
<306> 96-100
<307> 1996-04-29

<400> 46

Gly Phe Ile Ala Thr Leu Thr Lys Val Leu Asp Phe Gly Ile Asp Lys
1 5 10 15

Leu Ile Gln Leu Ile Glu Asp Lys
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<210> 47
<211> 24
<212> PRT
<213> Artificial Sequence

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<300>
<301> Andrä J, Berninghausen O, Wülfken J, Leippe M.
<302> Shortened amoebapore analogs with enhanced antibacterial and cytolytic activity.
<303> FEBS Lett.
<304> 385
<305> 1
<306> 96-100
<307> 1996-04-29

<400> 47

Gly Phe Leu Gly Thr Leu Glu Lys Ile Leu Ser Phe Gly Val Asp Glu
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Leu Val Lys Leu Ile Glu Asn His
20

<210> 48
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> effector

<300>
<301> Ines Neundorf, Robert Rennert, Jan Hoyer, Franziska Schramm, Kristin Löbner Igor Kitanovic and Stefan Wölfl
<302> Fusion of a Short HA2-Derived Peptide Sequence to Cell-Penetrating Peptides Improves Cytosolic Uptake, but Enhances Cytotoxic Activity.
<303> Pharmaceuticals
<304> 2
<305> 2
<306> 49-65
<307> 2009

<400> 48

Gly Leu Leu Glu Ala Leu Ala Glu Leu Leu Glu Gly
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<210> 49
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<309> 2003-04-27
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<400> 49

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Trp Asp Gly Lys Ile Asp Gly Thr Gly Thr His Ala Met Ile Val Thr
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Gln Gly Val Ser Ile Leu Glu Asn Asp Met Ser Lys Asn Glu Pro Glu
            20                  25                  30

Ser Val Arg Lys Asn Leu Glu Ile Leu Lys Asp Asn Met His Glu Leu
        35                  40                  45

Gln Leu Gly Ser Thr Tyr Pro Asp Tyr Asp Lys Asn Ala Tyr Asp Leu
    50                  55                  60

Tyr Gln Asp His Phe Trp Asp Pro Asp Thr Asn Asn Asn Phe Ser Lys
65                  70                  75                  80

Asp Asn Ser Trp Tyr Leu Ala Tyr Ser Ile Pro Asp Thr Gly Glu Ser
                85                  90                  95

Gln Ile Arg Lys Phe Ser Ala Leu Ala Arg Tyr Glu Trp Gln Arg Gly
            100                 105                 110

Asn Tyr Lys Gln Ala Thr Phe Tyr Leu Gly Glu Ala Met His Tyr Phe
        115                 120                 125

Gly Asp Ile Asp Thr Pro Tyr His Pro Ala Asn Val Thr Ala Val Asp
    130                 135                 140

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

Gln Tyr Lys Ile Asn Thr Val Gly Cys Lys Thr Asn Glu Asp Phe Tyr
                165                 170                 175

Ala Asp Ile Leu Lys Asn Lys Asp Phe Asn Ala Trp Ser Lys Glu Tyr
            180                 185                 190

Ala Arg Gly Phe Ala Lys Thr Gly Lys Ser Ile Tyr Tyr Ser His Ala
        195                 200                 205

Ser Met Ser His Ser Trp Asp Asp Trp Asp Tyr Ala Ala Lys Val Thr
    210                 215                 220

Leu Ala Asn Ser Gln Lys Gly Thr Ala Gly Tyr Ile Tyr Arg Phe Leu
225                 230                 235                 240

His Asp Val Ser Glu Gly Asn
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<210> 50
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<309> 2008-08-26
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<400> 50

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His Ala Asp Glu Ile Asp Lys Tyr Ile Gln Gly Leu Asp Tyr Asn Lys
1               5                  10                  15

Asn Asn Val Leu Val Tyr His Gly Asp Ala Val Thr Asn Val Pro Pro
            20                  25                  30

Arg Lys Gly Tyr Lys Asp Gly Asn Glu Tyr Ile Val Val Glu Lys Lys
        35                  40                  45

Lys Lys Ser Ile Asn Gln Asn Asn Ala Asp Ile Gln Val Val Asn Ala
    50                  55                  60

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

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

Thr Leu Ser Ile Asp Leu Pro Gly Met Thr Asn Gln Asp Asn Lys Ile
            100                 105                 110

Val Val Lys Asn Ala Thr Lys Ser Asn Val Asn Asn Ala Val Asn Thr
        115                 120                 125

Leu Val Glu Arg Trp Asn Glu Lys Tyr Ala Gln Ala Tyr Pro Asn Val
    130                 135                 140

Ser Ala Lys Ile Asp Tyr Asp Asp Glu Met Ala Tyr Ser Glu Ser Gln
145                 150                 155                 160

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

Asn Val Asn Phe Gly Ala Ile Ser Glu Gly Lys Met Gln Glu Glu Val
            180                 185                 190
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Ile Ser Phe Lys Gln Ile Tyr Tyr Asn Val Asn Val Asn Glu Pro Thr
        195                 200                 205

Arg Pro Ser Arg Phe Phe Gly Lys Ala Val Thr Lys Glu Gln Leu Gln
    210                 215                 220

Ala Leu Gly Val Asn Ala Glu Asn Pro Pro Ala Tyr Ile Ser Ser Val
225                 230                 235                 240

Ala Tyr Gly Arg Gln Val Tyr Leu Lys Leu Ser Thr Asn Ser His Ser
                245                 250                 255

Thr Lys Val Lys Ala Ala Phe Asp Ala Ala Val Ser Gly Lys Ser Val
            260                 265                 270

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

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

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

Asn Arg Glu Thr Pro Gly Val Pro Ile Ala Tyr Thr Thr Asn Phe Leu
                325                 330                 335

Lys Asp Asn Glu Leu Ala Val Ile Lys Asn Asn Ser Glu Tyr Ile Glu
            340                 345                 350

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

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

Asp Pro Glu Gly Asn Glu Ile Val Gln His Lys Asn Trp Ser Glu Asn
385                 390                 395                 400

Asn Lys Ser Lys Leu Ala His Phe Thr Ser Ser Ile Tyr Leu Pro Gly
                405                 410                 415

Asn Ala Arg Asn Ile Asn Val Tyr Ala Lys Glu Cys Thr Gly Leu Ala
            420                 425                 430

Trp Glu Trp Trp Arg Thr Val Ile Asp Asp Arg Asn Leu Pro Leu Val
        435                 440                 445
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Lys Asn Arg Asn Ile Ser Ile Trp Gly Thr Thr Leu Tyr Pro Lys Tyr
450 455 460

Ser Asn Ser Val
465

<210> 51
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<400> 51

Lys Phe Lys Lys Val Val Leu Gly Met Cys Leu Thr Ala Ser Val Leu
1 5 10 15

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

Lys Pro Pro Ala Ala Pro His Asp Ile Asp Ser Lys Leu Pro His Lys
35 40 45

Leu Ser Trp Ser Ala Asp Asn Pro Thr Asn Thr Asp Val Asn Thr His
50 55 60

Tyr Trp Leu Phe Lys Gln Ala Glu Lys Ile Leu Ala Lys Asp Val Asp
65 70 75 80

His Met Arg Ala Asn Leu Met Asn Glu Leu Lys Asn Phe Asp Lys Gln
85 90 95

Ile Ala Gln Gly Ile Tyr Asp Ala Asp His Lys Asn Pro Tyr Tyr Asp
100 105 110

Thr Ser Thr Phe Leu Ser His Phe Tyr Asn Pro Asp Lys Asp Asn Thr
115 120 125

Tyr Leu Pro Gly Phe Ala Asn Ala Lys Ile Thr Gly Ala Lys Tyr Phe
130 135 140

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

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Tyr Lys Leu Gly Leu Ala Ile His Tyr Tyr Thr Asp Ile Ser Gln Pro
                165                 170                 175

Met His Ala Asn Asn Phe Thr Ala Ile Ser Tyr Pro Pro Gly Tyr His
            180                 185                 190

Cys Ala Tyr Glu Asn Tyr Val Asp Thr Ile Lys His Asn Tyr Gln Ala
        195                 200                 205

Thr Glu Asp Met Val Val Gln Arg Phe Cys Ser Asn Asp Val Lys Glu
    210                 215                 220

Trp Leu Tyr Glu Asn Ala Lys Arg Ala Lys Ala Asp Tyr Pro Lys Ile
225                 230                 235                 240

Val Asn Ala Lys Thr Lys Lys Ser Tyr Leu Val Gly Asn Ser Glu Trp
                245                 250                 255

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

Gln Thr Leu Ala Gly Phe Leu Glu Phe Trp Ser Lys Lys Thr Asn Glu
        275                 280                 285

Gly
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<210> 52
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<309> 2009-07-10
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<400> 52

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Ser Ala Asp Val Ala Gly Ala Val Ile Asp Gly Ala Ser Leu Ser Phe
1               5                   10                  15

Asp Ile Leu Lys Thr Val Leu Glu Ala Leu Gly Asn Val Lys Arg Lys
            20                  25                  30

Ile Ala Val Gly Val Asp Asn Glu Ser Gly Lys Thr Trp Thr Ala Leu
        35                  40                  45
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Asn Thr Tyr Phe Arg Ser Gly Thr Ser Asp Ile Val Leu Pro His Lys
50 55 60

Val Pro His Gly Lys Ala Leu Leu Tyr Asn Gly Gln Lys Asp Arg Gly
65 70 75 80

Pro Val Ala Thr Gly Ala Val Gly Val Leu Ala Tyr Leu Met Ser Asp
85 90 95

Gly Asn Thr Leu Ala Val Leu Phe Ser Val Pro Tyr Asp Tyr Asn Trp
100 105 110

Tyr Ser Asn Trp Trp Asn Val Arg Ile Tyr Lys Gly Lys Arg Arg Ala
115 120 125

Asp Gln Arg Met Tyr Glu Glu Leu Tyr Tyr Asn Leu Ser Pro Phe Arg
130 135 140

Gly Asp Asn Gly Trp His Thr Arg Asn Leu Gly Tyr Gly Leu Lys Ser
145 150 155 160

Arg Gly Phe Met Asn Ser Ser Gly His Ala Ile Leu Glu Ile His Val
165 170 175

Thr Lys Ala

<210> 53
<211> 46
<212> PRT
<213> Artificial Sequence

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<300>
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<309> 2011-05-31
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<400> 53

Lys Ser Cys Cys Pro Asn Thr Thr Gly Arg Asn Ile Tyr Asn Ala Cys
1 5 10 15

Arg Leu Thr Gly Ala Pro Arg Pro Thr Cys Ala Lys Leu Ser Gly Cys
20 25 30

Lys Ile Ile Ser Gly Ser Thr Cys Pro Ser Asp Tyr Pro Lys
35 40 45

<210> 54
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<309> 2008-10-07
<313> (21)..(53)

<400> 54

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

Phe Val Pro Gly Ala Trp Leu Ala Gly Glu Gly Val Asp Val Thr Ser
20 25 30

Leu

<210> 55
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<309> 2009-03-27
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<400> 55

Asp Val Ile Arg Glu Tyr Leu Met Phe Asn Glu Leu Ser Ala Leu Ser
1 5 10 15

Ser Ser Pro Glu Ser Val Arg Ser Arg Phe Ser Ser Ile Tyr Gly Thr
20 25 30

Asn Pro Asp Gly Ile Ala Leu Asn Asn Glu Thr Tyr Phe Asn Ala Val
35 40 45

Lys Pro Pro Ile Thr Ala Gln Tyr Gly Tyr Tyr Cys Tyr Lys Asn Val
50 55 60

Gly Thr Val Gln Tyr Val Asn Arg Pro Thr Asp Ile Asn Pro Asn Val
65 70 75 80

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Ile Leu Ala Gln Asp Thr Leu Thr Asn Asn Thr Asn Glu Pro Phe Thr
                85                  90                  95

Thr Thr Ile Thr Ile Thr Gly Ser Phe Thr Asn Thr Ser Thr Val Thr
            100                 105                 110

Ser Ser Thr Thr Thr Gly Phe Lys Phe Thr Ser Lys Leu Ser Ile Lys
        115                 120                 125

Lys Val Phe Glu Ile Gly Gly Glu Val Ser Phe Ser Thr Thr Ile Gly
    130                 135                 140

Thr Ser Glu Thr Thr Thr Glu Thr Ile Thr Val Ser Lys Ser Val Thr
145                 150                 155                 160

Val Thr Val Pro Ala Gln Ser Arg Arg Thr Ile Gln Leu Thr Ala Lys
                165                 170                 175

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

Tyr Phe Gly Ala Asn Phe Pro Lys Arg Val Gly Pro Gly Gly His Tyr
        195                 200                 205

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

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

Val Gln Pro Ala Arg Ser Leu Leu Asp Glu Gln
                245                 250
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<210> 56
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<310> WO2010064207
<311> 2009-12-03
<312> 2010-06-10

<400> 56

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Tyr Lys Trp Tyr Gly Tyr Thr Pro Gln Asn Val Ile Gly Gly Gly Lys
1               5                   10                  15
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Leu Leu Leu Lys Leu Leu Lys Lys Leu Leu Lys Leu Leu Lys Lys Lys
20 25 30

<210> 57
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catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttttattata tttatagcca gacctatttt cgctttcagg aagaaattaa agaaaatacc 240

aaaaatgaca aacaaatggt gcagtatatc tacaaataca ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggcctgtat 360

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 420

accaatgaac atctgattga tatggatcat gaagccagct ttttttggtgc atttctggtt 480

ggtggtggta gcggtccgct gggtctggca ggtcgtgttg ttcgtggtcg tgattatcgt 540

acctgtctga ccattgtgca gaaactgaaa aaaatggtgg ataaaccgac ccagcgtagc 600

gttagcaatg cagcaacccg tgtttgtcgt accggtcgta gccgttggcg tgatgtttgt 660

cgtaatttca tgcgtcgtta tcagagccgt gttacccagg gtctggttgc cggtgaaacc 720

gcacagcaga tttgtgaaga tctgcgtctg tgtattccga gcaccggtcc gctg 774

<210> 58
<211> 783
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 58
ggtcgtgatt atcgtacctg tctgaccatt gttcagaaac tgaaaaaaat ggtggataaa 60

ccgacccagc gtagcgttag caatgcagca acccgtgttt gtcgtaccgg tcgtagccgt 120

tggcgtgatg tttgtcgtaa ctttatgcgt cgttatcaga gccgtgttac ccagggtctg 180

gttgccggtg aaaccgcaca gcagatttgt gaagatctgc gtctgtgtat tccgagcacc 240

ggtccgctgc gtgttgttcg tccgctgggt ctggcaggcg gtggtggtgg tagtccgcag 300

cgtgttgcag cacatattac cggcacccgt ggtcgtagca ataccctgag cagcccgaat 360

agcaaaaatg aaaaagcact gggtcgcaaa attaatagct gggaaagcag ccgtagcggt 420

catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 480

ttttattata tttatagcca gacctatttt cgctttcaag aagaaattaa agaaaatacc 540

aaaaatgata agcagatggt gcagtatatc tataaatata ccagctatcc ggatccgatt 600

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 660

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 720

accaatgaac atctgattga tatggatcat gaagccagct ttttttggtgc atttctggtt 780

ggt 783

<210> 59
<211> 558
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 59
cgtgttgcag cacatattac cggcacccgt ggtcgtagca ataccctgag cagcccgaat 60

agcaaaaatg aaaaagccct gggtcgcaaa attaatagct gggaaagcag ccgtagcggt 120

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 tggcctgtat 360

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 420

accaatgaac atctgattga tatggatcat gaagccagct ttttttggtgc atttctggtt 480

ggtccgctgg gtctggcagg tcgtgttgtt cgtaaactgc tgctgcgttt actgaaaaaa 540

ttactgcgcc tgctgaaa 558

<210> 60
<211> 681
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 60
ggtctgggta gcgtttttgg tcgtctggca cgtattctgg gtcgtgttat tccgaaagtt 60

gcaaaaaaac tgggtccgaa agtggccaaa gttctgccga aagttatgaa agaagcaatt 120

ccgatggcag ttgaaatggc aaaaagccaa gaagaacagc agccgcagcg tgttgttcgt 180

ccgctgggtc tggcaggtcg tgttgcagca catattaccg gcacccgtgg tcgtagcaat 240

accctgagca gcccgaatag caaaaatgaa aaagcactgg gtcgcaaaat caatagctgg 300

gaaagcagcc gtagcggtca tagctttctg agcaatctgc atctgcgtaa tggtgaactg 360

gtgattcatg aaaaaggctt ttattatatt tatagccaga cctatttttcg ctttcaagaa 420

gagattaaag aaaataccaa aaatgataaa caaatggtgc agtacattta caaatatacc 480

agctatccgg acccgattct gctgatgaaa agcgcacgta atagctgttg gagcaaagat 540

gcagaatatg gtctgtatag catttatcag ggtggcatct ttgagctgaa agaaaatgat 600

cgcatctttg ttagcgtgac caacgaacat ctgatcgata tggatcatga agccagcttt 660

tttggtgcat ttctggtggg t 681

<210> 61
<211> 792
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 61
accagcgaag aaaccattag caccgttcaa gaaaaacagc agaatattag tccgctggtt 60

cgtgaacgtg gtccgcagcg tgttgcagca catattaccg gcacccgtgg tcgtagcaat 120

accctgagca gcccgaatag caaaaatgaa aaagccctgg gtcgcaaaat taacagctgg 180

gaaagcagcc gtagcggtca tagctttctg agcaatctgc atctgcgtaa tggtgaactg 240

gtgattcacg agaaaggctt ctattatatc tatagccaga cctatttttcg ctttcaagaa 300

gaaattaaag aaaacaccaa aaatgataaa caaatggtgc agtatattta caaatatacc 360

agctatccgg atccgattct gctgatgaaa agcgcacgta atagctgttg gagcaaagat 420

gcagaatatg gcctgtatag catctatcag ggtggcattt ttgaactgaa agaaaacgat 480

cgcatctttg tgagcgtgac caatgaacat ctgattgata tggatcacga agccagcttt 540

tttggtgcat ttctggttgg ttgtgcagca tgtgcagccg catgtggtgg tggtccgctg 600

ggtctggcag gtcgtgttgt tcgtggtctg ggtagcgttt ttggtcgtct ggcacgtatt 660

ctgggtcgtg ttattccgaa agttgcaaaa aaactgggtc cgaaagtggc caaagttctg 720

ccgaaagtta tgaaagaagc aattccgatg gccgttgaaa tggcaaaaag ccaagaagaa 780

cagcagccgc ag 792

<210> 62
<211> 897
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 62
accagcgaag aaaccattag caccgttcaa gaaaaacagc agaatattag tccgctggtt 60

cgtgaacgtg gtccgcagcg tgttgcagca catattaccg gcacccgtgg tcgtagcaat 120

accctgagca gcccgaatag caaaaatgaa aaagcactgg gtcgcaaaat caatagctgg 180

gaaagcagcc gtagcggtca tagctttctg agcaatctgc atctgcgtaa tggtgaactg 240

gtgattcatg aaaaaggctt ctactatatc tatagccaga cctatttccg cttccaagaa 300

gaaatcaaag aaaataccaa aaatgataaa caaatggtgc agtatattta caaatatacc 360

agctatccgg atccgattct gctgatgaaa agcgcacgta atagctgttg gagcaaagat 420

gcagaatatg gtctgtatag catttatcag ggtggcatct ttgagctgaa agaaaatgat 480

cgcatctttg ttagcgtgac caacgaacat ctgatcgata tggatcatga agccagcttt 540

tttggtgcat ttctggttgg tggtagcggt tgtgcagcat gtgcagccgc atgtccgctg 600

ggtctggcag gtcgtgttgt tcgtggtaaa ctgagctgtc tgagcctggc actggcaatt 660

attctgattc tggcaattgt tcatagcccg aatatggaag ttaaagcact ggcagatccg 720

gaagcagatg catttggtga agcaaatgcc tttggcgaag ccgatgcgtt tgccgaagcc 780

aatgcagatg ttaaaggtat gaaaaaagcc attaaagaaa ttctggattg cgtgatcgag 840

aaaggctatg ataaactggc agccaaactg aaaaaagtta ttcagcagct gtgggaa 897

<210> 63
<211> 672
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 63
accagcgaag aaaccattag caccgttcaa gaaaaacagc agaatattag tccgctggtt 60

cgtgaacgtg gtccgcagcg tgttgcagca catattaccg gcacccgtgg tcgtagcaat 120

accctgagca gcccgaatag caaaaatgaa aaagcactgg gtcgcaaaat taatagctgg 180

gaaagcagcc gtagcggtca tagctttctg agcaatctgc atctgcgtaa tggtgaactg 240

gtgattcatg aaaaaggctt ttattatatt tatagccaga cctattttcg ctttcaagaa 300

gaaattaaag aaaacaccaa aaatgataaa caaatggtgc agtacattta taaatatacc 360

agctatccgg atccgattct gctgatgaaa agcgcacgta atagctgttg gagcaaagat 420

gcagaatatg gtctgtatag catttatcag ggtggcattt ttgaactgaa agaaaatgat 480

cgcatttttg tgagcgtgac caatgaacat ctgattgata tggatcatga agccagcttt 540

tttggtgcat ttctggttgg ttgtgcagca tgtgcagccg catgtggtgg tccgctgggt 600

ctggcaggtc gtgttgttcg taaatggtgt tttcgtgttt gctatcgcgg tatttgttat 660

cgtcgttgcc gc 672

<210> 64
<211> 606
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 64
gttcgtgaac gtggtccgca gcgtgttgca gcacatatta ccggcacccg tggtcgtagc 60

aataccctga gcagcccgaa tagcaaaaat gaaaaagcac tgggtcgcaa aattaatagc 120

tgggaaagca gccgtagcgg tcatagcttt ctgagcaatc tgcatctgcg taatggtgaa 180

ctggtgattc atgaaaaagg cttttattat atttatagcc agacctattt tcgctttcaa 240

gaggaaatta aagaaaatac caaaaatgat aaacaaatgg tgcagtacat ctataaatac 300

accagctatc cggatccgat tctgctgatg aaaagcgcac gtaatagctg ttggagcaaa 360

gatgcagaat atggtctgta tagcatttat cagggtggca tttttgaact gaaagaaaat 420

gatcgcattt ttgtgagcgt gaccaatgaa catctgattg atatggatca tgaagccagc 480

ttttttggtg catttctggt tggtccgctg ggtctggcag gtcgtgttgt gcgtcgtcgc 540

cgtcgccgtc gtcgtaaatg gtgttttcgt gtttgttatc gcggtatttg ttatcgtcgt 600

tgccgc 606

<210> 65
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 65
ggtattggca aatttctgca tagcgccaaa aaattcggca aagcatttgt gggcgaaatt 60

atgaatagcg gtggtcagcg tctgggtaat cagtgggcag ttggtcatct gatgcgtgtt 120

gttcgtccgc tgggtctggc aggttgtgca gcagcatgtg cagcctgtac cagcgaagaa 180

accattagca ccgttcaaga aaaacagcag aatattagtc cgctggttcg tgaacgtggt 240

ccgcagcgtg ttgcagcaca tattaccggc acccgtggtc gtagcaatac cctgagcagc 300

ccgaatagca aaaatgaaaa agcactgggt cgcaaaatca atagctggga aagcagccgt 360

agcggtcata gctttctgag caatctgcat ctgcgtaatg gtgaactggt gattcatgaa 420

aaaggcttct actatatcta tagccagacc tatttccgct tccaagaaga aatcaaagaa 480

aacaccaaaa atgataaaca aatggtgcag tatatctaca aatataccag ctatccggat 540

ccgattctgc tgatgaaaag cgcacgtaat agctgttgga gcaaagatgc agaatatggt 600

ctgtatagca tttatcaggg tggcatcttt gagctgaaag aaaatgatcg catctttgtt 660

agcgtgacca acgaacatct gatcgatatg gatcatgaag ccagcttttt tggtgcattt 720

ctggtgggt 729

<210> 66
<211> 588
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 66
ggtattggca aatttctgca tagcgccaaa aaatttggca aagcatttgt gggcgaaatt 60

atgaatagcc gtgttgttcg tccgctgggt ctggcaggtc cgcagcgtgt tgcagcacat 120

attaccggca cccgtggtcg tagcaatacc ctgagcagcc cgaatagcaa aaatgaaaaa 180

gcactgggtc gcaaaattaa tagctgggaa agcagccgta gcggtcatag ctttctgagc 240

aatctgcatc tgcgtaatgg tgaactggtg attcatgaaa aaggctttta ttatatttat 300

agccagacct attttcgctt tcaagaggaa attaaagaaa ataccaaaaa tgataaacaa 360

atggtgcagt acatctataa atacaccagc tatccggatc cgattctgct gatgaaaagc 420

gcacgtaata gctgttggag caaagatgca gaatatggtc tgtatagcat ttatcagggt 480

ggcatttttg aactgaaaga aaatgatcgc atttttgtga gcgtgaccaa tgaacatctg 540

attgatatgg atcatgaagc cagcttttt ggtgcatttc tggtgggt 588

<210> 67
<211> 606
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 67
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 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 gcggtagcgg tggtggtggt cgtgttgttc gtccgctggg tctggcaggt 540

cgtcgtcgtc gccgtcgtcg gcgtaaactg gcaaaactgg ccaaaaaact ggcgaaactg 600

gctaaa 606

<210> 68
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 68
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 gcagtatatc tacaaatata ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 360

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 420

accaatgaac atctgattga tatggatcat gaagccagct ttttttggtgc atttctggtt 480

ggtggtggtg caagcggttg tggtccggaa ggtggtggtg gtccgctggg tctggcaggt 540

cgtgttgttc gtcgtcgtcg tcgccgtcgc cgtaaactgg caaaactggc caaaaaactg 600

gcgaaactgg ctaaa 615

<210> 69
<211> 684
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 69
accagcgaag aaaccattag caccgttcag gaaaaacagc agaatattag tccgctggtt 60

cgtgaacgtg gtccgcagcg tgttgcagca catattaccg gcacccgtgg tcgtagcaat 120

accctgagca gcccgaatag caaaaatgaa aaagcactgg gtcgcaaaat taatagctgg 180

gaaagcagcc gtagcggtca tagctttctg agcaatctgc atctgcgtaa tggtgaactg 240

gtgattcatg aaaaaggctt ttattatatt tatagccaga cctattttcg ctttcaggaa 300

gaaattaaag aaaataccaa aaatgataaa caaatggtgc agtatatcta taaatacacc 360

agctatccgg atccgattct gctgatgaaa agcgcacgta atagctgttg gagcaaagat 420

gcagaatatg gtctgtatag catttatcag ggtggcattt ttgaactgaa agaaaatgat 480

cgcatttttg tgagcgtgac caatgaacat ctgattgata tggatcatga agccagcttt 540

tttggtgcat ttctggttgg tggtggtggc ggtagcggtg gtggtggtcg tgttgttcgt 600

ccgctgggtc tggcaggtcg tcgtcgtcgt agacgtcgtc gtaaactggc aaaactggcc 660

aaaaaactgg cgaaactggc taaa 684

<210> 70
<211> 576
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 70
catcatcatc accatcacaa actggcaaaa ctggccaaaa aactggcgaa actggctaaa 60

tgtcgtgttg ttcgtccgct gggtctggca ggtcgtgttg cagcacatat taccggcacc 120

cgtggtcgta gcaataccct gagcagcccg aatagcaaaa atgaaaaagc actgggtcgc 180

aaaatcaata gctgggaaag cagccgtagc ggtcatagct ttctgagcaa tctgcatctg 240

cgtaatggtg aactggtgat tcatgaaaaa ggcttttatt atatttatag ccagacctat 300

tttcgctttc aagaagagat taaagaaaat accaaaaatg ataaacaaat ggtgcagtat 360

atctataaat ataccagcta tccggacccg attctgctga tgaaaagcgc acgtaatagc 420

tgttggagca aagatgcaga atatggtctg tatagcattt atcagggtgg catctttgag 480

ctgaaagaaa atgatcgcat ctttgttagc gtgaccaacg aacatctgat cgatatggat 540

catgaagcca gctttttgg tgcatttctg gtgggt 576

<210> 71
<211> 600
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 71
catcatcatc accatcacaa actggcaaaa ctggccaaaa aactggcgaa actggctaaa 60

tgtcgtcgtc gtcgccgtcg gcgtcgtcgt gttgttcgtc cgctgggtct ggcaggtcgt 120

gttgcagcac atattaccgg cacccgtggt cgtagcaata ccctgagcag cccgaatagc 180

aaaaatgaaa aagcactggg tcgcaaaatc aatagctggg aaagcagccg tagcggtcat 240

agctttctga gcaatctgca tctgcgtaat ggtgaactgg tgattcatga aaaaggcttt 300

tattatattt atagccagac ctattttcgc tttcaagaag agattaaaga aaataccaaa 360

aatgataaac aaatggtgca gtatatctat aaatacacca gctatccgga cccgattctg 420

ctgatgaaaa gcgcacgtaa tagctgttgg agcaaagatg cagaatatgg tctgtatagc 480

atttatcagg gtggcatctt tgagctgaaa gaaaatgatc gcatctttgt tagcgtgacc 540

aacgaacatc tgatcgatat ggatcatgaa gccagctttt ttggtgcatt tctggtgggt 600

<210> 72
<211> 606
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 72
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 gcagtatatc tataaataca 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 gcggtagcgg tggtggtggt cgtgttgttc gtccgctggg tctggcaggt 540

cgtcgtcgtc gtagacgtcg tcgtaaactg gcaaaactgg ccaaaaaact ggcgaaactg 600

gctaaa 606

<210> 73
<211> 624
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 73
aaatggaaac tgtttaaaaa aattggcatt ggtgccgttc tgaaagttct gaccaccggt 60

ctgcctgcac tgattagccg tgttgttcgt ccgctgggtc tggcaggcga acgtggtccg 120

cagcgtgttg cagcacatat taccggcacc cgtggtcgta gcaataccct gagcagcccg 180

aatagcaaaa atgaaaaagc actgggtcgc aaaattaata gctgggaaag cagccgtagc 240

ggtcatagct ttctgagcaa tctgcatctg cgtaatggtg aactggtgat tcatgaaaaa 300

ggcttttatt atatttatag ccagacctat tttcgctttc aagaggaaat taaagaaaat 360

accaaaaatg ataaacaaat ggtgcagtat atctataaat ataccagcta tccggatccg 420

attctgctga tgaaaagcgc acgtaatagc tgttggagca aagatgcaga atatggtctg 480

tatagcattt atcagggtgg catttttgaa ctgaaagaaa atgatcgcat ttttgtgagc 540

gtgaccaatg aacatctgat tgatatggat catgaagcca gctttttttgg tgcatttctg 600

gttggtccgc tgggcctggc tggt 624

<210> 74
<211> 609
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 74
tttcgcaaaa gcaaagaaaa aattggcaaa ttttttaaac gcattgtgca gcgcattttt 60

gattttctgc gtaatctggt tcgtgttgtt cgtccgctgg gtctggcagg cgaacgtggt 120

ccgcagcgtg ttgcagcaca tattaccggc acccgtggtc gtagcaatac cctgagcagc 180

ccgaatagca aaaatgaaaa agcactgggt cgcaaaatta atagctggga aagcagccgt 240

agcggtcata gctttctgag caatctgcat ctgcgtaatg gtgaactggt gattcatgaa 300

aaaggctttt attatattta tagccagacc tattttcgct ttcaagagga aattaaagaa 360

aataccaaaa atgataaaca aatggtgcag tatatctata aatataccag ctatccggat 420

ccgattctgc tgatgaaaag cgcacgtaat agctgttgga gcaaagatgc agaatatggt 480

ctgtatagca tttatcaggg tggcattttt gaactgaaag aaaatgatcg cattttgtg 540

agcgtgacca atgaacatct gattgatatg gatcatgaag ccagcttttt tggtgcattt 600

ctggttggt 609

<210> 75
<211> 609
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 75
ggtggtctgc gtagcctggg tcgtaaaatt ctgcgtgcat ggaaaaaata tggtccgatt 60

attgtgccga ttattcgtat tcgtgttgtt cgtccgctgg gtctggcagg cgaacgtggt 120

ccgcagcgtg ttgcagcaca tattaccggc acccgtggtc gtagcaatac cctgagcagc 180

ccgaatagca aaaatgaaaa agcactgggt cgcaaaatta atagctggga aagcagccgt 240

agcggtcata gctttctgag caatctgcat ctgcgtaatg gtgaactggt gattcatgaa 300

aaaggctttt attatattta tagccagacc tattttcgct ttcaagagga aattaaagaa 360

aataccaaaa atgataaaca aatggtgcag tatatctata aatataccag ctatccggat 420

ccgattctgc tgatgaaaag cgcacgtaat agctgttgga gcaaagatgc agaatatggt 480

ctgtatagca tttatcaggg tggcattttt gaactgaaag aaaatgatcg cattttgtg 540

agcgtgacca atgaacatct gattgatatg gatcatgaag ccagcttttt tggtgcattt 600

ctggttggt 609

<210> 76
<211> 600
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 76
cgtgttgcag cacatattac cggcacccgt ggtcgtagca ataccctgag cagcccgaat 60

agcaaaaatg aaaaagcact gggtcgcaaa attaatagct gggaaagcag ccgtagcggt 120

catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

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ggtggtggta gcggtggtcc gctgggtctg gcaggtcgtg ttgttcgtgg tctggttgaa 540

accctgacca aaattgttag ctatggtatt gataaactga ttgaaaaaat tctggaaggt 600

<210> 77
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<400> 77
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catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

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aaaaatgata agcagatggt gcagtatatc tataaatata ccagctatcc ggatccgatt 300

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accaatgaac atctgattga tatggatcat gaagccagct tttttggtgc atttctggtt 480

ggtggtggta gcggtggtcc gctgggtctg gcaggtcgtg ttgttcgtgg ttttattgca 540

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<210> 78
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<220>
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<400> 78
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catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

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aaaaatgata agcagatggt gcagtatatc tataaatata ccagctatcc ggatccgatt 300

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accaatgaac atctgattga tatggatcat gaagccagct tttttggtgc atttctggtt 480

ggtggtggta gcggtggtcc gctgggtctg gcaggtcgtg ttgttcgtgg ttttctgggc 540

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<211> 570
<212> DNA
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<220>
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cgtagcaata ccctgagcag cccgaatagc aaaaatgaaa aagcactggg tcgcaaaatt 180

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agcaaagatg cagaatatgg tctgtatagc atttatcagg gtggcatttt tgaactgaaa 480

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gccagctttt ttggtgcatt tctggttggt 570

<210> 80
<211> 1287
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

<400> 80
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cagtataaaa ttaataccgt gggctgcaaa accaatgaag atttttatgc cgatatcctg 540

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gcaaaagtta ccctggcaaa tagccagaaa ggcaccgcag gttatattta tcgttttctg 720

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<210> 81
<211> 1974
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<220>
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<210> 82
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<220>
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<400> 82
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<210> 83
<211> 1083
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Peptide

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<210> 84
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<210> 85
<211> 672
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<400> 85
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gattatccga aa 672

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<220>
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<220>
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<210> 90
<211> 281
<212> PRT
<213> Homo sapiens

<400> 90

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

Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
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

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

Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
100 105 110

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
245 250 255

Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
260 265 270

Ser Phe Phe Gly Ala Phe Leu Val Gly
275 280

<210> 91
<211> 223
<212> PRT
<213> Artificial Sequence

<220>
<223> -

<400> 91

Lys Leu Leu Leu Lys Leu Leu Lys Lys Leu Leu Lys Leu Leu Lys Lys
1 5 10 15

Lys Gly Gly Gly Tyr Gly Arg Pro Arg Gln Ser Gly Lys Lys Arg Lys
20 25 30

Arg Lys Arg Leu Lys Pro Thr Arg Val Val Arg Pro Leu Gly Leu Ala
35 40 45

Gly Gly Gly Cys Ala Ala Ala Cys Ala Ala Cys Ser Gly Gly Arg Val
50 55 60

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

Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp
85 90 95

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

Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser
        115                 120                 125

Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn
    130                 135                 140

Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp
145                 150                 155                 160

Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp
                165                 170                 175

Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu
            180                 185                 190

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

Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
    210                 215                 220
```

<210> 92
<211> 223
<212> PRT
<213> Artificial Sequence

<220>
<223> -

<400> 92

```
Lys Leu Ala Lys Leu Ala Lys Lys Leu Ala Lys Leu Ala Lys Arg Arg
1               5                   10                  15

Arg Arg Arg Arg Arg Arg Lys Lys Arg Gly Gly Gly Cys Ala Ala Ala
            20                  25                  30

Cys Ala Ala Cys Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys
        35                  40                  45

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

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

```
Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp
                85                  90                  95

Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg
            100                 105                 110

Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser
        115                 120                 125

Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn
    130                 135                 140

Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp
145                 150                 155                 160

Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp
                165                 170                 175

Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu
            180                 185                 190

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

Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
    210                 215                 220
```

<210> 93
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> -

<400> 93

```
Lys Leu Ala Lys Leu Ala Lys Lys Leu Ala Lys Leu Ala Lys Arg Arg
1               5                   10                  15

Arg Arg Arg Arg Arg Arg Lys Lys Arg His Arg Gln Pro Arg Gly Trp
            20                  25                  30

Glu Gln Gly Gly Gly Cys Ala Ala Ala Cys Ala Ala Cys Thr Ser Glu
        35                  40                  45

Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu
    50                  55                  60
```

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Val Arg Glu Arg Gly Pro Gln 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
210 215 220

Phe Phe Gly Ala Phe Leu Val Gly
225 230

<210> 94
<211> 207
<212> PRT
<213> Artificial Sequence

<220>
<223> -

<400> 94

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 Gly Gly Gly Gly Pro Leu Gly Leu Ala Gly
165 170 175

Arg Val Val Arg Tyr Ala Arg Ala Ala Ala Arg Gln Ala Arg Ala Gly
180 185 190

Gly Lys Leu Ala Lys Leu Ala Lys Lys Leu Ala Lys Leu Ala Lys
195 200 205

<210> 95
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> -

<400> 95

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 Gly Gly Gly Gly Pro Leu Gly Leu Ala Gly
                165                 170                 175

Arg Val Val Arg Tyr Ala Arg Ala Ala Ala Arg Gln Ala Arg Ala Gly
            180                 185                 190

Gly Arg Trp Gly Lys Trp Phe Lys Lys Ala Thr His Val Gly Lys His
        195                 200                 205

Val Gly Lys Ala Ala Leu Thr Ala Tyr Leu
    210                 215
```

<210> 96
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> -

<400> 96

```
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 Gly Gly Gly Gly Pro Leu Gly Leu Ala Gly
                165                 170                 175

Arg Val Val Arg Tyr Ala Arg Ala Ala Ala Arg Gln Ala Arg Ala Gly
            180                 185                 190

Gly Gly Arg Arg Lys Arg Lys Trp Leu Arg Arg Ile Gly Lys Gly Val
        195                 200                 205

Lys Ile Ile Gly Gly Ala Ala Leu Asp His Leu
    210                 215
```

<210> 97
<211> 212
<212> PRT
<213> Artificial Sequence

<220>
<223> -

<400> 97

```
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 Gly Gly Gly Gly Pro Leu Gly Leu Ala Gly
                165                 170                 175

Arg Val Val Arg Thr His Arg Pro Pro Met Trp Ser Pro Val Trp Pro
            180                 185                 190

Gly Gly Gly Lys Leu Leu Leu Lys Leu Leu Lys Lys Leu Leu Lys Leu
        195                 200                 205

Leu Lys Lys Lys
    210
```

<210> 98
<211> 207
<212> PRT
<213> Artificial Sequence

<220>
<223> -

<400> 98

```
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 Gly Gly Gly Gly Pro Leu Gly Leu Ala Gly
165 170 175

Arg Val Val Arg Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly
180 185 190

Gly Lys Leu Ala Lys Leu Ala Lys Lys Leu Ala Lys Leu Ala Lys
195 200 205

<210> 99
<211> 211
<212> PRT
<213> Artificial Sequence

<220>
<223> -

<400> 99

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 Gly Gly Gly Gly Pro Leu Gly Leu Ala Gly
                165                 170                 175

Arg Val Val Arg Gly Arg Phe Lys Arg Phe Arg Lys Lys Phe Lys Lys
            180                 185                 190

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

His Leu Met
    210
```

<210> 100
<211> 210
<212> PRT
<213> Artificial Sequence

<220>
<223> -

<400> 100

```
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 Gly Gly Gly Gly Pro Leu Gly Leu Ala Gly
                165                 170                 175

Arg Val Val Arg Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly
            180                 185                 190

Gly Arg Phe Lys Arg Phe Arg Lys Lys Phe Lys Lys Leu Phe Lys Lys
        195                 200                 205

Leu Ser
    210
```

<210> 101
<211> 211
<212> PRT
<213> Artificial Sequence

<220>

<223> -

<400> 101

```
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 Gly Gly Gly Gly Pro Leu Gly Leu Ala Gly
                165                 170                 175

Arg Val Val Arg Gly Gly Leu Arg Ser Leu Gly Arg Lys Ile Leu Arg
            180                 185                 190

Ala Trp Lys Lys Tyr Gly Gln Arg Leu Gly Asn Gln Trp Ala Val Gly
        195                 200                 205

His Leu Met
    210
```

<210> 102
<211> 234
<212> PRT

<213> Artificial Sequence

<220>
<223> -

<400> 102

```
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 Gly Gly Gly Gly Pro Leu Gly Leu Ala Gly
                165                 170                 175

Arg Val Val Arg Gly Gly Gly Ile Gly Ala Arg Leu Lys Val Leu Thr
            180                 185                 190

Thr Gly Leu Pro Arg Ile Ser Trp Ile Lys Arg Lys Arg Gln Gln Gly
        195                 200                 205

Gly Gly Gly Ser Lys Leu Ala Lys Leu Ala Lys Lys Leu Ala Lys Leu
    210                 215                 220
```

Ala Lys Arg Arg Arg Arg Arg Arg Arg
225 230

<210> 103
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> -

<400> 103

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 Gly Gly Gly Gly Pro Leu Gly Leu Ala Gly
165 170 175

Arg Val Val Arg Gly Ile Gly Ala Arg Leu Lys Val Leu Thr Thr Gly
180 185 190

Leu Pro Arg Ile Ser Trp Ile Lys Arg Lys Arg Gln Gln

195 200 205

<210> 104
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> -

<400> 104

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 Gly Gly Gly Gly Pro Leu Gly Leu Ala Gly
165 170 175

Arg Val Val Arg Arg Arg Arg Arg Arg Arg Arg Arg Gly Gly Gly Ile
180 185 190

Gly Ala Arg Leu Lys Val Leu Thr Thr Gly Leu Pro Arg Ile Ser Trp
195 200 205

Ile Lys Arg Lys Arg Gln Gln
210 215

<210> 105
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> -

<400> 105

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 Gly Gly Gly Gly Pro Leu Gly Leu Ala Gly
165 170 175

Arg Val Val Arg Gly Gly Gly Ile Gly Ala Arg Leu Lys Val Leu Thr
180 185 190

```
Thr Gly Leu Pro Arg Ile Ser Trp Ile Lys Arg Lys Arg Gln Gln Arg
        195                 200                 205

Arg Arg Arg Arg Arg Arg Arg
    210                 215
```

<210> 106
<211> 203
<212> PRT
<213> Artificial Sequence

<220>
<223> -

<400> 106

```
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 Gly Gly Gly Gly Pro Leu Gly Leu Ala Gly
                165                 170                 175
```

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Arg Val Val Arg Arg Arg Arg Arg Arg Arg Arg Lys Leu Leu Leu
180 185 190

Arg Leu Leu Lys Lys Leu Leu Arg Leu Leu Lys
195 200

<210> 107
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> -

<400> 107

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 Gly Gly Gly Gly Pro Leu Gly Leu Ala Gly
165 170 175

Arg Val Val Arg Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly

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180 185 190

Gly Lys Leu Leu Leu Arg Leu Leu Lys Lys Leu Leu Arg Leu Leu Lys
195 200 205

<210> 108
<211> 669
<212> DNA
<213> Artificial Sequence

<220>
<223> -

<400> 108
aaactgctgc tgaaactgct gaaaaaactg ctgaaactgc tgaaaaaaaa aggtggtggt 60

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gttgttcgtc cgctgggtct ggcaggcggt ggttgtgcag cagcatgtgc agcctgtagc 180

ggtggtcgtg ttgcagcaca tattaccggc acccgtggtc gtagcaatac cctgagcagc 240

ccgaatagca aaaatgaaaa agcactgggt cgcaaaatta acagctggga aagcagccgt 300

agtggtcata gctttctgag caatctgcat ctgcgtaatg gtgaactggt gattcatgaa 360

aaaggcttct actatatcta cagccagacc tattttcgct tccaagaaga gattaaagaa 420

aacaccaaaa acgataaaca aatggtgcag tacatctata aatacaccag ctatccggat 480

ccgattctgc tgatgaaaag cgcacgtaat agctgttgga gcaaagatgc agaatatggc 540

ctgtatagca tttatcaggg tggcatcttt gaactgaaag aaaacgatcg tattttcgtg 600

agcgtgacca atgaacatct gatcgatatg gatcatgaag ccagcttttt tggtgcattt 660

ctggtgggt 669

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accattagca ccgttcaaga aaaacagcag aatattagtc cgctggttcg tgaacgtggt 180

ccgcagcgtg ttgcagcaca tattaccggc acccgtggtc gtagcaatac cctgagcagc 240

ccgaatagca aaaatgaaaa agcactgggt cgcaaaatta acagctggga aagcagccgt 300

agcggtcata gctttctgag caatctgcat ctgcgtaatg gtgaactggt gattcatgaa 360

aaaggcttct actatatcta cagccagacc tattttcgct tccaagaaga gattaaagaa 420

aacaccaaaa acgataaaca aatggtgcag tacatctata aatacaccag ctatccggat 480

ccgattctgc tgatgaaaag cgcacgtaat agctgttgga gcaaagatgc agaatatggc 540

ctgtatagca tttatcaggg tggcatcttt gaactgaaag aaaacgatcg tattttcgtg 600

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ctggtgggt 669

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<211> 696
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gcatgtgcag cctgtaccag cgaagaaacc attagcaccg ttcaagaaaa acagcagaat 180

attagtccgc tggttcgtga acgtggtccg cagcgtgttg 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

catgaagcga gctttttgg tgcatttctg gtgggt 696

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<212> DNA
<213> Artificial Sequence

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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

accaacgaac atctgattga tatggatcat gaagcgagct ttttttggcgc gtttctggtg 480

ggcggcggcg gcggcagcgg cggcggcggc ccgctgggcc tggcgggccg tgtggtgcgt 540

tatgcgcgtg cggcggcgcg tcaggcgcgt gcgggcggca aactggcgaa actggcgaaa 600

aaactggcga aactggcgaa a 621

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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

accaacgaac atctgattga tatggatcat gaagcgagct ttttttggcgc gtttctggtg 480

ggcggcggcg gcggcagcgg cggcggcggc ccgctgggcc tggcgggccg tgtggtgcgt 540

tatgcgcgtg cggcggcgcg tcaggcgcgt gcgggcggcc gttggggcaa atggtttaaa 600

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

<220>
<223> -

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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

accaacgaac atctgattga tatggatcat gaagcgagct ttttttggcgc gtttctggtg 480

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tatgcgcgtg cggcggcgcg tcaggcgcgt gcgggcggcg gccgtcgtaa acgtaaatgg 600

ctgcgtcgta ttggcaaagg cgtgaaaatt attggcggcg cggcgctgga tcatctg 657

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<211> 636
<212> DNA
<213> Artificial Sequence

<220>
<223> -

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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

accaacgaac atctgattga tatggatcat gaagcgagct ttttttggcgc gtttctggtg 480

ggcggcggcg gcggcagcgg cggcggcggc ccgctgggcc tggcgggccg tgtggtgcgt 540

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<212> DNA
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catagctttc tgagcaacct gcatctgcgc aacggcgaac tggtgattca tgaaaaaggc 180

ttttattata tttatagcca gacctatttt cgctttcagg aagaaattaa agaaaacacc 240

aaaaacgata aacagatggt gcagtatatt tataaatata ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcgcg caacagctgc tggagcaaag atgcggaata tggcctgtat 360

agcatttatc agggcggcat ttttgaactg aaagaaaacg atcgcatttt tgtgagcgtg 420

accaacgaac atctgattga tatggatcat gaagcgagct ttttttggcgc gtttctggtg 480

ggcggcggcg gcggcagcgg cggcggcggc ccgctgggcc tggcgggccg cgtggtgcgc 540

tatggccgca aaaaacgccg ccagcgccgc cgcggcggca aactggcgaa actggcgaaa 600

aaactggcga aactggcgaa a 621

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<212> DNA
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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

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ggtggtggtg gcggtagtgg cggtggtggt cctctgggtc tggcaggtcg tgttgttcgt 540

ggtcgtttta aacgttttcg caaaaaattt aaaaaactgt tcaaaaaact gagccagcgc 600

ctgggtaatc agtgggcagt tggtcatctg atg 633

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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

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ggtggtggtg gcggtagtgg cggtggtggt cctctgggtc tggcaggtcg tgttgttcgt 540

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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

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ggtggtctgc gtagcctggg acgtaaaatt ctgcgtgcat ggaagaaata tggtcagcgt 600

ctgggtaatc agtgggcagt tggtcatctg atg 633

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<212> DNA
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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 gcggtagtgg cggtggtggt cctctgggtc tggcaggtcg tgttgttcgc 540

ggaggtggta ttggtgcacg tctgaaagtt ctgaccaccg gtctgcctcg tattagctgg 600

attaaacgta aacgtcagca gggtgggggt ggtagcaaac tggcaaaact ggcgaaaaaa 660

ctggctaaac tggccaaacg tcgtcgtcgc cgtcgtcggc gt 702

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catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttctactata tctacagcca gacctatttt cgcttccaag aagagattaa agaaaacacc 240

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agcatttatc agggtggcat ctttgaactg aaagaaaacg atcgtatttt cgtgagcgtg 420

accaatgaac atctgatcga tatggatcat gaagccagct tttttggtgc atttctggtg 480

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cgtaaacgtc agcag 615

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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

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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

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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

agcatttatc agggtggcat ctttgaactg aaagaaaacg atcgtatttt cgtgagcgtg 420

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ctgctgaaa 609

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<220>
<223> -

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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 ttttttggtgc atttctggtg 480

ggtggtggtg gcggtagtgg cggtggtggt cctctgggtc tggcaggtcg tgttgttcgt 540

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<211> 39
<212> PRT
<213> Artificial Sequence

<220>
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<400> 125

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Arg Lys Arg Leu Lys Pro Thr
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<300>
<301> Hilchie AL, Doucette CD, Pinto DM, Patrzykat A, Douglas S, Hoskin DW.
<302> Pleurocidin-family cationic antimicrobial peptides are cytolytic for breast carcinoma cells and prevent growth of tumor xenografts
<303> Breast Cancer Res.
<304> 13
<305> 5
<306> R102
<307> 2011-10-24

<400> 126

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Gly Lys Ala Ala Leu Thr Ala Tyr Leu
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<300>
<301> Hilchie AL, Doucette CD, Pinto DM, Patrzykat A, Douglas S, Hoskin DW.
<302> Pleurocidin-family cationic antimicrobial peptides are cytolytic for breast carcinoma cells and prevent growth of tumor xenografts.
<303> Breast Cancer Res.
<304> 13
<305> 5
<306> R102
<307> 2011-10-24

<400> 127

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1 5 10 15

eolf-seql

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<210> 128
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> -

<300>
<301> Papo N, Shai Y.
<302> New lytic peptides based on the D,L-amphipathic helix motif preferentially kill tumor cells compared to normal cells.
<303> Biochemistry
<304> 42
<305> 31
<306> 9346-54
<307> 2003-08-12

<400> 128

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<211> 31
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<220>
<223> -

<300>
<301> Cai H, Yang H, Xiang B, Li S, Liu S, Wan L, Zhang J, Li Y, Cheng J, Lu X.
<302> Selective apoptotic killing of solid and hematologic tumor cells by bombesin-targeted delivery of mitochondria-disrupting peptides.
<303> Molecular Pharmacology
<304> 7
<305> 2
<306> 586-96
<307> 2010-04-05

<400> 129

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<301> Cai H, Yang H, Xiang B, Li S, Liu S, Wan L, Zhang J, Li Y, Cheng J, Lu X.
<302> Selective apoptotic killing of solid and hematologic tumor cells by bombesin-targeted delivery of mitochondria-disrupting peptides.
<303> Molecular Pharmacology
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<302> Selective apoptotic killing of solid and hematologic tumor cells by bombesin-targeted delivery of mitochondria-disrupting peptides.
<303> Molecular Pharmacology
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