SEQUENCE LISTING

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<120> Anticancer fusion protein

<130> KP1

<150> PL394618
<151> 2011-04-19

<160> 78

<170> PatentIn version 3.5

<210> 1
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Leu Ser Glu Asp Lys Leu Leu Ala Cys Gly Glu Gly Ala Ala Asp Ile
1 5 10 15

Ile Ile Gly His Leu Cys Ile Arg His Glu Met Thr Pro Val Asn Pro
20 25 30

Gly Arg Val Val Arg 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> 2
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<400> 2

Glu Met Thr Pro Val Asn Pro Gly Arg Val Val Arg Glu Arg Gly Pro
1 5 10 15

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

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

Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu
50 55 60

His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr
65 70 75 80

Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn
85 90 95

Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser
100 105 110

Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp
115 120 125

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

```
Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu
145                 150                 155                 160

His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu
                165                 170                 175

Val Gly
```

<210> 3
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<400> 3

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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 Pro Leu Gly Leu Ala Gly Arg Val Val Arg Glu Met Thr Pro Val
165 170 175

Asn Pro Gly

<210> 4
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<213> Artificial Sequence

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<400> 4

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 Leu Ser Glu Asp Lys
165 170 175

Leu Leu Ala Cys Gly Glu Gly Ala Ala Asp Ile Ile Ile Gly His Leu
180 185 190

Cys Ile Arg His Glu Met Thr Pro Val Asn Pro Gly
195 200

<210> 5
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<213> Artificial Sequence

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<223> fusion protein

<400> 5

Leu Ser Glu Asp Lys Leu Leu Ala Cys Gly Glu Gly Ala Ala Asp Ile
1 5 10 15

Ile Ile Gly His Leu Cys Ile Arg His Glu Met Thr Pro Val Asn Pro
20 25 30

Gly Arg Val Val Arg Pro Leu Gly Leu Ala Gly Thr Ser Glu Glu Thr
35 40 45

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

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

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

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

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

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

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

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

Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr

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180 185 190

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

Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe
210 215 220

Gly Ala Phe Leu Val Gly
225 230

<210> 6
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<213> Artificial Sequence

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<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 Cys Ala Ala Cys Ala
            180                 185                 190

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

Asp Lys Leu Leu Ala Cys Gly Glu Gly Ala Ala Asp Ile Ile Ile Gly
    210                 215                 220

His Leu Cys Ile Arg His Glu Met Thr Pro Val Asn Pro Gly
225                 230                 235
```

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

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<223> fusion protein

<400> 7

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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 Pro Leu Gly Leu Ala Gly Arg Val Val Arg Glu Met Thr
        195                 200                 205

Pro Val Asn Pro Gly
    210
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<210> 8
<211> 197
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 8

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Lys Arg Arg Gln Thr Ser Ala Thr Asp Phe Tyr His Ser Lys Arg Arg
1               5                   10                  15

Leu Ile Phe Ser Lys Pro Arg Arg Pro Tyr Arg Val Val Arg Pro Leu
            20                  25                  30

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

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

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

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

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

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

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

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

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

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

Ala Phe Leu Val Gly
195

<210> 9
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 9

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

Gln Thr Ser Ala Thr Asp Phe Tyr His Ser Lys Arg Arg Leu Ile Phe
210 215 220

Ser Lys Pro Arg Arg Pro Tyr
225 230

<210> 10
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 10

Met Trp Tyr Arg Pro Asp Leu Asp Glu Arg Lys Gln Gln Lys Arg Glu
1 5 10 15

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

Cys Ala Ala Cys Gly Gly Gln 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> 11
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 11

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

Arg Arg Arg Arg Arg Arg Arg Gly Gly Gly Phe Gln Leu Arg Gln Pro
    210                 215                 220

Pro Leu Val Pro Ser Arg Lys Gly Glu
225                 230
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<210> 12
<211> 590
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 12

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Ser Gly Met Ser Val Phe Asp Ser Lys Phe Lys Gly Ile His
            180                 185                 190

Val Tyr Ser Glu Ile Gly Glu Leu Glu Ser Val Leu Val His Glu Pro
        195                 200                 205

Gly Arg Glu Ile Asp Tyr Ile Thr Pro Ala Arg Leu Asp Glu Leu Leu
    210                 215                 220

Phe Ser Ala Ile Leu Glu Ser His Asp Ala Arg Lys Glu His Lys Gln
225                 230                 235                 240

Phe Val Ala Glu Leu Lys Ala Asn Asp Ile Asn Val Val Glu Leu Ile
                245                 250                 255

Asp Leu Val Ala Glu Thr Tyr Asp Leu Ala Ser Gln Glu Ala Lys Asp
            260                 265                 270

Lys Leu Ile Glu Glu Phe Leu Glu Asp Ser Glu Pro Val Leu Ser Glu
        275                 280                 285

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

Arg Glu Leu Val Glu Ile Met Met Ala Gly Ile Thr Lys Tyr Asp Leu
305                 310                 315                 320
```

```
Gly Ile Glu Ala Asp His Glu Leu Ile Val Asp Pro Met Pro Asn Leu
                325                 330                 335

Tyr Phe Thr Arg Asp Pro Phe Ala Ser Val Gly Asn Gly Val Thr Ile
            340                 345                 350

His Tyr Met Arg Tyr Lys Val Arg Gln Arg Glu Thr Leu Phe Ser Arg
        355                 360                 365

Phe Val Phe Ser Asn His Pro Lys Leu Ile Asn Thr Pro Trp Tyr Tyr
    370                 375                 380

Asp Pro Ser Leu Lys Leu Ser Ile Glu Gly Gly Asp Val Phe Ile Tyr
385                 390                 395                 400

Asn Asn Asp Thr Leu Val Val Gly Val Ser Glu Arg Thr Asp Leu Gln
                405                 410                 415

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

Phe Lys Arg Ile Val Ala Ile Asn Val Pro Lys Trp Thr Asn Leu Met
        435                 440                 445

His Leu Asp Thr Trp Leu Thr Met Leu Asp Lys Asp Lys Phe Leu Tyr
    450                 455                 460

Ser Pro Ile Ala Asn Asp Val Phe Lys Phe Trp Asp Tyr Asp Leu Val
465                 470                 475                 480

Asn Gly Gly Ala Glu Pro Gln Pro Val Glu Asn Gly Leu Pro Leu Glu
                485                 490                 495

Gly Leu Leu Gln Ser Ile Ile Asn Lys Lys Pro Val Leu Ile Pro Ile
            500                 505                 510

Ala Gly Glu Gly Ala Ser Gln Met Glu Ile Glu Arg Glu Thr His Phe
        515                 520                 525

Asp Gly Thr Asn Tyr Leu Ala Ile Arg Pro Gly Val Val Ile Gly Tyr
    530                 535                 540

Ser Arg Asn Glu Lys Thr Asn Ala Ala Leu Glu Ala Ala Gly Ile Lys
545                 550                 555                 560

Val Leu Pro Phe His Gly Asn Gln Leu Ser Leu Gly Met Gly Asn Ala
                565                 570                 575
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Arg Cys Met Ser Met Pro Leu Ser Arg Lys Asp Val Lys Trp
580 585 590

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

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<400> 13

Phe Leu Asp Thr Leu Val Val Leu His Arg Lys Pro Arg Arg Pro Tyr
1 5 10 15

Arg Val Val Arg Pro Leu Gly Leu Ala Gly 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
180 185

<210> 14
<211> 203
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 14

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

Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys Gly Met
            180                 185                 190

Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn
        195                 200
```

<210> 15
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 15

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

Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys Ala Val
            180                 185                 190

Thr Asp His Pro Asp Arg Leu Trp Ala Trp Glu Lys Phe
        195                 200                 205
```

<210> 16

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

<220>
<223> fusion protein

<400> 16

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Phe Trp Leu Arg Phe Thr Lys Pro Arg Arg Pro Tyr Arg Val Val Arg
1               5                   10                  15

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

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

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

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

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

Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile
            100                 105                 110

Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala
        115                 120                 125

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

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

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

Phe Gly Ala Phe Leu Val Gly
            180
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<210> 17
<211> 190
<212> PRT
<213> Artificial Sequence

<220>

<223> fusion protein

<400> 17

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Phe Arg Arg Lys Ala Phe Leu His Trp Tyr Thr 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
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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
180 185

<210> 19
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<400> 19

Gly Ile Gly Ala Arg Leu Lys Val Leu Thr Thr Gly Leu Pro Arg Ile
1 5 10 15

Ser Trp Ile Lys Arg Lys Arg Gln Gln Arg Val Val Arg Pro Leu Gly
20 25 30

Leu Ala Gly 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> 20
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<400> 20

Ala Leu Tyr Leu Ala Ile Arg Arg Arg Arg Arg Arg Arg Arg Val Val
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Arg Pro Leu Gly Leu Ala Gly Arg Val Ala Ala His Ile Thr Gly Thr
20 25 30

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

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

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

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

Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr
            100                 105                 110

Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser
        115                 120                 125

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

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

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

Phe Phe Gly Ala Phe Leu Val Gly
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<400> 21

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Ala Gly Ala Pro Ser Gly His Tyr Lys Gly Gly Gly Arg Val Ala Ala
            20                  25                  30

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

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

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

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

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

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

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

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

Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
180 185

<210> 22
<211> 188
<212> PRT
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<220>
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<400> 22

Val Asn Trp Lys Lys Val Leu Gly Lys Ile Ile Lys Val Ala Lys Arg
1 5 10 15

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

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

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

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

65 70 75 80

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

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

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

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

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

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

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

<210> 23
<211> 193
<212> PRT
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<220>
<223> fusion protein

<400> 23

Lys Trp Val Val Ser His Ala Arg Leu Met Tyr Ser Phe Arg Arg Arg
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

Gly

<210> 24
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
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<400> 24

Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile
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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

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

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

Arg Val Val Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys
225                 230                 235                 240

Trp Lys Lys
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<210> 25
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<220>
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<400> 25

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Asp Lys Arg Pro Ala Arg Asp Tyr Asn Arg Lys Arg Val Val Arg Pro
            20                  25                  30

Leu Gly Leu Ala Gly Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg
        35                  40                  45
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Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala
50 55 60

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

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

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

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

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

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

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

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

Phe Gly Ala Phe Leu Val Gly
195

<210> 26
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<300>
<301> Kono K, Ueba T, Takahashi JA, Murai N, Hashimoto N, Myoumoto A, Itoh N,Fukumoto M
<302> In vitro growth suppression of human glioma cells by a 16-mer oligopeptide: a potential new treatment modality for malignant glioma.
<303> . J Neurooncol
<304> 63
<305> 2
<306> 163-71
<307> 2003-07-30

<400> 26

Met Trp Tyr Arg Pro Asp Leu Asp Glu Arg Lys Gln Gln Lys Arg Glu

1 5 10 15

<210> 27
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<300>
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<309> 2008-10-16
<313> (464)..(496)

<400> 27

Leu Ser Glu Asp Lys Leu Leu Ala Cys Gly Glu Gly Ala Ala Asp Ile
1 5 10 15

Ile Ile Gly His Leu Cys Ile Arg His Glu Met Thr Pro Val Asn Pro
20 25 30

Gly Arg

<210> 28
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<309> 2008-10-16
<313> (489)..(496)

<400> 28

Glu Met Thr Pro Val Asn Pro Gly
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<210> 29
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<309> 2008-08-02
<313> (141)..(160)

<400> 29

Lys Arg Arg Gln Thr Ser Ala Thr Asp Phe Tyr His Ser Lys Arg Arg
1 5 10 15

Leu Ile Phe Ser
20

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

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<308> NCBI/
<309> 2010-03-04
<313> (417)..(431)

<400> 30

Gly Gly Gly Phe Gln Leu Arg Gln Pro Pro Leu Val Pro Ser Arg Lys
1 5 10 15

Gly Glu

<210> 31
<211> 410
<212> PRT
<213> Mycoplasma arginini

<300>
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<309> 2004-09-09
<313> (1)..(410)

<400> 31

Met Ser Val Phe Asp Ser Lys Phe Lys Gly Ile His Val Tyr Ser Glu
1 5 10 15

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

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

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

Leu Lys Ala Asn Asp Ile Asn Val Val Glu Leu Ile Asp Leu Val Ala
65 70 75 80

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

Glu Phe Leu Glu Asp Ser Glu Pro Val Leu Ser Glu Glu His Lys Val
100 105 110

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

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Glu Ile Met Met Ala Gly Ile Thr Lys Tyr Asp Leu Gly Ile Glu Ala
    130                 135                 140

Asp His Glu Leu Ile Val Asp Pro Met Pro Asn Leu Tyr Phe Thr Arg
145                 150                 155                 160

Asp Pro Phe Ala Ser Val Gly Asn Gly Val Thr Ile His Tyr Met Arg
                165                 170                 175

Tyr Lys Val Arg Gln Arg Glu Thr Leu Phe Ser Arg Phe Val Phe Ser
            180                 185                 190

Asn His Pro Lys Leu Ile Asn Thr Pro Trp Tyr Tyr Asp Pro Ser Leu
        195                 200                 205

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

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

Leu Ala Lys Asn Ile Val Ala Asn Lys Glu Cys Glu Phe Lys Arg Ile
                245                 250                 255

Val Ala Ile Asn Val Pro Lys Trp Thr Asn Leu Met His Leu Asp Thr
            260                 265                 270

Trp Leu Thr Met Leu Asp Lys Asp Lys Phe Leu Tyr Ser Pro Ile Ala
        275                 280                 285

Asn Asp Val Phe Lys Phe Trp Asp Tyr Asp Leu Val Asn Gly Gly Ala
    290                 295                 300

Glu Pro Gln Pro Val Glu Asn Gly Leu Pro Leu Glu Gly Leu Leu Gln
305                 310                 315                 320

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

Ala Ser Gln Met Glu Ile Glu Arg Glu Thr His Phe Asp Gly Thr Asn
            340                 345                 350

Tyr Leu Ala Ile Arg Pro Gly Val Val Ile Gly Tyr Ser Arg Asn Glu
        355                 360                 365

Lys Thr Asn Ala Ala Leu Glu Ala Ala Gly Ile Lys Val Leu Pro Phe
    370                 375                 380
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His Gly Asn Gln Leu Ser Leu Gly Met Gly Asn Ala Arg Cys Met Ser
385                 390                 395                 400


Met Pro Leu Ser Arg Lys Asp Val Lys Trp
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<210> 32
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<400> 32

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1               5                   10
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<210> 33
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<308> NCBI NP_001182061.1
<309> 2011-02-19
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Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
1               5                   10                  15


Ala Gly Ala Arg Val Val Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg
            20                  25                  30


Arg Met Lys Trp Lys Lys
        35
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<210> 34
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<309> 2010-04-19
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1 5 10

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<309> 2006-07-15
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<400> 35

Ala Val Thr Asp His Pro Asp Arg Leu Trp Ala Trp Glu Lys Phe
1 5 10 15

<210> 36
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<213> Homo sapiens

<300>
<302> Transcription factor E2F DNA-binding domain inhibitor peptides and their use
<308> USPTO
<309> 2003-01-16
<310> US6841385
<311> 2001-07-26
<312> 2003-01-16

<400> 36

Phe Trp Leu Arg Phe Thr
1 5

<210> 37
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<300>
<301> Pieraccini, S., Salamino, G., Cappelletti, G., Cartelli, D., Francescato, P., Speranza, G., Manisto, P., Sironi, M
<302> In silico design of tubulin - targeted antimitotic peptides
<303> Nature Chemistry
<304> 23
<306> 642 - 648
<307> 2009-09-23

<400> 37

Phe Arg Arg Lys Ala Phe Leu His Trp Tyr Thr Gly Arg
1 5 10

<210> 38
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<300>
<301> Pieraccini, S., Salamino, G., Cappelletti, G., Cartelli, D., Francescato, P., Speranza, G., Manisto, P., Sironi, M.,
<302> In silico design of tubulin - targeted antimitotic peptides,
<303> Nature Chemistry
<304> 1
<306> 642 - 648
<307> 2009-10-23

<400> 38

Trp Cys Pro Thr Gly Phe Lys Val Gly Arg
1 5 10

<210> 39
<211> 25
<212> PRT
<213> Apis mellifera

<300>
<308> GenBank/ AAU87881.1
<309> 2004-10-04
<313> (1)..(25)

<400> 39

Gly Ile Gly Ala Arg Leu Lys Val Leu Thr Thr Gly Leu Pro Arg Ile
1 5 10 15

Ser Trp Ile Lys Arg Lys Arg Gln Gln
20 25

<210> 40
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<300>
<301> Iwasaki T, Ishibashi J, Kubo M, Taylor D, Yamakawa M.
<302> Multiple functions of short synthetic enantiomeric peptides based on beetle defensins
<303> Biosci Biotechnol Biochem
<304> 73
<305> 3
<306> 683-687
<307> 2009-03-23

<400> 40

Ala Leu Tyr Leu Ala Ile
1 5

<210> 41
<211> 8
<212> PRT

<213> Homo sapiens

<300>
<301> Kono K, Ueba T, Takahashi JA, Murai N, Hashimoto N, Myoumoto A, Itoh N,Fukumoto M
<302> In vitro growth suppression of human glioma cells by a 16-mer oligopeptide: a potential new treatment modality for malignant glioma.
<303> J Neurooncol
<304> 63
<305> 2
<306> 163-171
<307> 2003-07-30

<400> 41

Ala Pro Ser Gly His Tyr Lys Gly
1 5

<210> 42
<211> 15
<212> PRT
<213> Lasioglossum laticeps

<300>
<301> Cerovský V, Budesínský M, Hovorka O, Cvacka J, Voburka Z, Slaninová J, Borovicková L, Fucík V, Bednárová L, Votruba I, Straka
<302> Lasioglossins/ three novel antimicrobial peptides from the venom of the eusocial bee Lasioglossum laticeps (Hymenoptera/ Halictidae).
<303> JChembiochem.
<304> 10
<305> 12
<306> 2089-2099
<307> 2009-08-17

<400> 42

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

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

<220>
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<300>
<301> Pamonsinlapatham P, Hadj-Slimane R, Raynaud F, Bickle M, Corneloup C, Barthelaix A, Lepelletier Y, Mercier P, Schapira M, Samson J, Mathieu AL, Hugo N, Moncorgé O, Mikaelian I, Dufour S, Garbay C, Colas P.
<302> A RasGAP SH3 peptide aptamer inhibits RasGAP-Aurora interaction and induces caspase-independent tumor cell death
<303> PLoS One
<304> 3
<305> 8)/e2902
<306> doi:10.1371/journal.pone.0002902

<307> 2008-08-06

<400> 43

Lys Trp Val Val Ser His Ala Arg Leu Met Tyr Ser Phe
1   5   10

<210> 44
<211> 27
<212> PRT
<213> Streptococcus pneumoniae

<300>
<301> Dong Gun Lee1 , Kyung-Soo Hahm2 , Yoonkyung Park2 , Hai-Young
       Kim3 , Weontae Lee3 , Sung-Chul Lim4 , Youn-Kyung Seo5 and
       Cheol-Hee Choi5
<302> Functional and structural characteristics of anticancer peptide
       Pep27 analogues
<303> Cancer Cell International
<304> 5
<305> 21
<306> doi:10.1186/1475-2867-5-21
<307> 2005-07-11

<400> 44

Met Trp Lys Trp Phe His Asn Val Leu Ser Trp Trp Trp Leu Leu Ala
1   5   10   15

Asp Lys Arg Pro Ala Arg Asp Tyr Asn Arg Lys
            20   25

<210> 45
<211> 6
<212> PRT
<213> Homo sapiens

<400> 45

Pro Leu Gly Leu Ala Gly
1   5

<210> 46
<211> 4
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<213> Homo sapiens

<400> 46

Arg Val Val Arg
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<210> 47
<211> 8
<212> PRT
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<220>

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<400> 47

Cys Ala Ala Cys Ala Ala Ala Cys
1 5

<210> 48
<211> 17
<212> PRT
<213> Drosophila melanogaster

<300>
<301> Derossi D, Calvet S, Trembleau A, Brunissen A, Chassaing G, Prochiantz A
<302> Cell
<303> J Biol Chem
<304> 271
<305> 30
<306> 18188-93
<307> 1996-07-26

<400> 48

Asp Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys
1 5 10 15

Lys

<210> 49
<211> 6
<212> PRT
<213> Drosophila melanogaster

<300>
<301> Derossi D, Calvet S, Trembleau A, Brunissen A, Chassaing G, Prochiantz A.
<302> Cell internalization of the third helix of the Antennapedia homeodomain is
<303> J Biol Chem
<304> 271
<305> 30
<306> 18188-93
<307> 1996-07-26

<400> 49

Lys Pro Arg Arg Pro Tyr
1 5

<210> 50
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<212> DNA
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<400> 50
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ctgtgcattc gtcatgaaat gacgccggtt aacccgggtc gtgttgttcg tgaacgtggt 120

ccgcaacgcg ttgcggcaca tattacgggt acccgtggcc gcagcaacac gctgagctct 180

ccgaattcga aaaatgaaaa agcactgggc cgcaaaatta actcgtggga aagcagtcgt 240

tctggtcaca gctttctgtc gaatctgcac ctgcgcaatg gtgaactggt gattcatgaa 300

aaaggctttt actatatcta ttctcagacg tattttcgtt ttcaggaaga aattaaagaa 360

aacaccaaaa atgacaaaca gatggtgcag tacatttaca aatacaccag ttacccggac 420

ccgattctgc tgatgaaaag cgcccgtaac tcatgctgga gcaaagacgc tgaatatggc 480

ctgtattcta tttatcaggg tggcatcttc gaactgaaag aaaacgatcg tatttttgtt 540

tcggtgacca acgaacacct gattgatatg gatcatgaag catcgttttt cggcgcgttt 600

ctggtcggc 609

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gcacatatta cgggtacccg tggccgcagc aacacgctga gctctccgaa ttcgaaaaat 120

gaaaaagcac tgggccgcaa aattaactcg tgggaaagca gtcgttctgg tcacagcttt 180

ctgtcgaatc tgcacctgcg caatggtgaa ctggtgattc atgaaaaagg cttttactat 240

atctattctc agacgtattt tcgttttcag gaagaaatta aagaaaacac caaaaatgac 300

aaacagatgg tgcagtacat ttacaaatac accagttacc cggacccgat tctgctgatg 360

aaaagcgccc gtaactcatg ctggagcaaa gacgctgaat atggcctgta ttctatttat 420

cagggtggca tcttcgaact gaaagaaaac gatcgtattt ttgtttcggt gaccaacgaa 480

cacctgattg atatggatca tgaagcatcg tttttcggcg cgtttctggt cggc 534

<210> 52
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catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttttattata tttatagcca gacctatttt cgctttcagg aagaaattaa agaaaatacc 240

aaaaatgata aacaaatggt gcagtatatc tataaatata ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggcctgtat 360

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 420

accaatgaac atctgattga tatggatcat gaagccagct tttttggtgc atttctggtt 480

ggtccgctgg gtctggcagg tcgtgttgtt cgtgaaatga caccggttaa tccgggt 537

<210> 53
<211> 612
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial

<400> 53
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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 tttttggtgc atttctggtt 480

ggtccgctgg gtctggcagg tcgtgttgtt cgtctgagcg aagataaact gctggcatgt 540

ggtgaaggtg cagccgatat tattattggc catctgtgca ttcgtcatga aatgacaccg 600

gttaatccgg gt 612

<210> 54
<211> 690
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial

<400> 54
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ctgtgcattc gccatgaaat gacaccggtt aatccgggtc gtgttgttcg tcctctgggt 120

ctggcaggca ccagcgaaga aaccattagc accgttcagg aaaaacagca gaatattagt 180

ccgctggttc gtgaacgtgg tccgcagcgt gttgcagcac atattaccgg cacccgtggt 240

cgtagcaata ccctgagcag cccgaatagc aaaaatgaaa aagcactggg tcgcaaaatt 300

aatagctggg aaagcagccg tagcggtcat agctttctga gcaatctgca tctgcgtaat 360

ggtgaactgg tgattcatga aaaaggcttt tattatattt atagccagac ctattttcgc 420

tttcaggaag aaattaaaga aaataccaaa aatgataaac aaatggtgca gtatatctat 480

aaatacacca gctatccgga tccgattctg ctgatgaaaa gcgcacgtaa tagctgttgg 540

agcaaagatg cagaatatgg tctgtatagc atttatcagg gtggcatttt tgaactgaaa 600

gaaaatgatc gcatttttgt gagcgtgacc aatgaacatc tgattgatat ggatcatgaa 660

gccagctttt ttggtgcatt tctggtgggt 690

<210> 55
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial

<400> 55
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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 ttgtgcagca tgtgcagccg catgtccgct gggtctggca 600

ggtcgtgttg ttcgtctgag cgaagataaa ctgctggcat gtggtgaagg tgcagcagat 660

attatcattg gtcatctgtg cattcgccat gaaatgacac cggttaatcc gggt 714

<210> 56
<211> 639
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial

<400> 56

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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 ttgtgcagca tgtgcagccg catgtccgct gggtctggca 600

ggtcgtgttg ttcgtgaaat gacaccggtt aatccgggt 639

<210> 57
<211> 591
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial

<400> 57
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aaaccgcgtc gtccgtatcg tgttgttcgt ccgctgggtc tggcaggtcg tgttgcagca 120

catattaccg gcacccgtgg tcgtagcaat accctgagca gcccgaatag caaaaatgaa 180

aaagccctgg gtcgcaaaat taatagctgg gaaagcagcc gtagcggtca tagctttctg 240

agcaatctgc atctgcgtaa tggtgaactg gtgattcatg aaaaaggctt ttattatatt 300

tatagccaga cctattttcg ctttcaggaa gaaattaaag aaaataccaa aaatgataaa 360

caaatggtgc agtacattta taaatatacc agctatccgg atccgattct gctgatgaaa 420

agcgcacgta atagctgttg gagcaaagat gcagaatatg gcctgtatag catttatcag 480

ggtggcattt ttgaactgaa agaaaatgat cgcatttttg tgagcgtgac caatgaacat 540

ctgattgata tggatcatga agccagcttt tttggtgcat ttctggtggg c 591

<210> 58
<211> 693
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial

<400> 58
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cgtgaacgtg gtccgcagcg tgttgcagca catattaccg gcacccgtgg tcgtagcaat 120

accctgagca gcccgaatag caaaaatgaa aaagcactgg gtcgcaaaat caatagctgg 180

gaaagcagcc gtagcggtca tagctttctg agcaatctgc atctgcgtaa tggtgaactg 240

gtgattcatg aaaaaggctt ttattatatt tatagccaga cctattttcg ctttcaagaa 300

gagattaaag aaaataccaa aaatgataaa caaatggtgc agtatatcta taaatatacc 360

agctatccgg atccgatcct gctgatgaaa agcgcacgta atagctgttg gagcaaagat 420

gcagaatatg gtctgtatag catttatcag ggtggcatct ttgagctgaa agaaaatgat 480

cgcatctttg ttagcgtgac caacgaacat ctgatcgata tggatcatga agccagcttt 540

tttggtgcat ttctggttgg ttgtgcagca tgtgcagccg catgtccgct gggtctggca 600

ggtcgtgttg ttcgtaaacg tcgtcagacc agcgcaaccg atttttatca tagcaaacgt 660

cgcctgatct ttagcaaacc gcgtcgtccg tat 693

<210> 59
<211> 600
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial

<400> 59
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ccgctgggtc tggcgggtgg tggttgcgcg gcggcgtgcg cggcgtgcgg tggtcagcgt 120

gttgcggcgc acatcaccgg tacccgtggt cgttctaaca ccctgtcttc tccgaactct 180

aaaaacgaaa aagcgctggg tcgtaaaatc aactcttggg aatcttctcg ttctggtcac 240

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tactacatct actctcagac ctacttccgt ttccaggaag aaatcaaaga aaacaccaaa 360

aacgacaaac agatggttca gtacatctac aaatacacct cttacccgga cccgatcctg 420

ctgatgaaat ctgcgcgtaa ctcttgctgg tctaaagacg cggaatacgg tctgtactct 480

atctaccagg gtggtatctt cgaactgaaa gaaaacgacc gtatcttcgt ttctgttacc 540

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<210> 60
<211> 699
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial

<400> 60

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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

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ggtctggcag gtcgtgttgt tcgtcgtcgt cgccgtcgtc ggcgtggtgg tggttttcag 660

ctgcgtcagc ctccgctggt tccgagccgt aaaggtgaa 699

<210> 61
<211> 1770
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial

<400> 61
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agcaaaaatg aaaaagcact gggtcgcaaa atcaatagct gggaaagcag ccgtagcggt 120

catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttttattata tttatagcca gacctatttt cgctttcaag aagagattaa agaaaatacc 240

aaaaatgata aacaaatggt gcagtatatc tataaatata ccagctatcc ggacccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 360

agcatttatc agggtggcat ctttgagctg aaagaaaatg atcgcatctt tgttagcgtg 420

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gaaagcgttc tggttcatga accgggtcgt gaaattgatt atattacacc ggcacgtctg 660

gatgaactgc tgtttagcgc aattctggaa agccatgatg cacgtaaaga acataaacag 720

tttgtggcag aactgaaagc caacgatatt aatgtggtgg aactgattga tctggttgca 780

gaaacctatg atctggcaag ccaagaagca aaagataaac tgatcgaaga atttctggaa 840

gatagcgaac cggttctgag cgaagaacat aaagttgttg tgcgcaattt tctgaaagcc 900

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ggtattgaag ccgatcatga actgattgtt gatccgatgc cgaatctgta ttttacccgt 1020

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gaaattgaac gtgaaaccca ttttgatggc accaattatc tggcaattcg tccgggtgtt 1620

gttattggtt atagccgtaa tgagaaaacc aatgcagcac tggaagcagc aggtattaaa 1680

gttctgccgt ttcatggtaa tcagctgagc ctgggtatgg gtaatgcacg ttgtatgagc 1740

atgccgctga gccgtaaaga tgttaaatgg 1770

<210> 62
<211> 561
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial

<400> 62
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ccgctgggtc tggcaggtcg tgttgcagca catattaccg gcacccgtgg tcgtagcaat 120

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gtgattcatg aaaaaggctt ttattatatt tatagccaga cctattttcg ctttcaggaa 300

gaaattaaag aaaataccaa aaatgataaa caaatggtgc agtacattta caaatatacc 360

agctatccgg atccgattct gctgatgaaa agcgcacgta atagctgttg gagcaaagat 420

gcagaatatg gtctgtatag catttatcag ggtggcattt ttgaactgaa agaaaatgat 480

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<210> 63

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

<220>
<223> artificial

<400> 63
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catagctttc tgagcaatct gcatctgcgt aatggtgaac tggtgattca tgaaaaaggc 180

ttttattata tttatagcca gacctatttt cgctttcagg aagaaattaa agaaaatacc 240

aaaaatgata aacaaatggt gcagtatatc tataaatata ccagctatcc ggatccgatt 300

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgcagaata tggtctgtat 360

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 420

accaatgaac atctgattga tatggatcat gaagccagct tttttggtgc atttctggtt 480

ggtggtagtc cgctgggtct ggcaggtcgt gttgttcgtg atcgtcagat taaaatttgg 540

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cagctgaat 609

<210> 64
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial

<400> 64
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agcaaaaatg aaaaagcact 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 tggtctgtat 360

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 420

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gcatgggaaa aattt 615

<210> 65
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial

<400> 65
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gcaggtcgtg ttgcagcaca tattaccggc acccgtggtc gtagcaatac cctgagcagc 120

ccgaatagca aaaatgaaaa agcactgggt cgcaaaatta atagctggga aagcagccgt 180

agcggtcata gctttctgag caatctgcat ctgcgtaatg gtgaactggt gattcatgaa 240

aaaggctttt attatattta tagccagacc tattttcgct ttcaggaaga aattaaagaa 300

aataccaaaa atgataaaca aatggtgcag tacatttaca aatataccag ctatccggat 360

ccgattctgc tgatgaaaag cgcacgtaat agctgttgga gcaaagatgc agaatatggt 420

ctgtatagca tttatcaggg tggcattttt gaactgaaag aaaatgatcg cattttgtg 480

agcgtgacca atgaacatct gattgatatg gatcatgaag ccagcttttt tggtgcattt 540

ctggttggt 549

<210> 66
<211> 570
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial

<400> 66
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cgtagcaata ccctgagcag cccgaatagc aaaaatgaga aagcactggg tcgcaaaatc 180

aatagctggg aaagcagccg tagcggtcat agctttctga gcaatctgca tctgcgtaat 240

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<211> 561
<212> DNA

<213> Artificial Sequence

<220>
<223> artificial

<400> 67
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<210> 68
<211> 588
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial

<400> 68
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attaccggca cccgtggtcg tagcaatacc ctgagcagcc cgaatagcaa aaatgaaaaa 180

gcactgggtc gcaaaattaa tagctgggaa agcagccgta gcggtcatag ctttctgagc 240

aatctgcatc tgcgtaatgg tgaactggtg attcatgaaa aaggctttta ttatatttat 300

agccagacct attttcgctt tcaggaagaa attaaagaaa ataccaaaaa tgataaacaa 360

atggtgcagt acatttacaa atataccagc tatccggatc cgattctgct gatgaaaagc 420

gcacgtaata gctgttggag caaagatgca gaatatggtc tgtatagcat ttatcagggt 480

ggcatttttg aactgaaaga aaatgatcgc atttttgtga gcgtgaccaa tgaacatctg 540

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<210> 69
<211> 552
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<220>

<223> artificial

<400> 69
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agcccgaata gcaaaaatga aaaagcactg ggtcgcaaaa ttaatagctg ggaaagcagc 180

cgtagcggtc atagctttct gagcaatctg catctgcgta atggtgaact ggtgattcat 240

gaaaaaggct tttattatat ttatagccag acctattttc gctttcaaga agaaattaaa 300

gagaatacca aaaacgataa gcagatggtg cagtacattt ataaatatac cagctatccg 360

gatccgattc tgctgatgaa aagcgcacgt aatagctgtt ggagcaaaga tgcagaatat 420

ggtctgtata gcatttatca gggtggcatt tttgaactga aagaaaatga tcgcattttt 480

gtgagcgtga ccaatgaaca tctgattgat atggatcatg aagccagctt ttttggtgca 540

tttctggtgg gt 552

<210> 70
<211> 567
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial

<400> 70
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agtggacatt ataagggagg aggaagggtc gccgcccata taacaggaac aaggggaagg 120

agtaatacac taagtagtcc caatagtaag aatgagaagg ccctaggaag gaagataaat 180

agttgggaga gtagtaggag tggacatagt tttctaagta atctacatct aaggaatgga 240

gagctagtca tacatgagaa gggattttat tatatatata gtcaaacata ttttaggttt 300

caagaggaga taaaggagaa tacaaagaat gataagcaaa tggtccaata tatatataag 360

tatacaagtt atcccgatcc catactacta atgaagagtg ccaggaatag ttgttggagt 420

aaggatgccg agtatggact atatagtata tatcaaggag gaatatttga gctaaaggag 480

aatgatagga tatttgtcag tgtcacaaat gagcatctaa tagatatgga tcatgaggcc 540

agttttttg gagcctttct agtcgga 567

<210> 71
<211> 564
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial

<400> 71

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aataccctga gcagcccgaa tagcaaaaat gaaaaagcac tgggtcgcaa aatcaatagc 180

tgggaaagca gccgtagcgg tcatagcttt ctgagcaatc tgcatctgcg taatggtgaa 240

ctggtgattc atgaaaaagg cttttattat atttatagcc agacctattt tcgctttcaa 300

gaagagatta aagaaaatac caaaaatgac aaacaaatgg tgcaatatat ctacaaatat 360

accagctatc cggacccgat tctgctgatg aaaagcgcac gtaatagctg ttggagcaaa 420

gatgcagaat atggtctgta tagcatttat cagggtggca tctttgagct gaaagaaaat 480

gatcgcatct ttgttagcgt gaccaacgaa catctgatcg atatggatca tgaagccagc 540

ttttttggtg catttctggt gggt 564

<210> 72
<211> 579
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial

<400> 72
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cgtcgtgttg ttcgtccgct gggtctggca ggttgtcgtg ttgcagcaca tattaccggc 120

acccgtggtc gtagcaatac cctgagcagc ccgaatagca aaaatgaaaa agcactgggt 180

cgcaaaatca atagctggga aagcagccgt agcggtcata gctttctgag caatctgcat 240

ctgcgtaatg gtgaactggt gattcatgaa aaaggctttt attatattta tagccagacc 300

tattttcgct ttcaagaaga gattaaagaa aataccaaaa atgacaaaca aatggtgcaa 360

tatatctaca aatataccag ctatccggac ccgattctgc tgatgaaaag cgcacgtaat 420

agctgttgga gcaaagatgc agaatatggt ctgtatagca tttatcaggg tggcatcttt 480

gagctgaaag aaaatgatcg catctttgtt agcgtgacca acgaacatct gatcgatatg 540

gatcatgaag ccagcttttt tggtgcattt ctggtgggt 579

<210> 73
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial

<400> 73
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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

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ggtcgtgttg ttcgtgatgc agcacgtgaa ggttttctgg ataccctggt tgttctgcat 660

cgtgccggtg cacgtgttgt gcgtcagatt aaaatctggt ttcagaatcg tcgcatgaaa 720

tggaaaaag 729

<210> 74
<211> 597
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial

<400> 74
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gcacgtgatt ataatcgtaa acgtgttgtt cgtccgctgg gtctggcagg tcagcgtgtt 120

gcagcacata ttaccggtac ccgtggtcgt agcaataccc tgagcagccc gaatagcaaa 180

aatgaaaaag cactgggtcg taaaattaat agctgggaaa gcagccgtag cggtcatagc 240

tttctgagca atctgcatct gcgtaatggt gaactggtta ttcatgaaaa aggtttttat 300

tatatttata gccagaccta ttttcgtttt caggaagaaa ttaaagaaaa taccaaaaat 360

gataaacaga tggttcagta tatttataaa tataccagct atccggatcc gattctgctg 420

atgaaaagcg cacgtaatag ctgttggagc aaagatgcag aatatggtct gtatagcatt 480

tatcagggtg gtatttttga actgaaagaa aatgatcgta tttttgttag cgttaccaat 540

gaacatctga ttgatatgga tcatgaagca agctttttg gtgcatttct ggttggt 597

<210> 75
<211> 212
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 75

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Leu Ile Phe Ser Lys Pro Arg Arg Pro Tyr Arg Val Val Arg Pro Leu
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Gly Leu Ala Gly Gly Gly Gly Cys Ala Ala Ala Cys Ala Ala Cys Gly
        35                  40                  45

Ser Gly Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser
    50                  55                  60

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

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

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

Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys
        115                 120                 125

Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr
    130                 135                 140

Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser
145                 150                 155                 160

Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly
                165                 170                 175

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

Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala
        195                 200                 205

Phe Leu Val Gly
    210
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<210> 76
<211> 636
<212> DNA
<213> Artificial Sequence

<220>

<223> fusion protein

<400> 76
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aaaccgcgtc gtccgtatcg tgttgttcgt ccgctgggta ttgccggtgg tggtggttgt 120

gcagcagcat gtgcagcctg tggtagcggt cagcgtgttg cagcacatat taccggcacc 180

cgtggtcgta gcaataccct gagcagcccg aatagcaaaa atgaaaaagc actgggtcgc 240

aaaattaaca gctgggaaag cagccgtagt ggtcatagct ttctgagcaa tctgcatctg 300

cgtaatggtg aactggtgat tcatgaaaaa ggcttctact atatctacag ccagacctat 360

tttcgcttcc aagaagagat taaagaaaac accaaaaacg ataaacaaat ggtgcagtac 420

atctataaat acaccagcta tccggatccg attctgctga tgaaaagcgc acgtaatagc 480

tgttggagca aagatgcaga atatggcctg tatagcattt atcagggtgg catctttgaa 540

ctgaaagaaa acgatcgtat tttcgtgagc gtgaccaatg aacatctgat cgatatggat 600

catgaagcca gctttttgg tgcatttctg gtgggt 636

<210> 77
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 77

Gly Gly Gly Cys Ala Ala Ala Cys Ala Ala Cys Gly Ser Gly
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<210> 78
<211> 281
<212> PRT
<213> Homo sapiens

<400> 78

Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys
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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

eolf-seql

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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
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