SEQUENCE LISTING

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<120> DKK-1 Antibodies

<130> X-18097

<150> 61/168411
<151> 2009-04-10

<150> PCT/US2010/030039
<151> 2010-04-06

<160> 52

<170> PatentIn version 3.5

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Gly Phe Thr Phe Ser Ser Tyr Thr Met Ser
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<400> 2

Thr Ile Ser Gly Gly Gly Phe Gly Thr Tyr Tyr Pro Asp Ser Val Lys
1 5 10 15

Gly

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Pro Gly Tyr His Asn Tyr Tyr Phe Asp Ile
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<400> 4

Pro Gly Tyr Asn Asn Tyr Tyr Phe Asp Ile
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His Ala Ser Asp Ser Ile Ser Asn Ser Leu His
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<400> 6

Tyr Gly Arg Gln Ser Ile Gln
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Gln Gln Ser Glu Ser Trp Pro Leu His
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<400> 8

Tyr Ala Arg Gln Ser Ile Gln
1 5

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<400> 9

Gln Gln Ser Ala Ser Trp Pro Leu His
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Tyr Ala Arg Gln Ser Glu Gln
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<400> 11

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Gly Gly Gly Phe Gly Thr Tyr Tyr Pro Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Gly Tyr His Asn Tyr Tyr Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
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<400> 12

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Thr Ile Ser Gly Gly Gly Phe Gly Thr Tyr Tyr Pro Asp Ser Val
    50                  55                  60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Pro Gly Tyr Asn Asn Tyr Tyr Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser
        115
```

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<400> 13

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

Glu Arg Ala Thr Leu Ser Cys His Ala Ser Asp Ser Ile Ser Asn Ser
            20                  25                  30

Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45

Tyr Tyr Gly Arg Gln Ser Ile Gln Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60
```

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

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

His Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

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<212> PRT
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<223> Synthetic Construct

<400> 14

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys His Ala Ser Asp Ser Ile Ser Asn Ser
20 25 30

Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Tyr Ala Arg Gln Ser Ile Gln Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

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

His Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

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

<220>
<223> Synthetic Construct

<400> 15

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys His Ala Ser Asp Ser Ile Ser Asn Ser
20 25 30

Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Tyr Gly Arg Gln Ser Ile Gln Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

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

His Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys His Ala Ser Asp Ser Ile Ser Asn Ser
20 25 30

Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

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

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

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

His Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

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

<220>
<223> Synthetic Construct

<400> 17

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Thr Ile Ser Gly Gly Gly Phe Gly Thr Tyr Tyr Pro Asp Ser Val
    50                  55                  60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Pro Gly Tyr His Asn Tyr Tyr Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210>  18
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<223>  Synthetic Construct

<400>  18

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Thr Ile Ser Gly Gly Gly Phe Gly Thr Tyr Tyr Pro Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Pro Gly Tyr Asn Asn Tyr Tyr Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 19
<211> 214
<212> PRT
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<220>
<223> Synthetic Construct

<400> 19

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

Glu Arg Ala Thr Leu Ser Cys His Ala Ser Asp Ser Ile Ser Asn Ser
            20                  25                  30

Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45

Tyr Tyr Gly Arg Gln Ser Ile Gln Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60

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

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

His Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110
```

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

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 20
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 20

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys His Ala Ser Asp Ser Ile Ser Asn Ser
20 25 30

Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Tyr Ala Arg Gln Ser Ile Gln Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

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

His Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

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

```
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

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

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

Phe Asn Arg Gly Glu Cys
    210
```

<210> 21
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 21

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

Glu Arg Ala Thr Leu Ser Cys His Ala Ser Asp Ser Ile Ser Asn Ser
            20                  25                  30

Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45

Tyr Tyr Gly Arg Gln Ser Ile Gln Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60

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

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

His Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125
```

```
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

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

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

Phe Asn Arg Gly Glu Cys
    210
```

<210> 22
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 22

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

Glu Arg Ala Thr Leu Ser Cys His Ala Ser Asp Ser Ile Ser Asn Ser
            20                  25                  30

Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45

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

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

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

His Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

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

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140
```

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 23
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<400> 23
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acagccgccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

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gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacaca gaagagcctc 1320

tccctgtctc tgggt 1335

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

<220>
<223> Synthetic Construct

<400> 24
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ccagggaagg ggctggagtg ggtggccacc atttccggtg gtggtttcgg cacatactat 180

cccgacagtg tgaagggtcg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagacctgga 300

tataataact actactttga catctggggc caagggacca cggtcaccgt ctcctcagcc 360

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aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac gaagacctac 600

acctgcaacg tagatcacaa gcccagcaac accaaggtgg acaagagagt tgagtccaaa 660

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ggccaggctc ccaggctcct catctattat ggcagacagt ccatccaggg catcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240

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ggccaggctc ccaggctcct catctattat gctagacagt ccatccaggg catcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240

gaagattttg cagtttatta ctgtcaacag agtgagagct ggccgctcca cttcggcgga 300

gggaccaagg tggagatcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gc 642

<210> 27
<211> 642
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 27
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgcc acgccagcga cagtattagc aacagcctac actggtacca acagaaacct 120

ggccaggctc ccaggctcct catctattat ggcagacagt ccatccaggg catcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240

gaagattttg cagtttatta ctgtcaacag agtgccagct ggccgctcca cttcggcgga 300

gggaccaagg tggagatcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gc 642

<210> 28
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 28
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgcc acgccagcga cagtattagc aacagcctac actggtacca acagaaacct 120

ggccaggctc ccaggctcct catctattat gctagacagt ccgagcaggg catcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240

gaagattttg cagtttatta ctgtcaacag agtgccagct ggccgctcca cttcggcgga 300

gggaccaagg tggagatcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gc 642

<210> 29
<211> 235
<212> PRT
<213> Homo sapiens

<400> 29

Thr Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro
1 5 10 15

```
Pro Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val Ser Ala Ala
            20                  25                  30

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

Tyr Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp Glu
    50                  55                  60

Tyr Cys Ala Ser Pro Thr Arg Gly Gly Asp Ala Gly Val Gln Ile Cys
65                  70                  75                  80

Leu Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Arg His Ala Met Cys
                85                  90                  95

Cys Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Val Ser Ser Asp Gln
            100                 105                 110

Asn His Phe Arg Gly Glu Ile Glu Glu Thr Ile Thr Glu Ser Phe Gly
        115                 120                 125

Asn Asp His Ser Thr Leu Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser
    130                 135                 140

Ser Lys Met Tyr His Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg
145                 150                 155                 160

Ser Ser Asp Cys Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser
                165                 170                 175

Lys Ile Cys Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His
            180                 185                 190

Arg Arg Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys
        195                 200                 205

Gly Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser
    210                 215                 220

Asn Ser Ser Arg Leu His Thr Cys Gln Arg His
225                 230                 235
```

<210> 30
<211> 234
<212> PRT
<213> Cebus albifrons

<400> 30

```
Thr Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro
1               5                   10                  15
```

```
Pro Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val Ser Ala Ala
            20                  25                  30

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

Tyr Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp Glu
    50                  55                  60

Tyr Cys Ala Ser Pro Thr Arg Gly Gly Asp Ala Gly Val Gln Ile Cys
65                  70                  75                  80

Leu Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Arg His Ala Met Cys
                85                  90                  95

Cys Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Val Ser Ser Asp Gln
            100                 105                 110

Asn Asn Phe Arg Gly Glu Ile Glu Glu Thr Ile Thr Glu Ser Phe Gly
        115                 120                 125

Asn Asp His Ser Thr Leu Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser
    130                 135                 140

Ser Lys Met Tyr His Ser Lys Gly Gln Glu Gly Ser Val Cys Leu Arg
145                 150                 155                 160

Ser Ser Asp Cys Ala Thr Gly Leu Cys Cys Ala Arg His Phe Trp Ser
                165                 170                 175

Lys Ile Cys Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His
            180                 185                 190

Arg Arg Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys
        195                 200                 205

Gly Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser
    210                 215                 220

Asn Ser Ser Arg Leu His Thr Cys Gln Arg
225                 230

<210>  31
<211>  252
<212>  PRT
<213>  Rattus rattus

<400>  31

Thr Leu Asn Ser Val Leu Ile Asn Ser Asn Ala Ile Lys Asn Leu Pro
1               5                   10                  15

Pro Pro Leu Gly Gly Ala Gly Gly Gln Pro Gly Ser Ala Val Ser Val
```

20 25 30

Ala Pro Gly Val Leu Tyr Glu Gly Gly Asn Lys Tyr Gln Thr Leu Asp
35 40 45

Asn Tyr Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp
50 55 60

Glu Tyr Cys Ser Ser Pro Ser Arg Gly Ala Ala Gly Val Gly Gly Val
65 70 75 80

Gln Ile Cys Leu Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Arg His
85 90 95

Ala Met Cys Cys Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Met Pro
100 105 110

Ser Asp His Ser His Leu Pro Arg Gly Glu Ile Glu Glu Gly Ile Ile
115 120 125

Glu Asn Leu Gly Asn Asp His Gly Ala Gly Asp Gly Tyr Pro Arg Arg
130 135 140

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

Val Cys Leu Arg Ser Ser Asp Cys Ala Thr Gly Leu Cys Cys Ala Arg
165 170 175

His Phe Trp Ser Lys Ile Cys Lys Pro Val Leu Lys Glu Gly Gln Val
180 185 190

Cys Thr Lys His Arg Arg Lys Gly Ser His Gly Leu Glu Ile Phe Gln
195 200 205

Arg Cys Tyr Cys Gly Glu Gly Leu Ala Cys Arg Ile Gln Lys Asp His
210 215 220

His Gln Thr Ser Asn Ser Ser Arg Leu His Thr Cys Gln Arg His Ala
225 230 235 240

Phe Ile Asp Tyr Lys Asp Asp Asp Asp Lys His Val
245 250

<210> 32
<211> 236
<212> PRT
<213> Lepus americanus

<400> 32

Thr Leu Asn Ser Val Leu Val Asn Ser Asn Ala Ile Lys Asn Leu Pro
1 5 10 15

```
Pro Pro Leu Gly Gly Ala Asn Gly His Pro Gly Ser Ala Val Ser Ala
            20                  25                  30

Thr Pro Gly Ile Leu Tyr Glu Gly Gly Asn Lys Tyr Leu Pro Leu Asp
        35                  40                  45

Asn Tyr Gln Pro Tyr Pro Cys Thr Glu Asp Glu Glu Cys Gly Thr Asp
    50                  55                  60

Glu Tyr Cys Ala Ser Pro Ala Arg Gly Gly Gly Ala Gly Val Gln Ile
65                  70                  75                  80

Cys Leu Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Arg His Ala Met
                85                  90                  95

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

His Asn His Phe His Arg Gly Glu Ile Glu Glu Thr Ile Val Glu Ser
        115                 120                 125

Phe Gly Asn Asp His Ser Thr Ser Asp Gly Tyr Ser Arg Arg Thr Thr
    130                 135                 140

Leu Ser Ser Lys Met Tyr His Ala Lys Gly Gln Glu Gly Ser Val Cys
145                 150                 155                 160

Leu Arg Ser Ser Asp Cys Ala Thr Gly Leu Cys Cys Ala Arg His Phe
                165                 170                 175

Trp Ser Lys Ile Cys Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr
            180                 185                 190

Lys His Arg Arg Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys
        195                 200                 205

Tyr Cys Gly Asp Gly Leu Ser Cys Arg Leu Gln Asn Asp Gln His Glu
    210                 215                 220

Ala Ser Asn Ser Ser Arg Leu His Thr Cys Gln Arg
225                 230                 235


<210>  33
<211>  241
<212>  PRT
<213>  Mus musculus

<400>  33

Thr Leu Asn Ser Val Leu Ile Asn Ser Asn Ala Ile Lys Asn Leu Pro
1               5                   10                  15
```

Pro Pro Leu Gly Gly Ala Gly Gly Gln Pro Gly Ser Ala Val Ser Val
20 25 30

Ala Pro Gly Val Leu Tyr Glu Gly Gly Asn Lys Tyr Gln Thr Leu Asp
35 40 45

Asn Tyr Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Ser Asp
50 55 60

Glu Tyr Cys Ser Ser Pro Ser Arg Gly Ala Ala Gly Val Gly Gly Val
65 70 75 80

Gln Ile Cys Leu Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Thr His
85 90 95

Ala Met Cys Cys Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Met Pro
100 105 110

Ser Asp His Ser His Phe Pro Arg Gly Glu Ile Glu Glu Ser Ile Ile
115 120 125

Glu Asn Leu Gly Asn Asp His Asn Ala Ala Ala Gly Asp Gly Tyr Pro
130 135 140

Arg Arg Thr Thr Leu Thr Ser Lys Ile Tyr His Thr Lys Gly Gln Glu
145 150 155 160

Gly Ser Val Cys Leu Arg Ser Ser Asp Cys Ala Ala Gly Leu Cys Cys
165 170 175

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

Gln Val Cys Thr Lys His Lys Arg Lys Gly Ser His Gly Leu Glu Ile
195 200 205

Phe Gln Arg Cys Tyr Cys Gly Glu Gly Leu Ala Cys Arg Ile Gln Lys
210 215 220

Asp His His Gln Ala Ser Asn Ser Ser Arg Leu His Thr Cys Gln Arg
225 230 235 240

His

<210> 34
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 34

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

Asp Ser Val Ser Leu Ser Cys Arg Ala Ser Asp Ser Ile Ser Gly Ser
20 25 30

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

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Thr
65 70 75 80

Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Asn Ser Trp Pro Leu
85 90 95

Asn Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala
100 105 110

Pro Thr Val Ser Ile Phe Pro Pro Ser Thr Glu Gln Leu Ala Thr Gly
115 120 125

Gly Ala Ser Val Val Cys Leu Met Asn Asn Phe Tyr Pro Arg Asp Ile
130 135 140

Ser Val Lys Trp Lys Ile Asp Gly Thr Glu Arg Arg Asp Gly Val Leu
145 150 155 160

Asp Ser Val Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
165 170 175

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

Thr Cys Glu Val Val His Lys Thr Ser Ser Ser Pro Val Val Lys Ser
195 200 205

Phe Asn Arg Asn Glu Cys
210

<210> 35
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 35

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

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
        35                  40                  45

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

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

Leu Gln Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Arg Pro Gly Tyr Asn Asn Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
        115                 120                 125

Pro Leu Ala Pro Gly Thr Ala Leu Lys Ser Asn Ser Met Val Thr Leu
    130                 135                 140

Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp
145                 150                 155                 160

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

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

Thr Trp Pro Ser Gln Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
        195                 200                 205

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

Cys Lys Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe Ile
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys
                245                 250                 255

Val Thr Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val His
            260                 265                 270
```

Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Arg
275 280 285

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

Pro Ile Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys
305 310 315 320

Val Thr Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys
325 330 335

Pro Glu Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro Thr
340 345 350

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

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

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

Ser Tyr Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp Gln
405 410 415

Gln Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn
420 425 430

His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
435 440 445

<210> 36
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 36

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

Asp Ser Val Ser Leu Ser Cys Arg Ala Ser Asp Ser Ile Ser Gly Ser
20 25 30

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

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Thr
65 70 75 80

Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Asn Ser Trp Pro Leu
85 90 95

Asn Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 37
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 37

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

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

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

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

Leu Gln Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Arg Pro Gly Tyr Asn Asn Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser
115

<210> 38
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 38

Thr Ile Ser Gly Gly Gly Gly Asn Thr Tyr Tyr Pro Asp Ser Val Lys

1 5 10 15

Gly

<210> 39
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 39

Pro Gly Tyr Asn Asn Tyr Tyr Phe Asp Tyr
1 5 10

<210> 40
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 40

Arg Ala Ser Asp Ser Ile Ser Gly Ser Leu His
1 5 10

<210> 41
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 41

Tyr Ala Ser Gln Ser Ile Ser
1 5

<210> 42
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 42

Gln Gln Ser Asn Ser Trp Pro Leu Asn
1 5

<210> 43
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa at position 7 = Phe or Gly

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa at position 8 = Gly or Asn

<400> 43

Thr Ile Ser Gly Gly Gly Xaa Xaa Thr Tyr Tyr Pro Asp Ser Val Lys
1 5 10 15

Gly

<210> 44
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa at position 4 = His or Asn

<400> 44

Pro Gly Tyr Xaa Asn Tyr Tyr Phe Asp Ile
1 5 10

<210> 45
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa at position 4 = His or Asn

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa at position 10 = Ile or Tyr

<400> 45

Pro Gly Tyr Xaa Asn Tyr Tyr Phe Asp Xaa
1 5 10

<210> 46
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa at position 1 = His or Arg

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa at position 8 = Asn or Gly

<400> 46

Xaa Ala Ser Asp Ser Ile Ser Xaa Ser Leu His
1 5 10

<210> 47
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa at position 2 = Gly or Ala

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa at position 6 = Ile or Glu

<400> 47

Tyr Xaa Arg Gln Ser Xaa Gln
1 5

<210> 48
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa at position 2 = Gly or Ala

<220>
<221> MISC_FEATURE
<222> (3)..(3)

<223> Xaa at position 3 = Arg or Ser

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa at position 6 = Ile or Glu

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa at position 7 = Gln or Ser

<400> 48

Tyr Xaa Xaa Gln Ser Xaa Xaa
1 5

<210> 49
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa at position 4 = Glu or Ala

<400> 49

Gln Gln Ser Xaa Ser Trp Pro Leu His
1 5

<210> 50
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa at position 4 = Glu, Ala or Asn

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa at position 9 = His or Asn

<400> 50

Gln Gln Ser Xaa Ser Trp Pro Leu Xaa
1 5

<210> 51
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (102)..(102)
<223> Xaa at position 102 = His or Asn

<400> 51

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Gly Gly Gly Phe Gly Thr Tyr Tyr Pro Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Pro Gly Tyr Xaa Asn Tyr Tyr Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 52
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (51)..(51)
<223> Xaa at position 51 = Gly or Ala

<220>
<221> MISC_FEATURE
<222> (55)..(55)
<223> Xaa at position 55 = Ile or Glu

<220>
<221> MISC_FEATURE
<222> (92)..(92)
<223> Xaa at position 92 = Glu or Ala

<400> 52

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

Glu Arg Ala Thr Leu Ser Cys His Ala Ser Asp Ser Ile Ser Asn Ser
            20                  25                  30

Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45

Tyr Tyr Xaa Arg Gln Ser Xaa Gln Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Xaa Ser Trp Pro Leu
                85                  90                  95

His Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
```