SEQUENCE LISTING

<110> SIAMAB THERAPEUTICS, INC.

<120> GLYCAN-INTERACTING COMPOUNDS AND METHODS OF USE

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<151> 2015-11-12

<160> 266

<170> PatentIn version 3.5

<210> 1
<211> 115
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<400> 1
Gln Val Gln Leu Leu Gln Tyr Asp Ala Glu Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30

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

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Ser Glu Lys Phe
    50   55   60

```
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80


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


Lys Arg Ser Ile Thr Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110


Val Ser Ala
        115
```

<210> 2
<211> 106
<212> PRT
<213> Mus sp.

<400> 2

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Asp Ile Gln Met Asn Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15


Asp Thr Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
            20                  25                  30


Leu Ser Trp Tyr Gln Gln Lys Pro Gly Asn Ile Pro Lys Leu Leu Ile
        35                  40                  45


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


Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Gln Ser Tyr Pro Tyr
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Leu Lys Lys
            100                 105
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<210> 3
<211> 115
<212> PRT

<213> Mus sp.

<400> 3
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30

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

Gly Tyr Ile Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80

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

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100   105   110

Val Ser Ala
        115

<210> 4
<211> 108
<212> PRT
<213> Mus sp.

<400> 4
Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly
1   5   10   15

Glu Arg Val Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Ile Tyr
            20   25   30

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

Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly

```
    50                  55                  60

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

Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105
```

<210> 5
<211> 115
<212> PRT
<213> Mus sp.

<400> 5

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30

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

Gly Tyr Val Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

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

Lys Arg Ser Leu Ile Gly Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
            100                 105                 110

Val Ser Ser
        115
```

<210> 6

<211> 107
<212> PRT
<213> Mus sp.

<400> 6
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Ser Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
            20   25   30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Phe Leu Ile
        35   40   45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
65   70   75   80

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 7
<211> 115
<212> PRT
<213> Mus sp.

<400> 7
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30

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

Gly Tyr Leu Ser Pro Gly Asn Asp Asp Ile Lys Tyr Ser Glu Lys Phe
    50   55   60

```
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80


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


Lys Arg Ser Ile Gly Gly Asp His Trp Gly Gln Gly Thr Thr Leu Thr
            100                 105                 110


Val Ser Ser
        115


<210> 8
<211> 108
<212> PRT
<213> Mus sp.

<400> 8
Asp Ile Gln Met Asn Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15


Asp Thr Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Asn Ile Pro Lys Leu Leu Ile
        35                  40                  45


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


Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Gly Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Gln Ser Tyr Pro Phe
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105


<210> 9
<211> 115
<212> PRT
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<213> Mus sp.

<400> 9
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30

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

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80

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

Gln Arg Gln Leu Gly Gln Gly Tyr Trp Gly Gln Gly Thr Thr Leu Thr
            100   105   110

Val Ser Ser
        115

<210> 10
<211> 113
<212> PRT
<213> Mus sp.

<400> 10
Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1   5   10   15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20   25   30

Tyr Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35   40   45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro

```
    50                  55                  60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Asn
                85                  90                  95

Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110

Arg
```

<210> 11
<211> 115
<212> PRT
<213> Mus sp.

<400> 11

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asp His
            20                  25                  30

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

Gly Tyr Ile Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

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

Glu Arg Ser Met Ile Gly Val Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110

Val Ser Ala
```

115

<210> 12
<211> 112
<212> PRT
<213> Mus sp.

<400> 12
Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Thr Val Ser Leu Gly
1 5 10 15

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

Asn Gly Asn Thr Tyr Leu Gln Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Cys Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

Thr His Ala Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 13
<211> 114
<212> PRT
<213> Mus sp.

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

Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

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

```
Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

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

Lys Ile Ser Tyr Tyr Gly Ile Trp Gly Gln Gly Thr Thr Leu Thr Val
            100                 105                 110

Ser Ser
```

<210> 14
<211> 107
<212> PRT
<213> Mus sp.

<400> 14

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

Glu Ser Val Thr Ile Thr Cys Arg Leu Ser Glu Asp Ile Tyr Ser Asn
            20                  25                  30

Leu Ala Trp Phe Gln Gln Arg Pro Gly Lys Ser Pro Gln Leu Leu Val
        35                  40                  45

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

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65                  70                  75                  80

Glu Asp Phe Gly Thr Tyr Tyr Cys Gln His Phe Trp Gly Thr Pro Phe
                85                  90                  95

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

<210> 15
<211> 114
<212> PRT
<213> Mus sp.

<400> 15
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30

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

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
    50   55   60

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

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

Lys Arg Ser Tyr Tyr Gly Asp Trp Gly Gln Gly Thr Thr Leu Thr Val
            100   105   110

Ser Ser

<210> 16
<211> 107
<212> PRT
<213> Mus sp.

<400> 16
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Val Ser Val Gly
1   5   10   15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser His
            20   25   30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val

```
        35                  40                  45

Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile His Ser Leu Gln Ser
65                  70                  75                  80

Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Gly Ala Pro Phe
                85                  90                  95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 17
<211> 115
<212> PRT
<213> Mus sp.

<400> 17

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30

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

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Val Lys Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

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

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

Val Ser Ser
```

115

<210> 18
<211> 108
<212> PRT
<213> Mus sp.

<400> 18
Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly
1 5 10 15

Glu Arg Val Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr
20 25 30

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

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

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

Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 19
<211> 115
<212> PRT
<213> Mus sp.

<400> 19
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Thr
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

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

```
Gly Tyr Ile Ser Pro Gly Asn Asp Asp Ile Lys Tyr Ser Glu Lys Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

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

Lys Arg Ser Leu Ser Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110

Val Ser Ala
        115
```

<210> 20
<211> 114
<212> PRT
<213> Mus sp.

<400> 20

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

Glu Lys Val Thr Met Ser Cys Arg Ser Ser Gln Ser Leu Leu Asn Ser
            20                  25                  30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
                85                  90                  95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
            100                 105                 110
```

Lys Arg

<210> 21
<211> 114
<212> PRT
<213> Mus sp.

<400> 21
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30

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

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Val Lys Tyr Ser Glu Arg Phe
    50   55   60

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

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

Lys Arg Ser Leu Ser Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100   105   110

Val Ser

<210> 22
<211> 114
<212> PRT
<213> Mus sp.

<400> 22
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1   5   10   15

Glu Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser

```
            20                  25                  30

Gly Asn Gln Lys Ser Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

Pro Pro Lys Leu Leu Ile Ser Trp Ala Ser Thr Arg Asp Ser Gly Val
    50                  55                  60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Ser
                85                  90                  95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
            100                 105                 110

Lys Arg
```

<210> 23
<211> 115
<212> PRT
<213> Mus sp.

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (111)..(111)
<223> Any amino acid

<400> 23

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
        35                  40                  45
```

```
Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60

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

Met Gln Leu Asn Ser Leu Ser Ser Asp Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95

Lys Arg Ser Leu Ser Thr Pro Tyr Trp Gly Gln Gly Thr Leu Xaa Thr
            100                 105                 110

Val Ser Ala
        115
```

<210> 24
<211> 114
<212> PRT
<213> Mus sp.

<400> 24

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

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Arg
            20                  25                  30

Gly Asn His Lys Asn Tyr Leu Thr Trp Tyr Arg Gln Lys Pro Gly Leu
        35                  40                  45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

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

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
                85                  90                  95

Asp Tyr Thr Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
            100                 105                 110
```

Lys Arg

<210> 25
<211> 115
<212> PRT
<213> Mus sp.

<400> 25
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30

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

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
    50   55   60

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

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

Lys Arg Ser Ile Thr Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100   105   110

Val Ser Ala
        115

<210> 26
<211> 114
<212> PRT
<213> Mus sp.

<400> 26
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1   5   10   15

```
Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
            20                  25                  30

Gly Lys Thr Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Asn
                85                  90                  95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
            100                 105                 110

Lys Arg
```

<210> 27
<211> 115
<212> PRT
<213> Mus sp.

<400> 27

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

Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30

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

Gly Tyr Ile Ser Pro Gly Asn Asp Asp Ile Lys Tyr Thr Glu Lys Phe
    50                  55                  60

Lys Gly Lys Val Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
```

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


Lys Arg Ser Ile Thr Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110


Val Ser Ala
        115


<210> 28
<211> 115
<212> PRT
<213> Mus sp.

<400> 28
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30


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


Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asp Glu Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80


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


Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110


Val Ser Ala
        115


<210> 29
<211> 115
<212> PRT
<213> Mus sp.
```

<400> 29
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30

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

Gly Tyr Ile Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80

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

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100   105   110

Val Ser Ala
        115

<210> 30
<211> 115
<212> PRT
<213> Mus sp.

<400> 30
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp His
            20   25   30

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

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

<210> 31
<211> 108
<212> PRT
<213> Mus sp.

<400> 31
Asp Ile Gln Met Asn Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Thr Ile Thr Ile Thr Cys His Ala Ser Gln His Ile Asn Phe Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Asn Ile Pro Lys Leu Leu Ile
35 40 45

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

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

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Asp Gln Ser Tyr Pro Tyr
85 90 95

Met Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 32
<211> 115

<212> PRT
<213> Mus sp.

<400> 32
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30

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

Gly Tyr Ile Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80

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

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100   105   110

Val Ser Ala
        115

<210> 33
<211> 115
<212> PRT
<213> Mus sp.

<400> 33
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30

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

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Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Thr Thr Ala Tyr
65                  70                  75                  80

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

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110

Val Ser Ala
        115
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<210> 34
<211> 107
<212> PRT
<213> Mus sp.

<400> 34

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Asp Ile Gln Met Asn Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15

Asp Thr Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
            20                  25                  30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Asn Ile Pro Lys Leu Leu Ile
        35                  40                  45

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

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln His Asp Gln Ser Tyr Pro Tyr
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105
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<210> 35
<211> 115
<212> PRT
<213> Mus sp.

<400> 35
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp His
            20   25   30

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

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Ile Glu Lys Phe
    50   55   60

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

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

Lys Arg Ser Leu Ser Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100   105   110

Val Ser Ala
        115

<210> 36
<211> 110
<212> PRT
<213> Mus sp.

<400> 36
Asn Ile Leu Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly
1   5   10   15

Glu Arg Val Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Asn Tyr
            20   25   30

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

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

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

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

Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100   105   110

<210> 37
<211> 109
<212> PRT
<213> Mus sp.

<400> 37
Asn Ile Leu Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly
1   5   10   15

Glu Arg Val Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Asn Tyr
            20   25   30

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

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

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

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

Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100   105

<210> 38
<211> 115

<212> PRT
<213> Mus sp.

<400> 38
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Thr
1   5   10   15

Ser Val Lys Ile Ser Cys Arg Ala Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30

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

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80

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

Lys Arg Ser Ile Thr Thr Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr
            100   105   110

Val Ser Ser
        115

<210> 39
<211> 105
<212> PRT
<213> Mus sp.

<400> 39
Ser Phe Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Asn Asn Asn
            20   25   30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Gln Leu Ile
        35   40   45

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

Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Tyr Thr Val Gln Ala
65                  70                  75                  80

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

Thr Phe Gly Gly Gly Thr Lys Leu Lys
            100                 105
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<210> 40
<211> 116
<212> PRT
<213> Mus sp.

<400> 40

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Asp Trp Ile
        35                  40                  45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60

Lys Asp Lys Val Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Cys
65                  70                  75                  80

Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95

Lys Arg Ser Leu Leu Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu
            100                 105                 110

Thr Val Ser Ser
        115
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<210> 41
<211> 107
<212> PRT
<213> Mus sp.

<400> 41
Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
1   5   10   15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Asn
            20   25   30

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

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

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

Glu Asp Leu Thr Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Phe Pro Leu
                85   90   95

Thr Phe Gly Val Gly Thr Lys Leu Glu Leu Lys
            100   105

<210> 42
<211> 116
<212> PRT
<213> Mus sp.

<400> 42
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Asp Trp Ile
        35   40   45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
    50   55   60

Lys Asp Lys Val Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser
65 70 75 80

Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Lys Arg Ser Leu Leu Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu
100 105 110

Thr Val Ser Ser
115

<210> 43
<211> 12
<212> PRT
<213> Mus sp.

<400> 43
Gly Tyr Thr Phe Thr Asp His Ala Ile His Trp Val
1 5 10

<210> 44
<211> 12
<212> PRT
<213> Mus sp.

<400> 44
Gly Tyr Thr Phe Ser Asp His Ala Ile His Trp Val
1 5 10

<210> 45
<211> 12
<212> PRT
<213> Mus sp.

<400> 45
Gly Tyr Ile Phe Thr Asp His Ala Ile His Trp Val
1 5 10

<210> 46
<211> 10
<212> PRT
<213> Mus sp.

<400> 46

Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr
1 5 10

<210> 47
<211> 10
<212> PRT
<213> Mus sp.

<400> 47
Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr
1 5 10

<210> 48
<211> 10
<212> PRT
<213> Mus sp.

<400> 48
Leu Ser Pro Gly Asn Asp Asp Ile Lys Tyr
1 5 10

<210> 49
<211> 10
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<213> Mus sp.

<400> 49
Val Ser Pro Gly Asn Gly Asp Ile Lys Tyr
1 5 10

<210> 50
<211> 10
<212> PRT
<213> Mus sp.

<400> 50
Ile Ser Pro Gly Asn Gly Asp Val Lys Tyr
1 5 10

<210> 51
<211> 10
<212> PRT
<213> Mus sp.

<400> 51
Ile Ser Pro Gly Asn Asp Asp Ile Lys Tyr
1 5 10

<210> 52
<211> 8
<212> PRT
<213> Mus sp.

<400> 52
Ser Val Gly Tyr Ala Leu Asp Tyr
1   5

<210> 53
<211> 7
<212> PRT
<213> Mus sp.

<400> 53
Lys Ile Ser Tyr Tyr Gly Ile
1   5

<210> 54
<211> 7
<212> PRT
<213> Mus sp.

<400> 54
Lys Arg Ser Tyr Tyr Gly Asp
1   5

<210> 55
<211> 8
<212> PRT
<213> Mus sp.

<400> 55
Lys Arg Ser Ile Gly Gly Asp His
1   5

<210> 56
<211> 8
<212> PRT
<213> Mus sp.

<400> 56
Gln Arg Gln Leu Gly Gln Gly Tyr
1   5

<210> 57
<211> 8
<212> PRT
<213> Mus sp.

<400> 57
Lys Arg Ser Leu Ile Gly Asp Tyr
1   5

<210> 58
<211> 8
<212> PRT
<213> Mus sp.

<400> 58
Lys Arg Ser Leu Ser Thr Pro Tyr
1   5

<210> 59
<211> 8
<212> PRT
<213> Mus sp.

<400> 59
Lys Arg Ser Ile Thr Thr Pro Tyr
1   5

<210> 60
<211> 8
<212> PRT
<213> Mus sp.

<400> 60
Glu Arg Ser Met Ile Gly Val Tyr
1   5

<210> 61
<211> 8
<212> PRT
<213> Mus sp.

<400> 61
Lys Arg Ser Ile Thr Thr Ser Tyr
1   5

<210> 62
<211> 6
<212> PRT
<213> Mus sp.

<400> 62
Glu Asn Val Val Thr Tyr
1   5

<210> 63
<211> 6
<212> PRT
<213> Mus sp.

<400> 63
Glu Asp Ile Tyr Ser Asn
1 5

<210> 64
<211> 6
<212> PRT
<213> Mus sp.

<400> 64
Glu Asn Ile Tyr Ser His
1 5

<210> 65
<211> 6
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<213> Mus sp.

<400> 65
Gln Asn Ile Asn Val Trp
1 5

<210> 66
<211> 11
<212> PRT
<213> Mus sp.

<400> 66
Gln Ser Leu Val His Ser Tyr Gly Asn Thr Tyr
1 5 10

<210> 67
<211> 6
<212> PRT
<213> Mus sp.

<400> 67
Gln Asn Val Gly Thr Ala
1 5

<210> 68
<211> 12

<212> PRT
<213> Mus sp.

<400> 68
Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Ser Tyr
1   5   10

<210> 69
<211> 6
<212> PRT
<213> Mus sp.

<400> 69
Gln Ser Val Asn Asn Asn
1   5

<210> 70
<211> 12
<212> PRT
<213> Mus sp.

<400> 70
Gln Ser Leu Leu Asn Arg Gly Asn His Lys Asn Tyr
1   5   10

<210> 71
<211> 11
<212> PRT
<213> Mus sp.

<400> 71
Gln Ser Leu Val Gln Ser Asn Gly Asn Thr Tyr
1   5   10

<210> 72
<211> 6
<212> PRT
<213> Mus sp.

<400> 72
Glu Asn Val Val Asn Tyr
1   5

<210> 73
<211> 12
<212> PRT
<213> Mus sp.

<400> 73

Gln Ser Leu Leu Asn Ser Gly Lys Thr Lys Asn Tyr
1   5   10

<210> 74
<211> 6
<212> PRT
<213> Mus sp.

<400> 74
Gln His Ile Asn Phe Trp
1   5

<210> 75
<211> 6
<212> PRT
<213> Mus sp.

<400> 75
Glu Asn Val Val Ile Tyr
1   5

<210> 76
<211> 12
<212> PRT
<213> Mus sp.

<400> 76
Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr
1   5   10

<210> 77
<211> 7
<212> PRT
<213> Mus sp.

<400> 77
Gly Ala Ser Asn Arg Tyr Thr
1   5

<210> 78
<211> 7
<212> PRT
<213> Mus sp.

<400> 78
Lys Ala Thr Asn Leu Ala Asp
1   5

<210> 79
<211> 7
<212> PRT
<213> Mus sp.

<400> 79
Gly Ala Thr Asn Leu Ala Asp
1 5

<210> 80
<211> 7
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<213> Mus sp.

<400> 80
Lys Ala Ser Asn Leu His Thr
1 5

<210> 81
<211> 7
<212> PRT
<213> Mus sp.

<400> 81
Lys Val Ser Asn Arg Phe Ser
1 5

<210> 82
<211> 7
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<213> Mus sp.

<400> 82
Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 83
<211> 7
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<213> Mus sp.

<400> 83
Trp Ala Ser Thr Arg Asp Ser
1 5

<210> 84
<211> 7
<212> PRT
<213> Mus sp.

<400> 84
Tyr Ala Ser Asn Arg Tyr Thr
1 5

<210> 85
<211> 7
<212> PRT
<213> Mus sp.

<400> 85
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 86
<211> 7
<212> PRT
<213> Mus sp.

<400> 86
Lys Val Ser Asn Arg Phe Cys
1 5

<210> 87
<211> 7
<212> PRT
<213> Mus sp.

<400> 87
Gly Ala Ser Asn Arg Tyr Ser
1 5

<210> 88
<211> 7
<212> PRT
<213> Mus sp.

<400> 88
Lys Val Ser Asn Leu His Thr
1 5

<210> 89
<211> 9
<212> PRT
<213> Mus sp.

<400> 89
Gly Gln Gly Tyr Ser Tyr Pro Tyr Thr
1 5

<210> 90
<211> 9
<212> PRT
<213> Mus sp.

<400> 90
Gln His Phe Trp Gly Thr Pro Phe Thr
1 5

<210> 91
<211> 9
<212> PRT
<213> Mus sp.

<400> 91
Gln His Phe Trp Gly Ala Pro Phe Thr
1 5

<210> 92
<211> 9
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<400> 92
Gln Gln Gly Gln Ser Tyr Pro Phe Thr
1 5

<210> 93
<211> 9
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<213> Mus sp.

<400> 93
Ser Gln Asn Thr His Val Pro Tyr Thr
1 5

<210> 94
<211> 9
<212> PRT
<213> Mus sp.

<400> 94
Gln Gln Tyr Ser Ser Tyr Arg Leu Thr
1 5

<210> 95
<211> 9

<212> PRT
<213> Mus sp.

<400> 95
Gln Ser Asp Tyr Ser Tyr Pro Tyr Thr
1   5

<210> 96
<211> 9
<212> PRT
<213> Mus sp.

<400> 96
Gln Gln Gly Tyr Ser Ser Pro Trp Thr
1   5

<210> 97
<211> 9
<212> PRT
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<400> 97
Gln Asn Asp Tyr Thr Tyr Pro Tyr Thr
1   5

<210> 98
<211> 9
<212> PRT
<213> Mus sp.

<400> 98
Ser Gln Ser Thr His Ala Pro Leu Thr
1   5

<210> 99
<211> 11
<212> PRT
<213> Mus sp.

<400> 99
Gly Ser Lys Trp Ile Thr Ser Tyr Pro Tyr Thr
1   5   10

<210> 100
<211> 10
<212> PRT
<213> Mus sp.

<400> 100

Gly Ala Arg Val Thr Ser Tyr Pro Tyr Thr
1 5 10

<210> 101
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<212> PRT
<213> Mus sp.

<400> 101
Gln Gln Asp Gln Ser Tyr Pro Tyr Thr
1 5

<210> 102
<211> 9
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<400> 102
Lys Asn Asp Tyr Ser Tyr Pro Tyr Thr
1 5

<210> 103
<211> 9
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<400> 103
Gln Gln Asp Gln Ser Tyr Pro Tyr Met
1 5

<210> 104
<211> 9
<212> PRT
<213> Mus sp.

<400> 104
Gln Asn Asp Tyr Ser Tyr Pro Tyr Thr
1 5

<210> 105
<211> 10
<212> PRT
<213> Mus sp.

<400> 105
Gly Tyr Thr Phe Thr Asp His Ala Ile His
1 5 10

<210> 106
<211> 10
<212> PRT
<213> Mus sp.

<400> 106
Gly Tyr Ile Phe Thr Asp His Ala Ile His
1 5 10

<210> 107
<211> 17
<212> PRT
<213> Mus sp.

<400> 107
Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 108
<211> 17
<212> PRT
<213> Mus sp.

<400> 108
Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe Arg
1 5 10 15

Gly

<210> 109
<211> 17
<212> PRT
<213> Mus sp.

<400> 109
Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Val

<210> 110
<211> 17

<212> PRT
<213> Mus sp.

<400> 110
Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe Lys
1   5   10   15

Val

<210> 111
<211> 17
<212> PRT
<213> Mus sp.

<400> 111
Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe Lys
1   5   10   15

Asp

<210> 112
<211> 17
<212> PRT
<213> Mus sp.

<400> 112
Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Lys Phe Lys
1   5   10   15

Gly

<210> 113
<211> 17
<212> PRT
<213> Mus sp.

<400> 113
Tyr Ile Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe Lys
1   5   10   15

Gly

<210> 114
<211> 6
<212> PRT
<213> Mus sp.

<400> 114
Ser Ile Thr Thr Ser Tyr
1 5

<210> 115
<211> 6
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<400> 115
Ser Leu Ser Thr Pro Tyr
1 5

<210> 116
<211> 5
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<400> 116
Ser Tyr Tyr Gly Asp
1 5

<210> 117
<211> 6
<212> PRT
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<400> 117
Ser Ile Thr Thr Pro Tyr
1 5

<210> 118
<211> 7
<212> PRT
<213> Mus sp.

<400> 118
Ser Leu Leu Ala Leu Asp Tyr
1 5

<210> 119
<211> 6
<212> PRT
<213> Mus sp.

<400> 119
Ser Leu Asn Met Ala Tyr
1 5

<210> 120
<211> 5
<212> PRT
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<400> 120
Ser Tyr Tyr Gly His
1 5

<210> 121
<211> 11
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<400> 121
Lys Ala Ser Glu Asn Val Val Thr Tyr Val Ser
1 5 10

<210> 122
<211> 11
<212> PRT
<213> Mus sp.

<400> 122
His Ala Ser Gln His Ile Asn Phe Trp Leu Ser
1 5 10

<210> 123
<211> 17
<212> PRT
<213> Mus sp.

<400> 123
Lys Ser Ser Gln Ser Leu Leu Asn Arg Gly Asn His Lys Asn Tyr Leu
1 5 10 15

Thr

<210> 124
<211> 11
<212> PRT
<213> Mus sp.

<400> 124
Arg Ala Ser Glu Asn Ile Tyr Ser His Leu Ala
1   5   10

<210> 125
<211> 17
<212> PRT
<213> Mus sp.

<400> 125
Lys Ser Ser Gln Ser Leu Leu Asn Ser Gly Lys Thr Lys Asn Tyr Leu
1   5   10   15

Thr

<210> 126
<211> 11
<212> PRT
<213> Mus sp.

<400> 126
Lys Ala Ser Gln Ser Val Asn Asn Asn Val Ala
1   5   10

<210> 127
<211> 11
<212> PRT
<213> Mus sp.

<400> 127
Lys Ala Ser Gln Asp Val Gly Thr Asn Ile Ala
1   5   10

<210> 128
<211> 17
<212> PRT
<213> Mus sp.

<400> 128
Lys Ser Ser Gln Ser Leu Leu Tyr Ser Gly Asn Gln Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 129
<211> 11
<212> PRT
<213> Mus sp.

<400> 129
Arg Ala Ser Glu Asn Ile Tyr Ser Asn Leu Ala
1 5 10

<210> 130
<211> 7
<212> PRT
<213> Mus sp.

<400> 130
Ser Ala Ser Thr Arg His Thr
1 5

<210> 131
<211> 7
<212> PRT
<213> Mus sp.

<400> 131
Trp Ala Ser Ala Arg Glu Ser
1 5

<210> 132
<211> 7
<212> PRT
<213> Mus sp.

<400> 132
Ala Ala Thr Asn Leu Ala Asp
1 5

<210> 133
<211> 9
<212> PRT
<213> Mus sp.

<400> 133
Gln Gln Tyr Ser Ser Phe Pro Leu Thr
1 5

<210> 134
<211> 9
<212> PRT
<213> Mus sp.

<400> 134
Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr
1 5

<210> 135
<211> 9
<212> PRT
<213> Mus sp.

<400> 135
Gln His Phe Trp Gly Thr Pro Tyr Thr
1 5

<210> 136
<211> 10
<212> PRT
<213> Mus sp.

<400> 136
Gly Tyr Thr Phe Ser Asp His Ala Ile His
1 5 10

<210> 137
<211> 17
<212> PRT
<213> Mus sp.

<400> 137
Tyr Ile Ser Pro Gly Asn Gly Asp Val Lys Tyr Ser Glu Arg Phe Lys
1 5 10 15

Gly

<210> 138
<211> 17
<212> PRT
<213> Mus sp.

<400> 138
Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Ser Glu Lys Phe Lys
1 5 10 15

Gly

<210> 139
<211> 17
<212> PRT
<213> Mus sp.

<400> 139
Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asp Glu Lys Phe Lys
1   5   10   15

Gly

<210> 140
<211> 6
<212> PRT
<213> Mus sp.

<400> 140
Gln Leu Gly Gln Gly Tyr
1   5

<210> 141
<211> 6
<212> PRT
<213> Mus sp.

<400> 141
Ser Met Ile Gly Val Tyr
1   5

<210> 142
<211> 11
<212> PRT
<213> Mus sp.

<400> 142
His Ala Ser Gln Asn Ile Asn Val Trp Leu Ser
1   5   10

<210> 143
<211> 17
<212> PRT
<213> Mus sp.

<400> 143
Lys Ser Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Ser Tyr Leu
1   5   10   15

Thr

<210> 144
<211> 11
<212> PRT
<213> Mus sp.

<400> 144
Lys Ala Ser Glu Asn Val Val Ile Tyr Val Ser
1 5 10

<210> 145
<211> 16
<212> PRT
<213> Mus sp.

<400> 145
Arg Ser Ser Gln Ser Leu Val His Ser Tyr Gly Asn Thr Tyr Leu His
1 5 10 15

<210> 146
<211> 16
<212> PRT
<213> Mus sp.

<400> 146
Arg Phe Ser Gln Ser Leu Val Gln Ser Asn Gly Asn Thr Tyr Leu Gln
1 5 10 15

<210> 147
<211> 7
<212> PRT
<213> Mus sp.

<400> 147
Lys Ala Ser Asn Leu Tyr Thr
1 5

<210> 148
<211> 9
<212> PRT
<213> Mus sp.

<400> 148
Gln His Asp Gln Ser Tyr Pro Thr Tyr
1 5

<210> 149
<211> 345
<212> DNA
<213> Mus sp.

<400> 149
caggttcagt tgctgcagta tgacgctgag ttggtgaaac ctgggggtc agtgaagata 60

tcgtgcaagg cctctggcta caccttcact gaccatgcta ttcactgggt gaagcagaag 120

cctgaacagg gcctggaatg gattggatat ttttctcccg gaaatgatga tattaagtac 180

agtgagaagt tcaagggcaa ggccacactg actgcagaca agtcctccag cactgcctac 240

atgcagctca acagcctgac atctgaggat tctgcagtgt atttctgtaa aagatccatt 300

actacgcctt actggggcca agggactctg gtcactgtct ctgca 345

<210> 150
<211> 319
<212> DNA
<213> Mus sp.

<400> 150
gacatccaga tgaaccagtc tccatccagt ctgtctgcat cccttggaga cacaattacc 60

atcacttgcc atgccagtca gaacattaat gtttggttaa gctggtacca gcagaaacca 120

ggaaatattc ctaaactatt gatctataag gtttccaact tgcacacagg cgtcccatca 180

aggtttagtg gcagtggatc tggaacaggt ttcacattaa ccatcagcag cctgcagcct 240

gaagacattg ccacttacta ctgtcaacag gatcaaagtt atccgtacac gttcggaggg 300

gggaccaagc tgaaaaaaa 319

<210> 151
<211> 345
<212> DNA
<213> Mus sp.

<400> 151
caggttcagc tgcagcagtc tgacgctgag ttggtgaaac ctggggcttc agtgaagata 60

tcctgcaagg cctctggcta caccttcact gaccatgcta ttcactgggt gaagcagaag 120

cctgaacagg gcctggaatg gattggatat atttctcccg gaaatgatga tattaagtac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cactgcctac 240

atgcagctca acagcctgac atctgaggat tctgcagtgt atttctgtaa aagatccatt 300

actacgtctt actggggcca agggactctg gtcactgtct ctgca 345

<210> 152
<211> 323
<212> DNA
<213> Mus sp.

<400> 152
aacattgtaa tgacccaatc tcccaaatcc atgtccatgt cagtaggaga gagggtcacc 60

ttgacctgca aggccagtga gaatgtggtt atttatgttt cctggtatca acagaaacca 120

gagcagtctc ctaaactgct gatatacggg gcatccaacc ggtacactgg ggtccccgat 180

cgcttcacag gcagtggatc tgcaacagat ttcactctga ccatcagcag tgtgcaggct 240

gaagaccttg cagattatca ctgtggacag ggttacagct atccgtacac gttcggaggg 300

gggaccaagc tggaaataaa acg 323

<210> 153
<211> 345
<212> DNA
<213> Mus sp.

<400> 153
caggttcagt tgcagcagtc tgacgctgag ttggtgaaac ctggggcttc agtgaagata 60

tcctgcaagg cttctggcta caccttcact gaccatgcca ttcattgggt gaagcagaag 120

cctgaacagg gcctggaatg gattggatat gtttctcccg gaaatggtga tattaagtac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cactgcctac 240

atgcagctca acagcctgac atcggaggat tctgcagtgt atttctgtaa aagatcttta 300

attggagact attggggcca aggcaccact ctcacagtct cctca 345

<210> 154
<211> 322
<212> DNA
<213> Mus sp.

<400> 154
gacattgtga tgacccagtc tcaaaaattc atgtcctcat cagtaggaga cagggtcacc 60

atcacctgca aggccagtca gaatgtgggt actgctgtag cctggtatca acagaaacca 120

ggacaatctc ctaaatttct gatttactcg gcatccaatc ggtacactgg agtccctgat 180

cgcttcacag gcagtggatc tgggacagat ttcactctca cgatcagcaa tatgcagtct 240

gaagacctgg cagattattt ctgccagcaa tatagcagct atcgtctgac gttcggtgga 300

ggcaccaagc tggaaatcaa ac 322

<210> 155
<211> 345
<212> DNA
<213> Mus sp.

<400> 155
caggttcagc tgcagcagtc tgacgctgaa ttggtgaaac ctggggcttc agtgaagata 60

tcctgcaagg cttctggcta caccttcact gaccatgcta ttcactgggt gaagcagaag 120

cctgaacagg gcctggaatg gattggatat ctttctcccg gaaatgatga tattaagtac 180

agtgagaagt tcaaggacaa ggccacactg actgcagaca aatcctccag cactgcctac 240

atgcagctca acagcctgac atctgaggat tctgcagtgt atttctgtaa aagatccata 300

gggggggacc actggggcca aggcaccact ctcacagtct cctca 345

<210> 156
<211> 323
<212> DNA
<213> Mus sp.

<400> 156
gacatccaga tgaaccagtc tccatccagt ctgtctgcat cccttggaga cacaattacc 60

atcacttgcc atgccagtca gaacattaat gtttggttaa actggtacca gcagaaacca 120

ggaaatattc ctaaactatt gatctataag gcttccaact tgcacacagg cgtcccatca 180

aggtttagtg gcagtggatc tggaacaggt ttcacattaa ccatcggcag cctgcagcct 240

gaagacattg ccacttacta ctgtcaacag ggtcaaagtt atccgttcac gttcggaggg 300

gggaccaagc tggaaataaa acg 323

<210> 157
<211> 345
<212> DNA
<213> Mus sp.

<400> 157
caggttcagc tgcagcagtc tgacgctgag ttggtgaaac ctggggcttc agtgaagata 60

tcctgcaagg cttctggcta caccttcact gaccatgcta ttcactgggt gaaacagaag 120

cctgaacagg gcctggaatg gattggatat atttctcccg gaaatggtga tattaagtat 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cactgcctac 240

atgcagctca acagcctgac atctgaggat tctgcagtgt atttctgtca aagacaactg 300

ggacaaggct actggggcca aggcaccact ctcacagtct cctca 345

<210> 158
<211> 338
<212> DNA
<213> Mus sp.

<400> 158
gatgttgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60

atctcttgca gatctagtca gagccttgta cacagttatg gaaacaccta tttacattgg 120

tacctgcaga agccaggcca gtctccaaag ctcctgattt acaaagtttc caaccgattt 180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240

agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaaatac acatgttccg 300

tacacgttcg gaggggggac caagctggaa ataaaacg 338

<210> 159
<211> 345
<212> DNA
<213> Mus sp.

<400> 159
caggttcagc tgcagcagtc tgacgctgag ttggggaaac ctggggcttc agtgaagata 60

tcctgcaagg cttctggcta caccttcagt gaccatgcta ttcactgggt gaagcagaag 120

cctgaacagg gcctggaatg gattggatat atctctcccg gaaacgatga tattaagtac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cactgcctac 240

atgcagctca acagcctgac atctgaggat tctgcagtgt atttctgtga aagatcgatg 300

attggggttt actggggcca agggactctg gtcactgtct ctgca 345

<210> 160
<211> 337
<212> DNA
<213> Mus sp.

<400> 160
gatgttgtga tgacccaaac tccactctcc ctgactgtca gtcttggcga tcaagcctcc 60

atctcttgca gatttagtca gagccttgta caaagtaatg gaaataccta tttacagtgg 120

tatctgcaga agccaggcca gtctccaaag ctcctgattt acaaagtctc caaccgattt 180

tgtggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240

agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgctccg 300

ctcacgttcg gtgctgggac caagctggag ctgaaac 337

<210> 161
<211> 342
<212> DNA
<213> Mus sp.

<400> 161
caggttcagc tgcagcagtc tgacgctgag ttggtgaaac ctggggcttc agtgaagata 60

tcctgcaaga cttctggcta caccttcact gaccatgcaa ttcactgggt gaagcagaag 120

cctgaacagg gcctggaatg gattggatat atttctcccg gaaatggtga tattaagtac 180

aatgagaagt tcaagggcaa ggccaccctg actgcagaca aatcctccag cactgcctat 240

atgcagctca gcagcctgac acctgaggat tctgcagtgt atttctgtaa aatatcttac 300

tacggtattt ggggccaagg caccactctc acagtctcct ca 342

<210> 162
<211> 322
<212> DNA
<213> Mus sp.

<400> 162
gacatccaga tgactcagtc tccagcctcc ctatctgtat ctgtgggaga gtctgtcacc 60

atcacatgtc gactaagtga agatatttac agtaatttag catggtttca gcagagaccg 120

ggaaaatctc ctcagctcct ggtttataaa gcaacaaact tagcagacgg tgtgccatca 180

aggttcagtg gcagtggatc aggcacacag tattccctca agatcaacag cctgcagtct 240

gaagattttg ggacttatta ctgtcaacat ttttggggta ctccattcac gttcggctcg 300

gggaccaagg tggaaataaa ac 322

<210> 163
<211> 342
<212> DNA
<213> Mus sp.

<400> 163
caggttcagc tgcagcagtc tgacgctgag ttggtgaaac ctggggcttc agtgaagata 60

tcctgcaagg cttctggcta caccttcact gaccatgcta ttcactgggt gaagcagaag 120

cctgaacagg gcctggaatg gattggatat ttttctcccg gaaatgatga tattaagtat 180

aatgagaagt tcaaggtcaa ggccacactg actgcagaca aatcctccag cactgcctac 240

atgcaactca ccagcctgac atctgaagat tctgcagtgt atttctgtaa aagatcttac 300

tacggtgatt ggggccaagg caccactctc acagtctcct ca 342

<210> 164
<211> 322
<212> DNA
<213> Mus sp.

<400> 164
gacatccaga tgactcagtc tccagcctcc ctatctgttt ctgtgggaga aactgtcacc 60

atcacatgtc gagcaagtga gaatatttac agtcatttag catggtatca acagaaacag 120

ggaaaatctc ctcaactcct ggtctatggt gcaactaact tagcagatgg tgtgccatca 180

aggttcagtg gcagtggatc aggcacacag ttttccctca agatccacag cctgcagtct 240

gaagattttg ggagttatta ctgtcaacat ttttggggtg ctccattcac gttcggctcg 300

gggacaaagt tggaaataaa ac 322

<210> 165
<211> 345
<212> DNA
<213> Mus sp.

<400> 165
caaattcagc tgcagcagtc tgacgctgag ttggtgaaac ctgggacttc agtgaagatg 60

tcctgcaagg cttctggcta caccttcact gaccatgcta ttcactgggt gaagcagaag 120

cctgaacagg gcctggaatg gattggatat ttttctcccg gaaatgatga tattaagtat 180

aatgtgaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cactgcctac 240

atgcagctca acagcctgac atctgaagat tctgcagtgt atttctgttc ggtgggatac 300

gcccttgact actggggcct aggcaccact ctcacagtct cctca 345

<210> 166

<211> 323
<212> DNA
<213> Mus sp.

<400> 166
aacattgtaa tgacccaatc tcccaaatcc atgtccatgt cagtaggaga gagggtcacc 60

ttgacctgca aggccagtga gaatgtggtt acttatgttt cctggtatca acagaaacca 120

gagcagtctc ctaaactgct gatatacggg gcatccaacc ggtacactgg ggtccccgat 180

cgcttcacag gcagtggatc tgcaacagat ttcactctga ccatcagcag tgtgcaggct 240

gaagaccttg cagattatca ctgtggacag ggttacagct atccgtacac gttcggaggg 300

gggaccaagc tggaaataaa acg 323

<210> 167
<211> 345
<212> DNA
<213> Mus sp.

<400> 167
caggttcagc tgcaacagtc tgacgctgag ttggtgaaac ctgggactac agtgaagata 60

tcctgcaagg cttctggcta cactttcact gaccatgcta ttcactgggt gaaggagaag 120

cctgaacagg gcctggaatg gatcggatat atttctcccg gaaatgatga tattaagtac 180

agtgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cactgcttac 240

atgcagctca acagcctgac atctgatgat tctgcagtgt atttctgtaa aagatcgctt 300

agtacgcctt actggggcca agggactctg gtcactgtct ctgca 345

<210> 168
<211> 477
<212> DNA
<213> Mus sp.

<400> 168
tttttaatac gactccctat agggcaagca gtggtatcaa tgcagattac aaggggggaaa 60

ggcatcagac cagcatgggc atcaaggtgg aatcacagac tctggtcttc atatccatac 120

tgtttgggtt atatggagct gatgggaaca cattaatgac ccaatctccc acatccatgt 180

acatgtcagt aggagagagg gtcaccttga cttgcaaggc cagtgagaat gagattaatt 240

atgtttcctg gtatcaacag aaaccagagc agtctcctaa actgttgata tacggggcat 300

ccaaccggta ctctggggtc cccgatcgct tcacaggcag tggatctgca acagatttca 360

ctctgaccat cagcagtgtg caggctgaag accttgcaga ttatccctgt ggagcaaggg 420

attaactagc tatccgtaca cgttcggagg ggggaccaag ctggaaataa aacgggc 477

<210> 169
<211> 341
<212> DNA
<213> Mus sp.

<400> 169
gacattgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60

atgagctgca ggtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120

tggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300

ccgtacacgt tcggaggggg gaccaagctg gaaataaaac g 341

<210> 170
<211> 343
<212> DNA
<213> Mus sp.

<400> 170
caggttcagc tgcagcagtc tgacgctgag ttggtgaaac ctggggcttc agtgaagata 60

tcctgcaagg cttctggcta caccttcact gaccatgcta ttcactgggt gatgcagatg 120

cctgaacagg gcctggaatg gattggatat atttctcccg gaaatggtga tgttaagtac 180

agtgagaggt tcaagggcag ggccacactg actgcagaca aatcctccag ctctgcctac 240

atgcagctca acagcctgac atctgaggat tctgcagttt atttctgtaa aagatcgctt 300

agtacgcctt actggggcca agggactctg gtcactgtct ctg 343

<210> 171
<211> 341
<212> DNA
<213> Mus sp.

<400> 171
gacattgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gagggtcact 60

atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagag ctacttgacc 120

tggtaccagc agaaaccagg gcagcctcct aaactgttga tctcctgggc atccactagg 180

gattctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240

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ccgtacacgt tcggaggggg gaccaagctg gaaataaaac g 341

<210> 172
<211> 345
<212> DNA
<213> Mus sp.

<220>
<221> modified_base
<222> (26)..(26)
<223> a, c, t, g, unknown or other

<220>
<221> modified_base
<222> (332)..(332)
<223> a, c, t, g, unknown or other

<400> 172
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tcctgtaagg cttctggcta caccttcact gaccatgcta ttcactgggt gaagcagaag 120

cctgaacagg gcctggaatg gattggatat ttttctcccg gaaatgatga tattaagtac 180

aatgagaagt ttaggggcaa ggccacactg actgcagaca aatcctccag cactgcctac 240

atgcagctca acagcctgtc atctgatgat tctgcagtgt atttctgtaa aagatcgctt 300

agtacgcctt actggggcca agggactctg gncactgtct ctgca 345

<210> 173
<211> 341
<212> DNA
<213> Mus sp.

<400> 173
gacattgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaagtcact 60

atgagctgca agtccagtca gagtctgtta aaccgtggaa atcataagaa ctacttgacc 120

tggtaccggc agaaaccagg gctgcctcct aaactgttga tttactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cgctctcacc 240

atcagcagtg ttcaggctga agacctggca gtttattact gtcagaatga ttatacttat 300

ccgtacacgt tcggaggggg gaccaagctg gagataaaac g 341

<210> 174
<211> 345
<212> DNA
<213> Mus sp.

<400> 174
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tcctgcaagg cttctggcta caccttcact gaccatgcta ttcactgggt gaagcagaag 120

cctgaacagg gcctggaatg gattggatat atttctcccg gaaatggtga tattaagtac 180

aatgagaagt tcaaggtcaa ggccacactg actgcagaca aatcctccag cactgcctac 240

atgcagctca acagcctgac atctgaggat tctgcagtgt atttctgtaa aagatcgatt 300

actacgcctt actggggcca agggactctg gtcactgtct ctgca 345

<210> 175
<211> 341
<212> DNA
<213> Mus sp.

<400> 175
gacattgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60

atgagctgca agtccagtca gagtctgtta aacagtggaa aaacaaagaa ctacttgacg 120

tggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240

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ccgtacacgt tcggaggggg gaccaagctg gaaataaaac g 341

<210> 176
<211> 345
<212> DNA
<213> Mus sp.

<400> 176
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tcctgcaaga cttctggcta caccttcact gaccatgcta ttcactgggt gaagcagaag 120

cctgaacagg gcctggaatg gattggatat atctctcccg gaaatgatga tattaagtac 180

actgagaagt tcaagggcaa ggtcacactg actgcagaca aatcctccag cactgcctac 240

atgcagctca acagcctgac atctgaggat tctgcagtct atttctgtaa aagatcgatt 300

actacgcctt actggggcca agggactctg gtcactgtct ctgca 345

<210> 177
<211> 480
<212> DNA
<213> Mus sp.

<220>
<221> modified_base
<222> (153)..(153)
<223> a, c, t, g, unknown or other

<220>
<221> modified_base
<222> (285)..(286)
<223> a, c, t, g, unknown or other

<220>
<221> modified_base
<222> (289)..(289)
<223> a, c, t, g, unknown or other

<220>
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<222> (297)..(298)
<223> a, c, t, g, unknown or other

<220>
<221> modified_base
<222> (332)..(332)
<223> a, c, t, g, unknown or other

<220>
<221> modified_base
<222> (405)..(405)
<223> a, c, t, g, unknown or other

<220>
<221> modified_base
<222> (412)..(412)
<223> a, c, t, g, unknown or other

<220>
<221> modified_base
<222> (429)..(429)
<223> a, c, t, g, unknown or other

<400> 177

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cttcatatcc agtacgctcg gggactatgg agnggaacag tacattttaa tgacccaatg 180

tcccaaaggc aagaacatgt cagtaggaga gagggtcact cagagtgcaa ggccaggaga 240

aatcaaaaca cttatgtttc ctggtatcaa cagaaaccag agcannctnt aaaatgnnga 300

ttacggggca tccaaccggg aatctggggt cnccgatcgc ttcacaggca gtggatctgg 360

aacagatttc actctcacca tcagcagtgt gcaggctgaa gaccnggcag tnttcactgt 420

ggacagggnt acagttatcc gtacacgttc ggaggggggga ccaagctgaa aaaaacgggc 480

<210> 178
<211> 345
<212> DNA
<213> Mus sp.

<400> 178
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cctgaacagg gcctggaatg gattggatat atttctcccg gaaatggtga tattaagtac 180

gatgagaagt ttaagggcaa ggccacactg actgcagaca aatcctcctc cactgcctac 240

atgcagctca acagcctgac atctgaagat tctgcagtgt atttctgtaa aagatcgatt 300

actacctctt actggggcca agggactctg gtcactgtct ctgca 345

<210> 179
<211> 345
<212> DNA
<213> Mus sp.

<400> 179
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tcctgcaagg cttctggcta caccttcact gaccatgcta ttcactgggt gaagcagaag 120

cctgaacagg gcctggaatg gattggatat atttctcccg gaaatgatga tattaagtac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca agtcctccag cactgcctac 240

atgcagctca acagcctgac atctgaggat tctgcagtgt ttttctgtaa aagatcgatt 300

actacctctt actggggcca agggactctg gtcactgtct ctgca 345

<210> 180
<211> 483
<212> DNA
<213> Mus sp.

<220>
<221> modified_base
<222> (3)..(3)
<223> a, c, t, g, unknown or other

<220>
<221> modified_base
<222> (137)..(137)
<223> a, c, t, g, unknown or other

<220>
<221> modified_base
<222> (193)..(193)
<223> a, c, t, g, unknown or other

<400> 180
ttnataggac tcaatatagg gcaagcagtg gtattaacgc cgagtacatg gggagggcaa 60

gggcagaaag tcactttcag tgaggataca ccatcagcat gagggtcctt gttgagctcc 120

tgggggggct ggtgttntgc tttttaggtg tgagatgtga catccagatg aaccagtctc 180

catccagtct gtntgcatcc tttggagaca caattaccat catttgccat tccagtcaga 240

acattaatgt ttggttaaga tggtaccagc agaaaccagg aaatattcct aaaatattga 300

tatataaggg ttccaacttg tacacaggcg tcccatcaag gtttagtggc agtggatttg 360

gaacaggttt cacattaacc atcagcagcg tgcagcggga agacattgcc acttactact 420

gtcaacagga tcaaagttat ccgtacacgt tcggaggggg gaccaagctg aaataaaacg 480

ggc 483

<210> 181
<211> 345
<212> DNA
<213> Mus sp.

<400> 181
caggttcagc tgcagcagtc tgacgccgag ttggtgaaac ctggggcttc agtgaagata 60

tcctgcaagg cttctggcta catcttcact gaccatgcta ttcactgggt gaagcagaag 120

cctgaacagg gcctggaatg gattggatat atttctcccg gaaatggtga tattaagtac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cactgcctac 240

atgcatctca acagcctgac atctgaggat tctgcagtgt atttctgtaa aagatcgatt 300

actacctctt actggggcca agggactctg gtcactgtct ctgca 345

<210> 182
<211> 323
<212> DNA
<213> Mus sp.

<400> 182
gacatccaga tgaaccagtc cccatccagt ctgtctgcat cccttggaga cacaattacc 60

atcacttgcc atgccagtca gcacattaat ttttggttaa gctggtacca gcagaaacca 120

ggaaatattc ctaaactctt gatctataag gcttccaact tgcacacagg cgtcccatca 180

aggtttagtg gcagtggatc tggaacaggt ttcacattaa ccatcagcag cctgctgcct 240

gaagacgttg ccacttacta ctgtcaacag gatcaaagtt atccgtatat gttcggaggg 300

gggaccaagc tggaaataaa acg 323

<210> 183
<211> 345
<212> DNA
<213> Mus sp.

<400> 183
caggttcagc tgcagcagtc tgacgctgag ttggtgaaac ctggggcttc agtgaagata 60

tcctgcaagg cttctggcta caccttcact gaccatgcta ttcactgggt gaagcagaag 120

cctgaacagg gcctggaatg gattggatat atttctcccg gaaatgatga tattaagtac 180

aatgagaagt ttaagggcaa ggccacactg actgcagaca aatcctccag cactgcctac 240

atgctgctca acagcctgac atctgaggat tctgcagtgt atttctgtaa aagatcgatt 300

actacctctt actggggcca agggactctg gtcactgtct ctgca 345

<210> 184
<211> 323
<212> DNA
<213> Mus sp.

<400> 184
aacattgtaa tgacccaatc tcccaaatcc atgtccatgt cagtaggaga gagggtcacc 60

ttgacctgca aggccagtga gaatgtggtt acttatgttt cctggtatca acagaaacca 120

gagcagtctc ctaaactgct gatatacggg gcatccaacc ggtacactgg ggtccccgat 180

cgcttcacag gcagtggatc tgcaacagat ttcactttga ccatcagcag tgtgcaggct 240

gaagaccttg cagattatca ctgtggacag ggttacagct atccgtacac gttcggaggg 300

gggaccaagc tggaaataaa acg 323

<210> 185
<211> 345
<212> DNA
<213> Mus sp.

<400> 185
caggttcaac tgcagcagtc tgacgctgag ttggtgaaac ctggggcttc agtgaagata 60

tcctgcaagg cttctggcta caccttcact gaccatgcta ttcactgggt gaagcagaag 120

cctgaacagg gcctggaatg gattggatat atttctcccg gaaatggtga tattaagtac 180

aatgagaagt tcaagggtaa ggccacactg actgcagaca cttcctccac cactgcctac 240

atgcagctca acagcctgac atctgaggat tctgcaatgt atttctgtaa aagatccatt 300

actacgtctt actggggcca agggactctg gtcactgtct ctgca 345

<210> 186
<211> 321
<212> DNA
<213> Mus sp.

<400> 186
gacatccaga tgaaccagtc tccatccagt ctgtctgcat cccttggaga cacaattacc 60

atcacttgcc atgccagtca gaacattaat gtttggttaa gctggtacca gcagaaacca 120

ggaaatattc ctaaactatt gatctataag gcttccaatt tgtatacagg cgtcccatca 180

aggtttagtg gcagtggatc tggaacaggt ttcacattaa ccatcagcag cctgcagcct 240

gaagacgttg ccacgtacta ctgtcaacac gatcaaagtt atccgtacac gttcggaggg 300

gggaccaagc tggaaataaa a 321

<210> 187
<211> 345
<212> DNA
<213> Mus sp.

<400> 187

caggttcagc tgcagcagtc tgacgctgag ttggtgaaac ctggggcttc agtgaagata 60

tcctgcaagg cttctggcta catcttcact gaccatgcaa ttcactgggt gaagcagaag 120

cctgaacagg gcctggaatg gattggatat atttctcccg gaaatggtga tattaagtac 180

attgagaagt tcaggggcaa ggccacactg actgcagaca aatcctccag cactgcctac 240

atgcagctca acagcctgac atctgaggat tctgcagtgt atttctgtaa aagatcgctt 300

agtacgcctt actggggcca agggactctg gtcactgtct ctgca 345

<210> 188
<211> 329
<212> DNA
<213> Mus sp.

<400> 188
aacattttaa tgacccaatc tcccaaatcc atgtccatgt cagtaggaga gagggtcacc 60

ttgacctgca aggccagtga gaatgtggtt aattatgttt cctggtatca acagaaacca 120

gagcagtctc ctaaactgct gatattcggg gcatccaacc ggtactctgg ggtccccgat 180

cgcttcacag gcagtggatc tgcaacagat ttcactctga ccatcagcag tgtgcaggct 240

gaagaccttg cagattatca ctgtggaagc aagtggatta ctagctatcc gtacacgttc 300

ggaggggggga ccaagctgga aataaaacg 329

<210> 189
<211> 326
<212> DNA
<213> Mus sp.

<400> 189
aacattttaa tgacccaatc tcccaaatcc atgtccatgt cagtaggaga gagggtcacc 60

ttgacctgca aggccagtga gaatgtggtt aattatgttt cctggtatca acagaaacca 120

gagcagtctc ctaaactgct gatatacggg gcatccaacc ggtactctgg ggtccccgat 180

cgcttcacag gcagtggatc tgcaacagat ttcactctga ccatcagcag tgtgcaggct 240

gaagaccttg cagattatca ctgtggagca agggttacta gctatccgta cacgttcgga 300

gggggggacca agctggaaat aaaacg 326

<210> 190
<211> 345
<212> DNA

<213> Mus sp.

<400> 190
caggttcagc tgcagcagtc tgacgctgag ttggtgaaac ctgggacttc agtgaagata 60

tcctgcaggg cttctggcta caccttcact gaccatgcta ttcactgggt gaagcagaag 120

cctgaacagg gcctggaatg gattggatat atttctcccg gaaatggtga tattaagtac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cactgcctac 240

atgcagctca acagcctgac atctgacgat tctgcagtgt atttctgtaa aagatccatt 300

actacgcctt actggggcca aggcaccact ctcacagtct cctca 345

<210> 191
<211> 315
<212> DNA
<213> Mus sp.

<400> 191
agttttgtga tgacccagac tcccaaattc ctgcttgtgt cagcaggaga cagggttacc 60

ataacctgca aggccagtca gagtgtgaat aataatgtag cttggtacca acagaagcca 120

gggcagtctc ctaaacagct gatatactat gcatccaatc gctacactgg agtccctgat 180

cgcttcactg gcagtggata tgggacggat ttcactttca ccatctacac tgtgcaggct 240

gaagacctgg cagtttattt ctgtcagcag ggttatagct ctccgtggac gttcggtgga 300

ggcaccaagc tgaaa 315

<210> 192
<211> 330
<212> PRT
<213> Mus sp.

<400> 192
Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Val Cys Gly
1 5 10 15

Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
20 25 30

Phe Pro Glu Pro Val Thr Leu Thr Trp Asn Ser Gly Ser Leu Ser Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu

```
    50                  55                  60

Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp Pro Ser Gln Ser Ile
65                  70                  75                  80

Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
                85                  90                  95

Ile Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys
            100                 105                 110

Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro
        115                 120                 125

Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys
    130                 135                 140

Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp
145                 150                 155                 160

Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg
                165                 170                 175

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

His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
        195                 200                 205

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

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

Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met
                245                 250                 255

Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu
            260                 265                 270
```

```
Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe
        275                 280                 285

Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn
    290                 295                 300

Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr
305                 310                 315                 320

Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
                325                 330
```

<210> 193
<211> 107
<212> PRT
<213> Mus sp.

<400> 193

```
Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
1               5                   10                  15

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
            20                  25                  30

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

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
    50                  55                  60

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
65                  70                  75                  80

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
                85                  90                  95

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
            100                 105
```

<210> 194
<211> 330
<212> PRT

<213> Homo sapiens

<400> 194

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

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

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

```
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

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

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
```

<210> 195
<211> 107
<212> PRT
<213> Homo sapiens

<400> 195

```
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1               5                   10                  15

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        35                  40                  45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
    50                  55                  60
```

```
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65                  70                  75                  80


Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
                85                  90                  95


Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            100                 105


<210> 196
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      hybrid polypeptide

<400> 196
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30


Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Asp Trp Ile
        35                  40                  45


Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Asp Lys Val Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Cys
65                  70                  75                  80


Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95


Lys Arg Ser Leu Leu Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu
            100                 105                 110


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

```
Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu
    130                 135                 140

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

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

Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp Pro
            180                 185                 190

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

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

Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe
225                 230                 235                 240

Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro
                245                 250                 255

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

Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr
        275                 280                 285

Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala
    290                 295                 300

Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys
305                 310                 315                 320

Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser
                325                 330                 335

Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro
```

340 345 350

Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val
355 360 365

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

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

Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp
405 410 415

Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His
420 425 430

Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
435 440 445

<210> 197
<211> 1401
<212> DNA
<213> Artificial Sequence

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

<400> 197
atggagaccg acaccctgct gctctgggtg ctgctgctct gggtgcccgg ctccaccgga 60

caggttcagc tgcagcagtc tgacgctgag ttggtgaaac ctggggcttc agtgaagata 120

tcctgcaagg cttctggcta caccttcact gaccatgcta ttcactgggt gaagcaaaag 180

cctgaacagg gcctggactg gattggatat atttctcccg gaaatggtga tattaagtac 240

aatgagaagt tcaaggacaa ggtcacactg actgcagaca aatcctccag cactgcctgc 300

atgcacctca acagcctgac atctgaggat tctgcagtgt atttctgcaa aagatcccta 360

ctagctcttg actactgggg ccaaggcacc actctcacag tctcctcagc taaaacaaca 420

gccccatcgg tctatccact ggcccctgtg tgtggagata caactggctc ctcggtgact 480

ctaggatgcc tggtcaaggg ttatttccct gagccagtga ccttgacctg gaactctggt 540

tccctgtcca gtggtgtgca caccttccca gctgtcctgc agtctgacct ctacaccctc 600

agctcaagcg tgactgtaac cagctcgacc tggcccagcc agtccatcac ctgcaatgtg 660

gcccacccgg caagcagcac caaggtggac aagaaaattg agcccagagg gcccacaatc 720

aagccctgtc ctccatgcaa atgcccagca cctaacctct tgggtggacc atccgtcttc 780

atcttccctc caaagatcaa ggatgtactc atgatctccc tgagccccat agtcacatgt 840

gtagtcgttg atgtgagcga ggatgaccca gatgtccaga tcagctggtt tgtgaacaac 900

gtggaagtgc acactgctca gacacagacg catagagagg attacaacag tactctccgg 960

gttgtcagtg ccctccccat ccagcaccag gactggatga gtggcaagga gttcaaatgc 1020

aaggtcaaca acaaagacct cccagcgccc atcgagagaa ccatctcaaa acccaaaggg 1080

tcagtaagag ctccacaggt atatgtcttg cctccaccag aagaggagat gactaagaaa 1140

caggtcactc tgacctgcat ggtcacagac ttcatgcctg aagacattta cgtggagtgg 1200

accaacaacg ggaaaacaga gctaaactac aagaacactg aaccagtcct ggactctgat 1260

ggttcttact tcatgtacag caagctgaga gtggagaaga agaactgggt ggagagaaat 1320

agctactcct gttcagtggt ccacgagggt ctgcacaatc accacacgac taagagcttc 1380

tcccggactc cgggtaaata g 1401

<210> 198
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 198
Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Asn
20 25 30

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

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

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

Glu Asp Leu Thr Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Phe Pro Leu
85 90 95

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

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

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

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

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
165 170 175

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

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

Phe Asn Arg Asn Glu Cys
210

<210> 199
<211> 705
<212> DNA
<213> Artificial Sequence

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

<400> 199

atggagaccg acaccctgct gctctgggtg ctgctgctct gggtgcccgg ctccaccgga 60

gacattgtga tgacccagtc tcacaaattc atgtccacat cagtaggaga cagggtcagc 120

atcacctgca aggccagtca ggatgtgggc actaatatag cctggtatca acagaaacca 180

ggccgatctc ctaaagtact gatttactcg gcatccaccc ggcacactgg agtccctgat 240

cgcttcacag gcagtggatc tgggacagat ttcactctca ccattagcaa tgtgcagtct 300

gaagacttga cagattattt ctgtcagcaa tatagcagct ttcctctcac gttcggtgtt 360

gggaccaagc tggagctgaa acgggcagat gctgcaccaa ctgtatccat cttcccacca 420

tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gcttcttgaa caacttctac 480

cccaaagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa tggcgtcctg 540

aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcacg 600

ttgaccaagg acgagtatga acgacataac agctatacct gtgaggccac tcacaagaca 660

tcaacttcac ccattgtcaa gagcttcaac aggaatgagt gttga 705

<210> 200
<211> 296
<212> DNA
<213> Homo sapiens

<400> 200
caggttcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggtta cacctttacc agctatggta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcagcgctt acaatggtaa cacaaactat 180

gcacagaagc tccagggcag agtcaccatg accacagaca catccacgag cacagcctac 240

atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagaga 296

<210> 201
<211> 286
<212> DNA
<213> Homo sapiens

<400> 201
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctc 286

<210> 202
<211> 305
<212> DNA
<213> Homo sapiens

<400> 202
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtgtttta tacagctcca acaataagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatagtact 300

cctcc 305

<210> 203
<211> 98
<212> PRT
<213> Homo sapiens

<400> 203
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
50 55 60

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

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

Ala Arg

<210> 204
<211> 95
<212> PRT
<213> Homo sapiens

<400> 204
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

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

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro
85 90 95

<210> 205
<211> 102
<212> PRT
<213> Homo sapiens

<400> 205
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

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

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

```
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80


Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95


Tyr Tyr Ser Thr Pro Cys
            100


<210> 206
<211> 25
<212> PRT
<213> Homo sapiens

<400> 206
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser
            20                  25


<210> 207
<211> 22
<212> PRT
<213> Homo sapiens

<400> 207
Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
1               5                   10                  15


Arg Val Thr Ile Thr Cys
            20


<210> 208
<211> 23
<212> PRT
<213> Homo sapiens

<400> 208
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Glu Arg Ala Thr Ile Asn Cys
            20
```

<210> 209
<211> 14
<212> PRT
<213> Homo sapiens

<400> 209
Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1   5   10

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

<400> 210
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
1   5   10   15

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

<400> 211
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
1   5   10   15

<210> 212
<211> 32
<212> PRT
<213> Homo sapiens

<400> 212
Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
1   5   10   15

Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg
            20   25   30

<210> 213
<211> 32
<212> PRT
<213> Homo sapiens

<400> 213
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1   5   10   15

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

<210> 214
<211> 32
<212> PRT
<213> Homo sapiens

<400> 214
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1   5   10   15

Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
            20   25   30

<210> 215
<211> 11
<212> PRT
<213> Homo sapiens

<400> 215
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1   5   10

<210> 216
<211> 10
<212> PRT
<213> Homo sapiens

<400> 216
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
1   5   10

<210> 217
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      hybrid polypeptide

<400> 217
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

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

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

Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Phe Trp Gly Ala Pro Phe
85 90 95

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

<210> 218
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 218
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Val
35 40 45

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

Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Phe Trp Gly Ala Pro Phe
85 90 95

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

<210> 219
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 219
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Val
35 40 45

Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Phe Trp Gly Ala Pro Phe
85 90 95

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

<210> 220
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 220
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30

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

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
    50   55   60

Lys Val Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65   70   75   80

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

Ala Arg Ser Tyr Tyr Gly Asp Trp Gly Gln Gly Thr Leu Val Thr Val
            100   105   110

Ser Ser

<210> 221
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      hybrid polypeptide

<400> 221
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30

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

```
Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60

Lys Val Arg Val Thr Met Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

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

Lys Arg Ser Tyr Tyr Gly Asp Trp Gly Gln Gly Thr Leu Val Thr Val
            100                 105                 110

Ser Ser
```

<210> 222
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 222

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30

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

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60

Lys Val Arg Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95
```

Lys Arg Ser Tyr Tyr Gly Asp Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser

<210> 223
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic hybrid polypeptide

<400> 223
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

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

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Val Arg Val Thr Met Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Lys Arg Ser Tyr Tyr Gly Asp Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser

<210> 224
<211> 114

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 224
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

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

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Val Arg Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Lys Arg Ser Tyr Tyr Gly Asp Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser

<210> 225
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 225
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys His Ala Ser Gln His Ile Asn Phe Trp
            20   25   30

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Gln Ser Tyr Pro Tyr
                85   90   95

Met Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 226
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      hybrid polypeptide

<400> 226
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys His Ala Ser Gln His Ile Asn Phe Trp
            20   25   30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
        35   40   45

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

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Gln Ser Tyr Pro Tyr
85 90 95

Met Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 227
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 227
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Ile Thr Ile Thr Cys His Ala Ser Gln His Ile Asn Phe Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Asp Gln Ser Tyr Pro Tyr
85 90 95

Met Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 228
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 228
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys His Ala Ser Gln His Ile Asn Phe Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Gln Ser Tyr Pro Tyr
85 90 95

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

<210> 229
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 229
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Ile Thr Ile Thr Cys His Ala Ser Gln His Ile Asn Phe Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Asp Gln Ser Tyr Pro Tyr
85 90 95

Phe Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 230
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 230
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp His
20 25 30

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

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

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

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

Ala Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 231
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 231
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp His
20 25 30

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

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

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

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

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 232
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 232

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


Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp His
            20                  25                  30


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


Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60


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


Met His Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95


Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110


Val Ser Ser
        115


<210> 233
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      hybrid polypeptide

<400> 233
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp His
            20                  25                  30


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

```
Gly Tyr Ile Ser Pro Gly Ser Gly Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60

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

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

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110

Val Ser Ser
        115
```

<210> 234
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic hybrid polypeptide

<400> 234

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp His
            20                  25                  30

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

Gly Tyr Ile Ser Pro Gly Ser Gly Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60

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

Met His Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95
```

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 235
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 235
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Arg
20 25 30

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Thr Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 236
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 236
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Arg
20 25 30

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Thr Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 237
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 237
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

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


Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60


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


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


Ala Arg Ser Leu Ser Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110


Val Ser Ser
        115


<210> 238
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      hybrid polypeptide

<400> 238
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30


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


Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Arg Gly Arg Val Thr Met Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
```

```
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95


Lys Arg Ser Leu Ser Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110


Val Ser Ser
        115


<210> 239
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      hybrid polypeptide

<400> 239
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30


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


Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Arg Gly Arg Val Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80


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


Lys Arg Ser Leu Ser Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110


Val Ser Ser
        115
```

<210> 240
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 240
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

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

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

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

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

Lys Arg Ser Leu Ser Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 241
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 241

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


Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30


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


Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Arg Gly Arg Val Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80


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


Lys Arg Ser Leu Ser Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110


Val Ser Ser
        115


<210> 242
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      hybrid polypeptide

<400> 242
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr
            20                  25                  30


Val Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
```

```
Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr
                85                  90                  95

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

<210> 243
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic hybrid polypeptide

<400> 243

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr
            20                  25                  30

Val Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr
                85                  90                  95

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

<210> 244
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 244
Asn Ile Val Met Thr Gln Ser Pro Ser Ser Met Ser Met Ser Val Gly
1 5 10 15

Asp Arg Val Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr
20 25 30

Val Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Leu Ala Thr Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 245
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 245
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

```
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


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


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


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Asp Gln Ser Tyr Pro Tyr
                85                  90                  95


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


<210> 246
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      hybrid polypeptide

<400> 246
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
            20                  25                  30


Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
        35                  40                  45


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


Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Asp Gln Ser Tyr Pro Tyr
                85                  90                  95
```

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

<210> 247
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic hybrid polypeptide

<400> 247
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Asp Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 248
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic hybrid polypeptide

<400> 248

```
Asp Ile Gln Met Asn Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
            20                  25                  30


Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
        35                  40                  45


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


Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Asp Gln Ser Tyr Pro Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 249
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      hybrid polypeptide

<400> 249
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30


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


Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60
```

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

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

Ala Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 250
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic hybrid polypeptide

<400> 250
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

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

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

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

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

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
        115

<210> 251
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      hybrid polypeptide

<400> 251
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30

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

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
    50   55   60

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

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

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100   105   110

Val Ser Ser
        115

<210> 252
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      hybrid polypeptide

<400> 252
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30

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

Gly Tyr Ile Ser Pro Gly Ser Gly Asp Ile Lys Tyr Asn Glu Lys Phe
    50   55   60

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

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

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100   105   110

Val Ser Ser
        115

<210> 253
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      hybrid polypeptide

<400> 253
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20   25   30

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

```
Gly Tyr Ile Ser Pro Gly Ser Gly Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60

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

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

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110

Val Ser Ser
        115
```

<210> 254
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 254

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Asn
            20                  25                  30

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

Tyr Ser Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser Phe Pro Leu
                85                  90                  95
```

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

<210> 255
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic hybrid polypeptide

<400> 255
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Asn
20 25 30

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

Tyr Ser Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

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

<210> 256
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic hybrid polypeptide

<400> 256

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


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30


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


Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80


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


Ala Arg Ser Leu Leu Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 257
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      hybrid polypeptide

<400> 257
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30


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

```
Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60

Lys Asp Arg Val Thr Met Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

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

Lys Arg Ser Leu Leu Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110

Thr Val Ser Ser
        115
```

<210> 258
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic hybrid polypeptide

<400> 258

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30

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

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
    50                  55                  60

Lys Asp Arg Val Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser
65                  70                  75                  80

Met His Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95
```

Lys Arg Ser Leu Leu Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 259
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 259
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

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

Gly Tyr Ile Ser Pro Gly Ser Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Lys Arg Ser Leu Leu Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 260
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 260
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

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

Gly Tyr Ile Ser Pro Gly Ser Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Val Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser
65 70 75 80

Met His Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
85 90 95

Lys Arg Ser Leu Leu Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 261
<211> 12
<212> PRT
<213> Artificial Sequence

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

<400> 261
Cys Gln Phe Asp Leu Ser Thr Arg Arg Leu Lys Cys
1 5 10

<210> 262
<211> 12

<212> PRT
<213> Artificial Sequence

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

<400> 262
Cys Gln Tyr Asn Leu Ser Ser Arg Ala Leu Lys Cys
1 5 10

<210> 263
<211> 122
<212> PRT
<213> Artificial Sequence

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

<400> 263
Met Ala Asn Val Gln Leu Asn Glu Ser Gly Gly Gly Leu Val Gln Pro
1 5 10 15

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

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

Trp Val Ser Asp Ile Ser Pro Ser Gly Ala Val Lys Ala Tyr Ser Asp
50 55 60

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

Leu Tyr Leu Gln Met Asn Ser Leu Thr Pro Glu Asp Thr Gly Glu Tyr
85 90 95

Phe Cys Thr Lys Val Gln Ser Pro Arg Thr Arg Ile Pro Ala Pro Ser
100 105 110

Ser Gln Gly Thr Gln Val Thr Val Ser Ser
115 120

<210> 264
<211> 122
<212> PRT
<213> Artificial Sequence

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

<400> 264
Met Ala Asn Val Gln Leu Asn Glu Ser Gly Gly Gly Leu Val Gln Pro
1 5 10 15

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

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

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

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

Leu Tyr Leu Gln Met Asn Ser Leu Thr Pro Glu Asp Thr Gly Glu Tyr
85 90 95

Phe Cys Thr Lys Val Gln Ser Pro Arg Thr Arg Ile Pro Ala Pro Ser
100 105 110

Ser Gln Gly Thr Gln Val Thr Val Ser Ser
115 120

<210> 265
<211> 10
<212> PRT
<213> Artificial Sequence

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

<400> 265
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 266
<211> 8
<212> PRT
<213> Artificial Sequence

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

<400> 266
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5