SEQUENCE LISTING

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<120> ANTIBODIES SPECIFIC FOR TROP-2 AND THIER USES

<130> PC71866A

<150> US 61/559,015
<151> 2011-11-11

<150> US 61/640,641
<151> 2012-04-30

<150> US 61/717,288
<151> 2012-10-23

<160> 130

<170> PatentIn version 3.5

<210> 1
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 1

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

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

Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

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

<210> 2
<211> 119

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 2

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


Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20                  25                  30


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


Gly Val Ile Trp Thr Gly Gly Ser Thr Asp Tyr Asn Ser Ala Leu Met
    50                  55                  60


Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65                  70                  75                  80


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


Arg Asp Gly Asp Tyr Asp Arg Tyr Thr Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Ser Val Thr Val Ser Ser
        115
```

<210> 3
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 3

```
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 Arg Ala Ser Lys Ser Val Ser Thr Ser
            20                  25                  30


Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


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


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

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

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

<210> 4
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 4

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

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

Gly Val Ile Trp Thr Gly Gly Ser Thr Asp Tyr Asn Ser Ala Leu Met
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Gly Asp Tyr Asp Arg Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 5

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

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

Gly Val Ile Trp Thr Ser Gly Val Thr Asp Tyr Asn Ser Ala Leu Met
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Gly Asp Tyr Asp Arg Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 6
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 6

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 Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30

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

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

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

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

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

<210> 7
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 7

```
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 Arg Ala Ser Lys Ser Val Ser Thr Ser
            20                  25                  30

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

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

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

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

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

<210> 8
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 8

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

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Thr Ile Gly Thr Ser
            20                  25                  30

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

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

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

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser Asn Ser Trp Pro Phe
                85                  90                  95
```

eolf-seql

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

<210> 9
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 9

Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Arg Pro Gly Ala
1 5 10 15

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

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

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

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

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

Thr Tyr Gly Ser Ser Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser
115

<210> 10
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 10

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Thr Ile Gly Thr Ser
20 25 30

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

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

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

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

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

<210> 11
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 11

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

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

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

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

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

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

Val Ser Ser
115

<210> 12
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 12

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Thr Ile Gly Thr Ser
            20                  25                  30

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

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

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

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

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

<210> 13
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 13

```
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

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

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

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

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

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

Val Ser Ser
        115
```

<210> 14
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 14
gacattgtgc tgacacagtc tcctgcttcc ttagctgtat ctctggggca gagggccacc 60

atctcatgca gggccagcaa aagtgtcagt acatctggct atagttatat gcactggtac 120

caacagaaac caggacagcc acccaaactc ctcatctatc ttgcatccaa cctagaatct 180

ggggtccctg ccaggttcag tggcagtggg tctgggacag acttcaccct caacatccat 240

cctgtggagg aggaggatgc tgcaacctat tactgtcagc acagtaggga gcttccgtac 300

acgttcggag gggggaccaa gctggagatc aaa 333

<210> 15
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 15
caggtccaac tgcaggaatc aggtccaggc ctggtgaaac cgtctgaaac cctgagcctg 60

acatgcaccg tgagcggtgg tagtattagc tcttacggcg tccattggat ccgtcaaccg 120

cctggtaaag gtctggaatg gattggcgtg atctggaccg gtggtagcac cgactataac 180

agcgcactga tgagccgcgt gaccatctcg gtagacacgt cgaaaaacca gttcagcctg 240

aaactgagca gcgtgaccgc cgcggatacc gctgtttatt actgcgcacg cgacggggat 300

tatgatcgct acaccatgga ttattggggc cagggtaccc tggtcaccgt ctcctca 357

<210> 16
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 16
gatatcgtaa tgacccaatc tccggattcg ctggcggtat cactgggcga acgtgccacg 60

attaactgcc gtgcaagcaa atcagtgtcg acctccggct acagctatat gcactggtat 120

caacagaaac cgggccagcc gccgaaactg ctgatctatc tggctagcaa cctggagagc 180

ggtgtgcctg atcgctttag tggctccggt agcggtaccg atttcacgct gaccatcagc 240

tccctgcagg cagaagacgt ggccgtgtat tattgtcagc acagccgtga gctgccgtat 300

actttggcc aggggacaaa actggaaatc aaa 333

<210> 17
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 17
caggtccaac tgcaggaatc aggtccaggc ctggtgaaac cgtctgaaac cctgagcctg 60

acatgcaccg tgagcggtgg tagtattagc tcttacggcg tccattggat ccgtcaaccg 120

cctggtaaag gtctggaatg gattggcgtg atctggaccg gtggtagcac cgactataac 180

agcgcactga tgagccgcgt gaccatctcg gtagacacgt cgaaaaacca gttcagcctg 240

aaactgagca gcgtgaccgc cgcggatacc gctgtttatt actgcgcacg cgacggggat 300

tatgatcgct acaccatgga ttattggggc cagggtaccc tggtcaccgt ctcctca 357

<210> 18
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 18
caggtccaac tgcaggaatc aggtccaggc ctggtgaaac cgtctgaaac cctgagcctg 60

acatgcaccg tgagcggtgg tagtattagc tcttacggcg tccattggat ccgtcaaccg 120

cctggtaaag gtctggaatg gattggcgtg atctggacca gtggtgtgac cgactataac 180

agcgcactga tgggccgcgt gaccatctcg gtagacacgt cgaaaaacca gttcagcctg 240

aaactgagca gcgtgaccgc cgcggatacc gctgtttatt actgcgcacg cgacggggat 300

tatgatcgct acaccatgga ttattggggc cagggtaccc tggtcaccgt ctcctca 357

<210> 19
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 19
gatatcgtaa tgacccaatc tccggattcg ctggcggtat cactgggcga acgtgccacg 60

attaactgcc gtgcaagcaa atcagtgtcg acctccttgt acagctatat gcactggtat 120

caacagaaac cgggccagcc gccgaaactg ctgatctatc tggctagcaa cctggagagc 180

ggtgtgcctg atcgctttag tggctccggt agcggtaccg atttcacgct gaccatcagc 240

tccctgcagg cagaagacgt ggccgtgtat tattgtcagc acagccgtga gctgccgtat 300

actttggcc aggggacaaa actggaaatc aaa 333

<210> 20
<211> 333

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 20
gatatcgtaa tgacccaatc tccggattcg ctggcggtat cactgggcga acgtgccacg 60

attaactgcc gtgcaagcaa atcagtgtcg acctccaatt acagctatat gcactggtat 120

caacagaaac cgggccagcc gccgaaactg ctgatctatc tggctagcaa cctggagagc 180

ggtgtgcctg atcgctttag tggctccggt agcggtaccg atttcacgct gaccatcagc 240

tccctgcagg cagaagacgt ggccgtgtat tattgtcagc acagccgtga gctgccgtat 300

acttttggcc aggggacaaa actggaaatc aaa 333

<210> 21
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 21
gacatcttgc tgactcagtc tccagccatc ctgtctgtga gtccaggaga aagagtcagt 60

ttctcctgca gggccagtca gaccattggc acaagcatac actggtatca gcaaagaaca 120

aatggttctc caaggcttct cataaagtat gcttctgagt ctatctctgg gatcccttcc 180

aggtttagtg gcagtggatc agggacagat tttactctta gcatcaacag tgtggagtct 240

gaagatattg cagattatta ctgtcaacaa agtaatagct ggccattcac gttcggctcg 300

gggaccaagc tggaaataaa a 321

<210> 22
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 22
caggtccaac tgcagcagcc tggggctgag ctggtgaggc ctggggcttc agtgaagctg 60

tcctgcaagg cttctggcta caccttcacc agctactgga taaactgggt gaagcagagg 120

cctggacatg gccttgagtg gatcggaaat atttatcctt ctgatagtta ttctaactac 180

aatcaaaagt tcaaggacaa ggccacattg actgtagaca aatcctccag cacagcctac 240

atgcaggtca gcagcccgac atctgaggac tctgcggtct attactgtac gtacggtagt 300

agctttgact actggggcca aggcaccacg gtcaccgtct cctca 345

<210> 23
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 23
gagatcgtgc tgacccaaag tccagccacc ctttccctgt ctccaggcga acgcgcaacc 60

ctgagctgcc gcgcttctca gaccattggt acctccattc attggtatca gcagaagccc 120

ggccaagccc cgcgtctgct gatctattac gcctcagaaa gtatttcagg catccccgct 180

cgcttctccg gctccggcag cggaaccgac ttcacactta caatctctag tttggagcca 240

gaagacttcg ccgtttacta ctgtcagcag tctaacagct ggccatttac ctttggccag 300

ggcacgaagc tggaaatcaa g 321

<210> 24
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 24
caggtgcagt tggttcagag cggcgcggaa gtcaagaaac ccggcgcctc cgtgaaagtg 60

agctgcaaag cgagcggcta caccttcacc agttattgga ttaactgggt gcgccaggcc 120

ccaggccagg ggctggagtg gatgggaaac atctacccat ctgactctta cagcaactat 180

aatcagaaat ttaaggatcg cgtaacaatg acccgtgaca ccagcaccag cactgtttac 240

atggagctga gttctctgcg ttctgaagat accgccgtgt actactgcgc acgcggttcc 300

agtttcgatt actggggcca ggggaccctg gtcaccgtct cctca 345

<210> 25
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 25
caggtgcagt tggttcagag cggcgcggaa gtcaagaaac ccggcgcctc cgtgaaagtg 60

agctgcaaag cgagcggcta caccttcacc agttattgga ttaactgggt gcgccaggcc 120

ccaggccagg ggctggagtg gatgggaaac atcttcccat ctgactctta cagcaactat 180

aataagaaat ttaaggatcg cgtaacaatg acccgtgaca ccagcaccag cactgtttac 240

atggagctga gttctctgcg ttctgaagat accgccgtgt actactgcgc acgcggttcc 300

gggttcgatt actggggcca ggggaccctg gtcaccgtct cctca 345

<210> 26
<211> 321
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 26

gagatcgtgc tgacccaaag tccagccacc ctttccctgt ctccaggcga acgcgcaacc 60

ctgagctgcc gcgcttctca gaccattggt acctccattc attggtatca gcagaagccc 120

ggccaagccc cgcgtctgct gatctattac gcctcagaaa gtatttcagg catccccgct 180

cgcttctccg gctccggcag cggaaccgac ttcacactta caatctctag tttggagcca 240

gaagacttcg ccgtttacta ctgttcgcag tcttttagct ggccatttac ctttggccag 300

ggcacgaagc tggaaatcaa g 321

<210> 27
<211> 323
<212> PRT
<213> Homo sapiens

<400> 27

Met Ala Arg Gly Pro Gly Leu Ala Pro Pro Pro Leu Arg Leu Pro Leu
1 5 10 15

Leu Leu Leu Val Leu Ala Ala Val Thr Gly His Thr Ala Ala Gln Asp
20 25 30

Asn Cys Thr Cys Pro Thr Asn Lys Met Thr Val Cys Ser Pro Asp Gly
35 40 45

Pro Gly Gly Arg Cys Gln Cys Arg Ala Leu Gly Ser Gly Met Ala Val
50 55 60

Asp Cys Ser Thr Leu Thr Ser Lys Cys Leu Leu Leu Lys Ala Arg Met
65 70 75 80

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

Leu Val Asp Asn Asp Gly Leu Tyr Asp Pro Asp Cys Asp Pro Glu Gly
100 105 110

Arg Phe Lys Ala Arg Gln Cys Asn Gln Thr Ser Val Cys Trp Cys Val
115 120 125

Asn Ser Val Gly Val Arg Arg Thr Asp Lys Gly Asp Leu Ser Leu Arg
130 135 140

Cys Asp Glu Leu Val Arg Thr His His Ile Leu Ile Asp Leu Arg His
145 150 155 160

Arg Pro Thr Ala Gly Ala Phe Asn His Ser Asp Leu Asp Ala Glu Leu
165 170 175

Arg Arg Leu Phe Arg Glu Arg Tyr Arg Leu His Pro Lys Phe Val Ala

180 185 190

Ala Val His Tyr Glu Gln Pro Thr Ile Gln Ile Glu Leu Arg Gln Asn
195 200 205

Thr Ser Gln Lys Ala Ala Gly Asp Val Asp Ile Gly Asp Ala Ala Tyr
210 215 220

Tyr Phe Glu Arg Asp Ile Lys Gly Glu Ser Leu Phe Gln Gly Arg Gly
225 230 235 240

Gly Leu Asp Leu Arg Val Arg Gly Glu Pro Leu Gln Val Glu Arg Thr
245 250 255

Leu Ile Tyr Tyr Leu Asp Glu Ile Pro Pro Lys Phe Ser Met Lys Arg
260 265 270

Leu Thr Ala Gly Leu Ile Ala Val Ile Val Val Val Val Val Ala Leu
275 280 285

Val Ala Gly Met Ala Val Leu Val Ile Thr Asn Arg Arg Lys Ser Gly
290 295 300

Lys Tyr Lys Lys Val Glu Ile Lys Glu Leu Gly Glu Leu Arg Lys Glu
305 310 315 320

Pro Ser Leu

<210> 28
<211> 317
<212> PRT
<213> Mus musculus

<400> 28

Met Ala Arg Gly Leu Asp Leu Ala Pro Leu Leu Leu Leu Leu Leu Ala
1 5 10 15

Met Ala Thr Arg Phe Cys Thr Ala Gln Ser Asn Cys Thr Cys Pro Thr
20 25 30

Asn Lys Met Thr Val Cys Asp Thr Asn Gly Pro Gly Gly Val Cys Gln
35 40 45

Cys Arg Ala Met Gly Ser Gln Val Leu Val Asp Cys Ser Thr Leu Thr
50 55 60

Ser Lys Cys Leu Leu Leu Lys Ala Arg Met Ser Ala Arg Lys Ser Gly
65 70 75 80

Arg Ser Leu Val Met Pro Ser Glu His Ala Ile Leu Asp Asn Asp Gly
85 90 95

```
Leu Tyr Asp Pro Glu Cys Asp Asp Lys Gly Arg Phe Lys Ala Arg Gln
            100                 105                 110

Cys Asn Gln Thr Ser Val Cys Trp Cys Val Asn Ser Val Gly Val Arg
        115                 120                 125

Arg Thr Asp Lys Gly Asp Gln Ser Leu Arg Cys Asp Glu Val Val Arg
    130                 135                 140

Thr His His Ile Leu Ile Glu Leu Arg His Arg Pro Thr Asp Arg Ala
145                 150                 155                 160

Phe Asn His Ser Asp Leu Asp Ser Glu Leu Arg Arg Leu Phe Gln Glu
                165                 170                 175

Arg Tyr Lys Leu His Pro Ser Phe Leu Ser Ala Val His Tyr Glu Glu
            180                 185                 190

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

Arg Asp Val Asp Ile Ala Asp Ala Ala Tyr Tyr Phe Glu Arg Asp Ile
    210                 215                 220

Lys Gly Glu Ser Leu Phe Met Gly Arg Arg Gly Leu Asp Val Gln Val
225                 230                 235                 240

Arg Gly Glu Pro Leu His Val Glu Arg Thr Leu Ile Tyr Tyr Leu Asp
                245                 250                 255

Glu Lys Pro Pro Gln Phe Ser Met Lys Arg Leu Thr Ala Gly Val Ile
            260                 265                 270

Ala Val Ile Ala Val Val Ser Val Ala Val Val Ala Gly Val Val Val
        275                 280                 285

Leu Val Val Thr Lys Arg Arg Lys Ser Gly Lys Tyr Lys Lys Val Glu
    290                 295                 300

Leu Lys Glu Leu Gly Glu Met Arg Ser Glu Pro Ser Leu
305                 310                 315


<210>  29
<211>  314
<212>  PRT
<213>  Homo sapiens

<400>  29

Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
1               5                   10                  15
```

```
Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
            20                  25                  30

Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
        35                  40                  45

Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
    50                  55                  60

Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
65                  70                  75                  80

Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
                85                  90                  95

Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
            100                 105                 110

Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
        115                 120                 125

Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
    130                 135                 140

Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
145                 150                 155                 160

Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
                165                 170                 175

Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
            180                 185                 190

Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
        195                 200                 205

Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
    210                 215                 220

Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
225                 230                 235                 240

Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
                245                 250                 255

Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile
            260                 265                 270

Val Val Val Val Ile Ala Val Val Ala Gly Ile Val Val Leu Val Ile
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Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
290 295 300

Met Gly Glu Met His Arg Glu Leu Asn Ala
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Gly Phe Ser Leu Thr Ser Tyr
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Gly Phe Ser Leu Thr Ser Tyr Gly Val His
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Val Ile Trp Thr Gly Gly Ser Thr Asp Tyr Asn Ser Ala Leu Met Ser
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Trp Thr Gly Gly Ser
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Asp Gly Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
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Gly Gly Ser Ile Ser Ser Tyr
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Gly Gly Ser Ile Ser Ser Tyr Gly Val His
1 5 10

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Trp Thr Ser Gly Val
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Gly Tyr Thr Phe Thr Ser Tyr Trp Ile Asn
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Asn Ile Tyr Pro Ser Asp Ser Tyr Ser Asn Tyr Asn Gln Lys Phe Lys
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Asp

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Tyr Pro Ser Asp Ser Tyr
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Gly Ser Ser Phe Asp Tyr
1 5

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Asn Ile Phe Pro Ser Asp Ser Tyr Ser Asn Tyr Asn Lys Lys Phe Lys
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Asp

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Phe Pro Ser Asp Ser Tyr
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Val Ile Trp Thr Xaa Gly Xaa Thr Asp Tyr Asn Ser Ala Leu Met Xaa
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Gly Ser Xaa Phe Asp Tyr

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Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met His
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Leu Ala Ser Asn Leu Glu Ser
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Gln His Ser Arg Glu Leu Pro Tyr Thr
1 5

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

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<400> 58

Arg Ala Ser Lys Ser Val Ser Thr Ser Asn Tyr Ser Tyr Met His
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<400> 59

Arg Ala Ser Gln Thr Ile Gly Thr Ser Ile His
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Tyr Ala Ser Glu Ser Ile Ser
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Gln Gln Ser Asn Ser Trp Pro Phe Thr
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Ser Gln Ser Phe Ser Trp Pro Phe Thr
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Xaa Gln Ser Xaa Ser Trp Pro Phe Thr
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Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

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

Gly Val Ile Trp Thr Ser Gly Val Thr Asp Tyr Asn Ser Ala Leu Met
50 55 60

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

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Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Gly Asp Tyr Asp Arg Tyr Thr Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110

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

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140

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

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

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

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

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

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

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

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

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
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Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

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

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

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

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

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

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

Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

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

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

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

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
        115                 120                 125
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Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

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

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

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

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

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

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

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

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Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
    130                 135                 140

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

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

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

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

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
    210                 215                 220

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

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

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            260                 265                 270

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

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

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

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

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

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

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

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385                 390                 395                 400
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Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Asp Cys Asp Xaa Xaa Gly Xaa Phe Lys Ala Lys Gln Cys Asn Xaa
100 105 110

Thr Ser Xaa Cys Trp Cys Val Asn Ser Xaa Gly Val Arg Arg Thr Asp
115 120 125

Lys Xaa Asp Xaa Xaa Ile Xaa Cys Xaa Glu Xaa Val Arg Thr His Xaa
130 135 140

Ile Ile Ile Asp Leu Lys His Lys Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa
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Xaa Xaa Leu Xaa Xaa Xaa Leu Xaa Lys Xaa Xaa Xaa Xaa Arg Tyr Xaa
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Leu Xaa Pro Lys Phe Ile Xaa Ala Ile Xaa Tyr Glu Asn Xaa Xaa Ile
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Xaa Ile Asp Leu Xaa Gln Asn Ser Ser Gln Lys Xaa Xaa Xaa Asp Val
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Asp Ile Ala Asp Xaa Ala Tyr Tyr Phe Glu Lys Asp Ile Lys Gly Glu
210 215 220

Ser Leu Phe Xaa Xaa Lys Xaa Xaa Leu Asp Leu Xaa Val Xaa Gly Glu
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Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Thr Leu Ile Tyr Tyr Leu Asp Glu
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Xaa Xaa Pro Xaa Phe Ser Met Xaa Xaa Leu Xaa Ala Gly Leu Ile Ala
260 265 270

Val Ile Val Val Val Val Ile Ala Leu Val Ala Gly Ile Xaa Val Leu
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            20                  25                  30

Asn Cys Thr Cys Pro Thr Asn Lys Met Thr Val Cys Xaa Xaa Xaa Gly
        35                  40                  45

Pro Gly Gly Xaa Cys Gln Cys Arg Ala Leu Gly Ser Xaa Met Xaa Val
    50                  55                  60

Asp Cys Ser Thr Leu Thr Ser Lys Cys Leu Leu Leu Lys Ala Arg Met
65                  70                  75                  80

Ser Ala Xaa Lys Xaa Ala Arg Ser Leu Val Xaa Pro Ser Glu His Ala
                85                  90                  95

Ile Leu Asp Asn Asp Gly Leu Tyr Asp Pro Asp Cys Asp Xaa Xaa Gly
            100                 105                 110

Arg Phe Lys Ala Arg Gln Cys Asn Gln Thr Ser Val Cys Trp Cys Val
        115                 120                 125
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Asn Ser Val Gly Val Arg Arg Thr Asp Lys Gly Asp Xaa Ser Leu Arg
130 135 140

Cys Asp Glu Leu Val Arg Thr His His Ile Leu Ile Asp Leu Arg His
145 150 155 160

Arg Pro Thr Xaa Xaa Ala Phe Asn His Ser Asp Leu Asp Ala Glu Leu
165 170 175

Arg Arg Leu Phe Xaa Glu Arg Tyr Lys Leu His Pro Xaa Phe Leu Ala
180 185 190

Ala Val His Tyr Glu Xaa Pro Thr Ile Gln Ile Glu Leu Arg Gln Asn
195 200 205

Xaa Ser Gln Lys Ala Xaa Xaa Asp Val Asp Ile Ala Asp Ala Ala Tyr
210 215 220

Tyr Phe Glu Arg Asp Ile Lys Gly Glu Ser Leu Phe Xaa Gly Arg Xaa
225 230 235 240

Gly Leu Asp Leu Xaa Val Arg Gly Glu Pro Leu Xaa Val Glu Arg Thr
245 250 255

Leu Ile Tyr Tyr Leu Asp Glu Xaa Pro Pro Xaa Phe Ser Met Lys Arg
260 265 270

Leu Thr Ala Gly Leu Ile Ala Val Ile Xaa Val Val Xaa Val Ala Leu
275 280 285

Val Ala Gly Met Xaa Val Leu Val Ile Thr Xaa Arg Arg Lys Ser Gly
290 295 300

Lys Tyr Lys Lys Val Glu Ile Lys Glu Leu Gly Glu Leu Arg Xaa Glu
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Pro Ser Leu

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

Gly Val Ile Trp Thr Gly Gly Ser Thr Asp Tyr Asn Ser Ala Leu Met
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

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

Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

Glu Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
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Trp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

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

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
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Ala Arg Gly Ser Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
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Val Ser Ser
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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Thr Ile Gly Thr Ser
20 25 30

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Asn Ser Trp Pro Phe
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Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
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Gly Xaa Ser Xaa Xaa Ser Tyr
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Gly Gly Leu Leu Gln Gly Gly
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Leu Leu Gln Gly Ala
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Gly Gly Leu Leu Gln Gly Ala

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Asp Tyr Asp Arg Tyr Thr Xaa Asp Tyr
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Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45


Gly Val Ile Trp Thr Ser Gly Val Thr Asp Tyr Asn Ser Ala Leu Met
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
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Arg Xaa Xaa Asp Tyr Asp Arg Tyr Thr Xaa Asp Tyr Trp Gly Gln Gly
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Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Trp Thr Ser Gly Val Thr Asp Tyr Asn Ser Ala Leu Met
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Xaa Xaa Asp Tyr Asp Arg Tyr Thr Xaa Asp Tyr Trp Gly Gln Gly
100 105 110

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<400> 87

Xaa Xaa Asp Tyr Asp Arg Tyr Thr Xaa Asp Tyr
1 5 10

<210> 88
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa can be G or P

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa can be A, G, P, or absent

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa can be A, G, K, P, or absent

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa can be G, K, or absent

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa can be K or absent

<400> 88

Leu Leu Gln Xaa Xaa Xaa Xaa Xaa
1 5

<210> 89
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa can be any naturally occurring amino acid or absent

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa can be any naturally occurring amino acid or absent

<220>
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<222> (7)..(7)
<223> Xaa can be any naturally occurring amino acid or absent

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa can be any naturally occurring amino acid or absent

<400> 89

Leu Leu Gln Xaa Xaa Xaa Xaa Xaa
1 5

<210> 90
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 90

Leu Leu Gln Gly Pro Gly Lys
1 5

<210> 91
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 91

Leu Leu Gln Gly Pro Gly
1 5

<210> 92
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 92

Leu Leu Gln Gly Pro Ala
1 5

<210> 93
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 93

Leu Leu Gln Gly Pro
1 5

<210> 94
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 94

Leu Leu Gln Pro
1

<210> 95
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 95

Leu Leu Gln Pro Gly Lys
1 5

<210> 96
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 96

Leu Leu Gln Gly Ala Pro Gly Lys
1 5

<210> 97
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 97

Leu Leu Gln Gly Ala Pro Gly
1 5

<210> 98
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 98

Leu Leu Gln Gly Ala Pro
1 5

<210> 99
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 99

Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5

<210> 100
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 100

Asp Tyr Asp Arg Tyr Thr Glu Asp Tyr
1 5

<210> 101
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> MISC_FEATURE
<222> (98)..(98)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (99)..(99)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (106)..(106)
<223> Xaa can be any naturally occurring amino acid

<400> 101

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


Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
            20                  25                  30


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


Gly Val Ile Trp Thr Ser Gly Val Thr Asp Tyr Asn Ser Ala Leu Met
    50                  55                  60


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95


Arg Xaa Xaa Asp Tyr Asp Arg Tyr Thr Xaa Asp Tyr Trp Gly Gln Gly
            100                 105                 110


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


Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140


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


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


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


Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205
```

```
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

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

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

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

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

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

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

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

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

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

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

Lys
```

<210> 102
<211> 449

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> MISC_FEATURE
<222> (98)..(98)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (99)..(99)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (106)..(106)
<223> Xaa can be E or M

<400> 102

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
            20                  25                  30

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

Gly Val Ile Trp Thr Ser Gly Val Thr Asp Tyr Asn Ser Ala Leu Met
    50                  55                  60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Xaa Xaa Asp Tyr Asp Arg Tyr Thr Xaa Asp Tyr Trp Gly Gln Gly
            100                 105                 110

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

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140

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

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
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```
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

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

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

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

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

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

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

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

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

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

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

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

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

<210> 103
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 103

Leu Gly Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 104
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 104

Tyr Gly Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 105
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 105

Phe Gly Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 106
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 106

His Gly Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 107
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 107

Ala Gly Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 108
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 108

Thr Gly Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 109
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 109

Ser Gly Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 110
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 110

Ile Gly Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 111
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<400> 111

Arg Gly Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 112
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 112

Val Gly Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 113
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 113

Trp Gly Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 114
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 114

Gln Gly Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 115
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 115

Gly Gly Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 116
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 116

Lys Gly Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 117
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 117

Asp Ser Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1   5   10

<210> 118
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 118

Asp Lys Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1   5   10

<210> 119
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 119

Asp His Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1   5   10

<210> 120
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 120

Asp Ala Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1   5   10

<210> 121
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 121

Asp Phe Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1   5   10

<210> 122
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 122

Asp Thr Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 123
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 123

Asp Arg Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 124
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 124

Asp Val Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 125
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 125

Asp Gln Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 126
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 126

Asp Leu Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 127
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 127

Asp Tyr Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 128
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 128

Asp Glu Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 129
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 129

Asp Asn Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10

<210> 130
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 130

Asp Trp Asp Tyr Asp Arg Tyr Thr Met Asp Tyr
1 5 10