SEQUENCE LISTING

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<120> COMPOSITIONS AND METHODS RELATED TO ENGINEERED Fc CONSTRUCTS

<130> 50937-012WO3

<150> US 62/081,923
<151> 2014-11-19

<150> US 61/987,863
<151> 2014-05-04

<160> 46

<170> PatentIn version 3.5

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Gly Gly Gly Gly Ser
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Gly Gly Ser Gly
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Ser Gly Gly Gly
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Gly Ser Gly Ser
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Gly Ser Gly Ser Gly Ser
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Gly Ser Gly Ser Gly Ser Gly Ser
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<400> 9

Gly Gly Ser Gly Gly Ser
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Gly Gly Ser Gly Gly Ser Gly Gly Ser
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Gly Gly Ser Gly
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Gly Gly Ser Gly
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Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
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Gly Gly Gly Gly Ser
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<400> 17

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
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<400> 18

Gly Glu Asn Leu Tyr Phe Gln Ser Gly Gly

1 5 10

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<220>
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<400> 19

Ser Ala Cys Tyr Cys Glu Leu Ser
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<400> 20

Arg Ser Ile Ala Thr
1 5

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<400> 21

Arg Pro Ala Cys Lys Ile Pro Asn Asp Leu Lys Gln Lys Val Met Asn
1 5 10 15

His

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<223> Synthetic Construct

<400> 22

Gly Gly Ser Ala Gly Gly Ser Gly Ser Gly Ser Ser Gly Gly Ser Ser
1   5   10   15

Gly Ala Ser Gly Thr Gly Thr Ala Gly Gly Thr Gly Ser Gly Ser Gly
            20   25   30

Thr Gly Ser Gly
        35

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Ala Ala Ala Asn Ser Ser Ile Asp Leu Ile Ser Val Pro Val Asp Ser
1   5   10   15

Arg

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<400> 24

Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly
1   5   10   15

Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser
            20   25   30

Gly Gly Gly Ser
        35

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<220>
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<400> 25

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10

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

<220>
<223> Synthetic Construct

<400> 26

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
1 5 10 15

Ser Gly Gly Gly
20

<210> 27
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 27

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
1 5 10 15

Gly Ser

<210> 28
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 28

Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp
1   5   10

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<211> 681
<212> DNA
<213> Homo sapiens

<400> 29
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ttcctgttcc ccccaaagcc caaggacacc ctgatgatca gccggacccc cgaagtgacc   120

tgcgtggtgg tggacgtgtc ccacgaggac cctgaagtga agttcaattg gtacgtggac   180

ggcgtggaag tgcacaacgc caagaccaag cccagagagg aacagtacaa cagcacctac   240

cgggtggtgt ccgtgctgac cgtgctgcac caggactggc tgaacggcaa agaatacaag   300

tgcaaagtct ccaacaaggc cctgcctgcc cccatcgaga aaaccatcag caaggccaag   360

ggccagcccc gcgagcccca ggtgtacaca ctgccccca gccgggacga gctgaccaag   420

aaccaggtgt ccctgacctg cctggtgaaa ggcttctacc ccagcgatat cgccgtggaa   480

tgggagagca acggccagcc cgagaacaac tacaagacca ccccccctgt gctggacagc   540

gacggctcat tcttcctgta cagcaagctg accgtggaca agagccggtg gcagcagggc   600

aacgtgttca gctgcagcgt gatgcacgag gccctgcaca accactacac ccagaagtcc   660

ctgagcctga gccccggcaa g   681

<210> 30
<211> 227
<212> PRT
<213> Homo sapiens

<400> 30

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1   5   10   15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30

```
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

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

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190

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

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225
```

<210> 31
<211> 681

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 31
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ttcctgttcc ccccaaagcc caaggacacc ctgatgatca gccggacccc cgaagtgacc 120

tgcgtggtgg tggacgtgtc ccacgaggac cctgaagtga agttcaattg gtacgtggac 180

ggcgtggaag tgcacaacgc caagaccaag cccagagagg aacagtacaa cagcacctac 240

cgggtggtgt ccgtgctgac cgtgctgcac caggactggc tgaacggcaa agaatacaag 300

tgcaaagtct ccaacaaggc cctgcctgcc cccatcgaga aaaccatcag caaggccaag 360

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aaccaggtgt ccctgtggtg cctggtgaaa ggcttctacc ccagcgatat cgccgtggaa 480

tgggagagca acggccagcc cgagaacaac tacaagacca ccccccctgt gctggacagc 540

gacggctcat tcttcctgta cagcaagctg accgtggaca agagccggtg gcagcagggc 600

aacgtgttca gctgcagcgt gatgcacgag gccctgcaca accactacac ccagaagtcc 660

ctgagcctga gccccggcaa g 681

<210> 32
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 32

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

```
    50                  55                  60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190

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

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225
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<210> 33
<211> 681
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 33
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ttcctgttcc ccccaaagcc caaggacacc ctgatgatca gccggacccc cgaagtgacc 120

tgcgtggtgg tggacgtgtc ccacgaggac cctgaagtga agttcaattg gtacgtggac 180

ggcgtggaag tgcacaacgc caagaccaag cccagagagg aacagtacaa cagcacctac 240

cgggtggtgt ccgtgctgac cgtgctgcac caggactggc tgaacggcaa agaatacaag 300

tgcaaagtct ccaacaaggc cctgcctgcc cccatcgaga aaaccatcag caaggccaag 360

ggccagcccc gcgagcccca agtgtgtaca ctgccccca gccgggacga gctgaccaag 420

aaccaggtgt ccctgagctg cgccgtgaaa ggcttctacc ccagcgatat cgccgtggaa 480

tgggagagca acggccagcc cgagaacaac tacaagacca ccccccctgt gctggacagc 540

gacggctcat tcttcctggt tagcaagctg accgtggaca agagccggtg gcagcagggc 600

aacgtgttca gctgcagcgt gatgcacgag gccctgcaca accactacac ccagaagtcc 660

ctgagcctga gccccggcaa g 681

<210> 34
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 34

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

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

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

```
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

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

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

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

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

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225
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<210> 35
<211> 681
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

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ttcctgttcc ccccaaagcc caaggacacc ctgatgatca gccggacccc cgaagtgacc 120

tgcgtggtgg tggacgtgtc ccacgaggac cctgaagtga agttcaattg gtacgtggac 180

ggcgtggaag tgcacaacgc caagaccaag cccagagagg aacagtacaa cagcacctac 240

cgggtggtgt ccgtgctgac cgtgctgcac caggactggc tgaacggcaa agaatacaag 300

tgcaaagtct ccaacaaggc cctgcctgcc cccatcgaga aaaccatcag caaggccaag 360

ggccagcccc gcgagcccca ggtgtacaca ctgcccccca gccgggacga gctgaccaag 420

aaccaggtgt ccctgacctg cctggtgaaa ggcttctacc ccagcgatat cgccgtggaa 480

tgggagagca acggccagcc cgagaacaac tacaagacca ccccccctgt gctgaaaagc 540

gacggctcat tcttcctgta cagcgacctg accgtggaca agagccggtg gcagcagggc 600

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ctgagcctga gccccggcaa g 681

<210> 36
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
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<400> 36

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

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

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

```
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val
            180                 185                 190

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

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225
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<210> 37
<211> 1398
<212> DNA
<213> Artificial Sequence

<220>
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ttcctgttcc ccccaaagcc caaggacacc ctgatgatca gccggacccc cgaagtgacc 120

tgcgtggtgg tggacgtgtc ccacgaggac cctgaagtga agttcaattg gtacgtggac 180

ggcgtggaag tgcacaacgc caagaccaag cccagagagg aacagtacaa cagcacctac 240

cgggtggtgt ccgtgctgac cgtgctgcac caggactggc tcaacggcaa agagtacaag 300

tgcaaggtgt ccaacaaggc cctgcctgcc cccatcgaga aaaccatcag caaggccaag 360

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aaccaggtct ccctgacctg cctggtgaaa ggcttctacc ccagcgatat cgccgtggaa 480

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tccctgtccc ccggcaag 1398

<210> 38
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 38

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

```
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

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

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190

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

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp
225                 230                 235                 240

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                245                 250                 255
```

```
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
    290                 295                 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
305                 310                 315                 320

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335

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

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
        355                 360                 365

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
    370                 375                 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385                 390                 395                 400

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
                405                 410                 415

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
            420                 425                 430

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
        435                 440                 445

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
    450                 455                 460

Gly Lys
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465

<210> 39
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
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<400> 39
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tgcgtggtgg tggacgtgtc ccacgaggac cctgaagtga agttcaattg gtacgtggac 180

ggcgtggaag tgcacaacgc caagaccaag cccagagagg aacagtacaa cagcacctac 240

cgggtggtgt ccgtgctgac cgtgctgcac caggactggc tgaacggcaa agagtacaag 300

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aagtttaatt ggtatgtcga tggggtcgag gtgcacaatg ccaaaacaaa acctcgggaa 960

gaacagtata actccacata cagagtggtg tctgtcctca cagtcctgca tcaggattgg 1020

ctcaatggga aagagtacaa atgtaaagtc tctaacaagg ctctccccgc tccgatcgaa 1080

aagaccatct ccaaagccaa agggcagccc agagaacctc aggtctacac actgcctccc 1140

agccgggacg agctgacaaa aaatcaagtg tctctgacct gcctcgtgaa gggcttttat 1200

ccctccgaca ttgccgtcga gtgggagtcc aatggacagc cggaaaacaa ttataagacc 1260

acgcctccag tgctgaagtc cgacggcagc ttctttctgt actccgacct gacagtggat 1320

aagtccagat ggcagcaagg gaatgtgttc tcctgttccg tgatgcatga agccctccat 1380

aatcactata cccagaaaag cctgtccctg tcccctggca ag 1422

<210> 40
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 40

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

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

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125

Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140

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

```
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190

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

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
225                 230                 235                 240

Gly Gly Gly Ser Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys
                245                 250                 255

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
    290                 295                 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
    370                 375                 380
```

```
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385                 390                 395                 400


Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415


Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe
            420                 425                 430


Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
        435                 440                 445


Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460


Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 41
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 41

```
gacaagaccc acacctgtcc cccttgccct gcccctgagc tgctgggagg ccccagcgtg       60

ttcctgttcc ccccaaagcc caaggacacc ctgatgatca gccggacccc cgaagtgacc      120

tgcgtggtgg tggacgtgtc ccacgaggac cctgaagtga agttcaattg gtacgtggac      180

ggcgtggaag tgcacaacgc caagaccaag cccagagagg aacagtacaa cagcacctac      240

cgggtggtgt ccgtgctgac cgtgctgcac caggactggc tgaacggcaa agagtacaag      300

tgcaaggtgt ccaacaaggc cctgcctgcc cccatcgaga aaaccatcag caaggccaag      360

ggccagcccc gcgagcccca ggtgtacacc ctgccccctt gcagagatga actgaccaag      420

aaccaggtgt ccctgtggtg cctggtcaag ggcttctacc ccagcgatat cgccgtggaa      480

tgggagagca acggccagcc cgagaacaac tacaagacca ccccccctgt gctggacagc      540

gacggctcat tcttcctgta cagcaagctg accgtggaca agagccggtg gcagcagggc      600
```

aacgtgttca gctgcagcgt gatgcacgag gccctgcaca accactacac ccagaagtcc 660

ctgagcctga gccccggcaa gtctgggggа ggatcagggg gtggaagtgg cggtggatct 720

ggtggtggaa gcggaggcgg cgataagaca cacacatgcc ccccctgtcc agctcccgaa 780

ctgctggggg gaccctccgt gtttctgttt ccacctaagc ctaaggatac gctcatgatc 840

tccagaaccc ctgaagtcac atgtgtggtg gtcgatgtgt ctcatgaaga tcccgaagtc 900

aagtttaact ggtatgtgga tggggtcgag gtccacaatg ccaaaacaaa gcctcgggaa 960

gaacagtata actccaccta cagagtcgtc agcgtgctga cagtcctgca tcaagattgg 1020

ctcaatggga aagagtataa gtgtaaagtc tcgaacaaag ccctccccgc tcctatcgaa 1080

aagaccatct ccaaagccaa agggcagccc agagaacctc aggtctacac actgcctcca 1140

tgtcgggacg agctgacaaa aaatcaggtg tcactgtggt gtctggtgaa ggggttttac 1200

ccttccgaca ttgctgtgga atgggaatcc aatgggcagc ctgaaaacaa ttataagaca 1260

acacctcccg tgctggactc cgatggctca ttttttctgt actctaaact gacagtggat 1320

aagtccagat ggcagcaggg aaatgtgttt tcctgctctg tgatgcatga agctctgcat 1380

aatcactata cacagaaaag cctgtccctg tcccctggca ag 1422

<210> 42
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 42

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

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

```
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190

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

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
225                 230                 235                 240

Gly Gly Gly Ser Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys
                245                 250                 255

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285
```

```
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
    290                 295                 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu
    370                 375                 380

Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr
385                 390                 395                 400

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            420                 425                 430

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
        435                 440                 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 43
<211> 1365
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 43
aggacagtgg ccgctcccag cgtgttcatc ttcccaccca gcgacgagca gctgaagtcc 60

ggcacagcca gcgtggtctg cctgctgaac aacttctacc cccgcgaggc caaggtgcag 120

tggaaggtgg acaacgccct gcagagcggc aacagccagg aaagcgtcac cgagcaggac 180

agcaaggact ccacctacag cctgtctagc accctgaccc tgagcaaggc cgactacgag 240

aagcacaagg tgtacgcctg cgaagtgacc caccagggcc tgtccagccc cgtgaccaag 300

agcttcaaca gaggcgagtg cggcggctct ggcggaggat ccgggggagg atcaggcggc 360

ggaagcggag gcagcgctag cacaaagggc ccctccgtgt tccccctggc ccccagcagc 420

aagagcacat ctggcggaac agccgccctg ggctgcctgg tgaaagacta cttccccgag 480

cccgtgaccg tgtcctggaa ctctggcgcc ctgaccagcg gcgtgcacac ctttccagcc 540

gtgctgcaga gcagcggcct gtactccctg agcagcgtgg tgacagtgcc tagcagcagc 600

ctgggcaccc agacctacat ctgcaacgtg aaccacaagc ccagcaacac caaagtggac 660

aagcgggtgg aacccaagag ctgcgacaag acccacacgt gtccccctg cccagccct 720

gaactgctgg gcggacctag cgtgttcctg ttcccccaa agcccaagga caccctgatg 780

atcagccgga cccccgaagt gacctgcgtg gtggtggacg tgtcccacga ggaccctgaa 840

gtgaagttca attggtacgt ggacggcgtg gaagtgcaca atgccaagac caagcccaga 900

gaggaacagt acaacagcac ctaccgggtg gtgtccgtgc tgaccgtgct gcaccaggac 960

tggctgaacg gcaaagagta caagtgcaag gtctccaaca aggccctgcc tgcccccatc 1020

gagaaaacca tcagcaaggc caagggccag ccccgcgagc cccaggtgta cacactgccc 1080

cccagccggg acgagctgac caagaaccag gtgtccctga cctgtctggt gaaaggcttc 1140

taccctccg atatcgccgt ggaatgggag agcaacggcc agcccgagaa caactacaag 1200

accacccccc ctgtgctgga ctccgacggc tcattcttcc tgtacagcaa gctgaccgtg 1260

gacaagagcc ggtggcagca gggcaacgtg ttcagctgct ccgtgatgca cgaggccctg 1320

cacaaccact acacccagaa gtccctgagc ctgagccccg gcaaa 1365

<210> 44
<211> 455
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 44

```
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 Gly Gly Ser Gly Gly
            100                 105                 110


Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Ala Ser Thr
        115                 120                 125


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


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


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


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


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

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

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
225                 230                 235                 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
                245                 250                 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
            260                 265                 270

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

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

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
305                 310                 315                 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
                325                 330                 335

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
        355                 360                 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
    370                 375                 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385                 390                 395                 400

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

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
```

```
            420                 425                 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
        435                 440                 445

Leu Ser Leu Ser Pro Gly Lys
    450                 455
```

<210> 45
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 45

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1               5                   10                  15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

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

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
```

```
Leu Ser Cys Ala Val Glu Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160


Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175


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


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


His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220


Pro Gly Lys
225
```

<210> 46
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 46

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1               5                   10                  15


Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30


Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45


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


His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80
```

```
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Tyr Thr Leu Pro Pro Cys Arg Asp Lys Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190

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

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
225                 230                 235                 240

Gly Gly Gly Ser Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys
                245                 250                 255

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
    290                 295                 300
```

```
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
    370                 375                 380

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385                 390                 395                 400

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415

Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe
            420                 425                 430

Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
        435                 440                 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470
```