SEQUENCE LISTING

<110> YANG, Zhi-yong
NABEL, Gary J.
WU, Lan
SEUNG, Edward
WEI, Ronnie
BENINGA, Jochen
RAO, Ercole
LEUSCHNER, Wulf Dirk
BEIL, Christian
LANGE, Christian
CORVEY, Carsten

<120> TRISPECIFIC AND/OR TRIVALENT BINDING PROTEINS

<130> 183952027140

<140> Not Yet Assigned
<141> Concurrently Herewith

<150> US 62/322,036
<151> 2016-04-13

<150> US 62/331,191
<151> 2016-05-03

<150> US 62/412,187
<151> 2016-10-24

<150> EP 17305298.6
<151> 2017-03-17

<160> 179

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 1
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30
Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

```
Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125
Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
    130                 135                 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190
Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
        195                 200                 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
    210                 215                 220
Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
225                 230                 235                 240
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255
Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
            260                 265                 270
Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285
Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320
Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
                325                 330                 335
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350
Pro Cys Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu
        355                 360                 365
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415
Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445
```

<210> 2
<211> 214
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 2
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
            20   25   30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100   105   110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165   170   175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180   185   190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195   200   205
Phe Asn Arg Gly Glu Cys
    210

<210> 3
<211> 571
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 3
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Val 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
Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Ser Ile Tyr Pro Gly Asn Val Asn Thr Asn Tyr Ala Gln Lys Phe
    50   55   60
Gln Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Ile Ser Thr Ala Tyr
65   70   75   80

```
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Thr Arg Ser His Tyr Gly Leu Asp Trp Asn Phe Asp Val Trp Gly Lys
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser Ser Gln Val Gln Leu Val Glu Ser
        115                 120                 125
Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala
    130                 135                 140
Ala Ser Gly Phe Thr Phe Thr Lys Ala Trp Met His Trp Val Arg Gln
145                 150                 155                 160
Ala Pro Gly Lys Gln Leu Glu Trp Val Ala Gln Ile Lys Asp Lys Ser
                165                 170                 175
Asn Ser Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
            180                 185                 190
Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser
        195                 200                 205
Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Arg Gly Val Tyr Tyr
    210                 215                 220
Ala Leu Ser Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
225                 230                 235                 240
Ser Ser Arg Thr Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
                245                 250                 255
Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
            260                 265                 270
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
        275                 280                 285
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
    290                 295                 300
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
305                 310                 315                 320
Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
                325                 330                 335
Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
            340                 345                 350
Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
        355                 360                 365
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    370                 375                 380
Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
385                 390                 395                 400
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                405                 410                 415
Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            420                 425                 430
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
        435                 440                 445
Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
    450                 455                 460
Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Gln Glu
465                 470                 475                 480
Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe
                485                 490                 495
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            500                 505                 510
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
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        515                 520                 525
Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
    530                 535                 540
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
545                 550                 555                 560
Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
                565                 570


<210> 4
<211> 338
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 4
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1               5                  10                  15
Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Val His Asn
            20                  25                  30
Asn Ala Asn Thr Tyr Leu Ser Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45
Pro Gln Ser Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gly Gln Gly
                85                  90                  95
Thr Gln Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Val Glu Ile Lys
            100                 105                 110
Gly Gln Pro Lys Ala Ala Pro Asp Ile Gln Met Thr Gln Ser Pro Ser
        115                 120                 125
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala
    130                 135                 140
Ser Gln Asn Ile Tyr Val Trp Leu Asn Trp Tyr Gln Gln Lys Pro Gly
145                 150                 155                 160
Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Asn Leu His Thr Gly
                165                 170                 175
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
            180                 185                 190
Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln
        195                 200                 205
Gln Gly Gln Thr Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu
    210                 215                 220
Ile Lys Thr Lys Gly Pro Ser Arg Thr Val Ala Ala Pro Ser Val Phe
225                 230                 235                 240
Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
                245                 250                 255
Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
            260                 265                 270
Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
        275                 280                 285
Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
```

```
    290                 295                 300
Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
305                 310                 315                 320
Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
                325                 330                 335
Glu Cys
```

<210> 5
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 5
gaagtgcagc tggtggaatc tggcggcgga ctggtgcagc ctggcggatc tctgagactg 60
agctgtgccg ccagcggctt caacatcaag gacacctaca tccactgggt gcgccaggcc 120
cctggcaagg gactggaatg ggtggccaga atctacccca ccaacggcta caccagatac 180
gccgacagcg tgaagggccg gttcaccatc agcgccgaca ccagcaagaa caccgcctac 240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgtag tagatgggga 300
ggcgacggct tctacgccat ggactattgg ggccagggca ccctcgtgac cgtgtctagt 360
gcgtcgacca agggcccatc ggtgttccct ctggcccctt gcagcagaag caccagcgaa 420
tctacagccg ccctgggctg cctcgtgaag gactactttc ccgagcccgt gaccgtgtcc 480
tggaactctg gcgctctgac aagcggcgtg cacacctttc cagccgtgct ccagagcagc 540
ggcctgtact ctctgagcag cgtcgtgaca gtgcccagca gcagcctggg caccaagacc 600
tacacctgta acgtggacca caagcccagc aacaccaagg tggacaagcg ggtggaatct 660
aagtacggcc ctccctgccc tccttgccca gcccctgaat ttctgggcgg accctccgtg 720
ttcctgttcc ccccaaagcc caaggacacc ctgatgatca gccggacccc cgaagtgacc 780
tgcgtggtgg tggatgtgtc ccaggaagat cccgaggtgc agttcaattg gtacgtggac 840
ggcgtggaag tgcacaacgc caagaccaag cccagagagg aacagttcaa cagcacctac 900
cgggtggtgt ccgtgctgac cgtgctgcac caggactggc tgaacggcaa agagtacaag 960
tgcaaggtgt ccaacaaggg cctgcccagc tccatcgaga aaaccatcag caaggccaag 1020
ggccagcccc gcgagcctca agtgtatacc ctgccccctt gccaggaaga gatgaccaag 1080
aaccaggtgt ccctgtggtg tctcgtgaaa ggcttctacc ccagcgacat tgccgtggaa 1140
tgggagagca acggccagcc cgagaacaac tacaagacca ccccccctgt gctggacagc 1200
gacggctcat tcttcctgta ctccaagctg accgtggaca agagccggtg gcaggaaggc 1260
aacgtgttca gctgctccgt gatgcacgag gccctgcaca accactacac ccagaagtcc 1320
ctgtctctgt ccctgggcaa g   1341

<210> 6
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 6
gacatccaga tgacccagag ccccagcagc ctgtctgcca gcgtgggcga cagagtgacc 60
atcacctgta gagccagcca ggacgtgaac accgccgtgg cctggtatca gcagaagcct 120
ggcaaggccc ccaagctgct gatctacagc gccagcttcc tgtacagcgg cgtgcccagc 180
agattcagcg gaagcagaag cggcaccgac ttcaccctga ccatcagctc cctgcagccc 240

gaggacttcg ccacctacta ctgccagcag cactacacca ccccccccac atttggccag 300
ggcaccaagg tggaaatcaa gcgtacggtg gccgctccca gcgtgttcat cttcccacct 360
agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 420
ccccgcgagg ccaaagtgca gtggaaggtg gacaacgccc tgcagagcgg caacagccag 480
gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgaca 540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600
ctgtctagcc ccgtgaccaa gagcttcaac cggggcgagt gt 642

<210> 7
<211> 1713
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 7
caggtgcagc tggtgcagtc tggcgccgag gtcgtgaaac ctggcgcctc tgtgaaggtg 60
tcctgcaagg ccagcggcta cacctttacc agctactaca tccactgggt gcgccaggcc 120
cctggacagg gactggaatg gatcggcagc atctaccccg gcaacgtgaa caccaactac 180
gcccagaagt tccagggcag agccaccctg accgtggaca ccagcatcag caccgcctac 240
atggaactga gccggctgag aagcgacgac accgccgtgt actactgcac ccggtcccac 300
tacggcctgg attggaactt cgacgtgtgg ggcaagggca ccaccgtgac agtgtctagc 360
agccaggtgc agctggtgga atctggcggc ggagtggtgc agcctggcag aagcctgaga 420
ctgagctgtg ccgccagcgg cttcaccttc accaaggcct ggatgcactg ggtgcgccag 480
gcccctggaa agcagctgga atgggtggcc cagatcaagg acaagagcaa cagctacgcc 540
acctactacg ccgacagcgt gaagggccgg ttcaccatca gccgggacga cagcaagaac 600
accctgtacc tgcagatgaa cagcctgcgg gccgaggaca ccgccgtgta ctactgtcgg 660
ggcgtgtact atgccctgag ccccttcgat tactggggcc agggaaccct cgtgaccgtg 720
tctagtcgga ccgccagcac aaagggccca tcggtgttcc ctctggcccc ttgcagcaga 780
agcaccagcg aatctacagc cgccctgggc tgcctcgtga aggactactt tcccgagccc 840
gtgaccgtgt cctggaactc tggcgctctg acaagcggcg tgcacacctt tccagccgtg 900
ctccagagca gcggcctgta ctctctgagc agcgtcgtga cagtgcccag cagcagcctg 960
ggcaccaaga cctacacctg taacgtggac cacaagccca gcaacaccaa ggtggacaag 1020
cgggtggaat ctaagtacgg ccctccctgc cctccttgcc cagccctga atttctgggc 1080
ggaccctccg tgttcctgtt ccccccaaag cccaaggaca ccctgatgat cagccggacc 1140
cccgaagtga cctgcgtggt ggtggatgtg tcccaggaag atcccgaggt gcagttcaat 1200
tggtacgtgg acggcgtgga agtgcacaac gccaagacca agcccagaga ggaacagttc 1260
aacagcacct accgggtggt gtccgtgctg accgtgctgc accaggactg gctgaacggc 1320
aaagagtaca agtgcaaggt gtccaacaag ggcctgccca gctccatcga gaaaaccatc 1380
agcaaggcca agggccagcc ccgcgagcct caagtgtgta ccctgccccc tagccaggaa 1440
gagatgacca agaaccaggt gtccctgagc tgtgccgtga aaggcttcta ccccagcgac 1500
attgccgtgg aatgggagag caacggccag cccgagaaca actacaagac cacccccct 1560
gtgctggaca gcgacggctc attcttcctg gtgtccaagc tgaccgtgga caagagccgg 1620
tggcaggaag gcaacgtgtt cagctgctcc gtgatgcacg aggccctgca caaccactac 1680
acccagaagt ccctgtctct gtccctgggc aag 1713

<210> 8
<211> 1014
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 8
gacatcgtga tgacccagac ccccctgagc ctgagcgtga cacctggaca gcctgccagc 60
atcagctgca agagcagcca gagcctggtg cacaacaacg ccaacaccta cctgagctgg 120
tatctgcaga agcccggcca gagcccccag tccctgatct acaaggtgtc caacagattc 180
agcggcgtgc ccgacagatt ctccggcagc ggctctggca ccgacttcac cctgaagatc 240
agccgggtgg aagccgagga cgtgggcgtg tactattgtg gccagggcac ccagtacccc 300
ttcacctttg gcagcggcac caaggtggaa atcaagggcc agcccaaggc cgcccccgac 360
atccagatga cccagagccc cagcagcctg tctgccagcg tgggcgacag agtgaccatc 420
acctgtcagg ccagccagaa catctacgtg tggctgaact ggtatcagca gaagcccggc 480
aaggccccca agctgctgat ctacaaggcc agcaacctgc acaccggcgt gcccagcaga 540
ttttctggca gcggctccgg caccgacttc accctgacaa tcagctccct gcagcccgag 600
gacattgcca cctactactg ccagcagggc cagacctacc cctacacctt tggccagggc 660
accaagctgg aaatcaagac caagggcccc agccgtacgg tggccgctcc cagcgtgttc 720
atcttcccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt gtgcctgctg 780
aacaacttct accccgcga ggccaaagtg cagtggaagg tggacaacgc cctgcagagc 840
ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 900
agcaccctga cactgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaagtg 960
acccaccagg gcctgtctag ccccgtgacc aagagcttca accggggcga gtgt 1014

<210> 9
<211> 571
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 9
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1   5   10   15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp 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 Ala Gly Gly Gly Thr Asn Tyr Asn Pro Ser Leu Lys
    50   55   60
Ser Arg Lys Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val 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 Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser Ser Gln Val Gln Leu Val Glu Ser
        115   120   125
Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala
    130   135   140
Ala Ser Gly Phe Thr Phe Thr Lys Ala Trp Met His Trp Val Arg Gln
145   150   155   160
Ala Pro Gly Lys Gln Leu Glu Trp Val Ala Gln Ile Lys Asp Lys Ser
                165   170   175
Asn Ser Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
            180   185   190
Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser
        195   200   205
Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Arg Gly Val Tyr Tyr

```
    210                 215                 220
Ala Leu Ser Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
225                 230                 235                 240
Ser Ser Arg Thr Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
                245                 250                 255
Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
            260                 265                 270
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
        275                 280                 285
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
    290                 295                 300
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
305                 310                 315                 320
Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
                325                 330                 335
Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
            340                 345                 350
Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
        355                 360                 365
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    370                 375                 380
Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
385                 390                 395                 400
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                405                 410                 415
Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            420                 425                 430
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
        435                 440                 445
Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
    450                 455                 460
Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Gln Glu
465                 470                 475                 480
Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe
                485                 490                 495
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            500                 505                 510
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        515                 520                 525
Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
    530                 535                 540
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
545                 550                 555                 560
Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
                565                 570
```

<210> 10
<211> 342
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 10
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1   5   10   15
Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Val His Asn
            20   25   30
Asn Ala Asn Thr Tyr Leu Ser Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35   40   45
Pro Gln Ser Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
    50   55   60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65   70   75   80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gly Gln Gly
                85   90   95
Thr Gln Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Val Glu Ile Lys
            100   105   110
Gly Gln Pro Lys Ala Ala Pro Asp Ile Val Leu Thr Gln Ser Pro Ala
        115   120   125
Ser Leu Ala Val Ser Pro Gly Gln Arg Ala Thr Ile Thr Cys Arg Ala
    130   135   140
Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln Trp Tyr Gln
145   150   155   160
Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Phe Ala Ala Ser Asn
                165   170   175
Val Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
            180   185   190
Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asn Asp Val Ala Asn
        195   200   205
Tyr Tyr Cys Gln Gln Ser Arg Lys Val Pro Tyr Thr Phe Gly Gln Gly
    210   215   220
Thr Lys Leu Glu Ile Lys Thr Lys Gly Pro Ser Arg Thr Val Ala Ala
225   230   235   240
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                245   250   255
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            260   265   270
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        275   280   285
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    290   295   300
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
305   310   315   320
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
                325   330   335
Phe Asn Arg Gly Glu Cys
            340

<210> 11
<211> 1713
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 11
caggtgcagc tgcaggaatc tggccctggc ctcgtgaagc ctagccagac cctgagcctg 60
acctgtaccg tgtccggctt cagcctgagc gactacggcg tgcactgggt gcgccagcca 120
cctggaaaag gcctggaatg gctgggcgtg atctgggctg gcggaggcac caactacaac 180
cccagcctga agtccagaaa gaccatcagc aaggacacca gcaagaacca ggtgtccctg 240
aagctgagca gcgtgacagc cgccgatacc gccgtgtact actgcgccag agacaagggc 300
tacagctact actacagcat ggactactgg ggccagggca ccaccgtgac cgtgtcatcc 360
tctcaggtgc agctggtgga atctggcggc ggagtggtgc agcctggcag aagcctgaga 420
ctgagctgtg ccgccagcgg cttcaccttc accaaggcct ggatgcactg ggtgcgccag 480
gcccctggaa agcagctgga atgggtggcc cagatcaagg acaagagcaa cagctacgcc 540
acctactacg ccgacagcgt gaagggccgg ttcaccatca gccgggacga cagcaagaac 600
accctgtacc tgcagatgaa cagcctgcgg gccgaggaca ccgccgtgta ctactgtcgg 660
ggcgtgtact atgccctgag ccccttcgat tactggggcc agggaaccct cgtgaccgtg 720
tctagtcgga ccgcttcgac caagggccca tcggtgttcc ctctggcccc ttgcagcaga 780
agcaccagcg aatctacagc cgccctgggc tgcctcgtga aggactactt tcccgagccc 840
gtgaccgtgt cctggaactc tggcgctctg acaagcggcg tgcacacctt tccagccgtg 900
ctccagagca gcggcctgta ctctctgagc agcgtcgtga cagtgcccag cagcagcctg 960
ggcaccaaga cctacacctg taacgtggac cacaagccca gcaacaccaa ggtggacaag 1020
cgggtggaat ctaagtacgg ccctccctgc cctccttgcc cagccctga atttctgggc 1080
ggaccctccg tgttcctgtt ccccccaaag cccaaggaca ccctgatgat cagccggacc 1140
cccgaagtga cctgcgtggt ggtggatgtg tcccaggaag atcccgaggt gcagttcaat 1200
tggtacgtgg acggcgtgga agtgcacaac gccaagacca agcccagaga ggaacagttc 1260
aacagcacct accgggtggt gtccgtgctg accgtgctgc accaggactg gctgaacggc 1320
aaagagtaca agtgcaaggt gtccaacaag ggcctgccca gctccatcga gaaaaccatc 1380
agcaaggcca agggccagcc ccgcgagcct caagtgtgta ccctgccccc tagccaggaa 1440
gagatgacca agaaccaggt gtccctgagc tgtgccgtga aaggcttcta ccccagcgac 1500
attgccgtgg aatgggagag caacggccag cccgagaaca actacaagac cacccccct 1560
gtgctggaca gcgacggctc attcttcctg gtgtccaagc tgaccgtgga caagagccgg 1620
tggcaggaag gcaacgtgtt cagctgctcc gtgatgcacg aggccctgca caaccactac 1680
acccagaagt ccctgtctct gtccctgggc aag 1713

<210> 12
<211> 1026
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 12
gacatcgtga tgacccagac ccccctgagc ctgagcgtga cacctggaca gcctgccagc 60
atcagctgca agagcagcca gagcctggtg cacaacaacg ccaacaccta cctgagctgg 120
tatctgcaga agcccggcca gagcccccag tccctgatct acaaggtgtc caacagattc 180
agcggcgtgc ccgacagatt ctccggcagc ggctctggca ccgacttcac cctgaagatc 240
agccgggtgg aagccgagga cgtgggcgtg tactattgtg gccagggcac ccagtacccc 300
ttcacctttg gcagcggcac caaggtggaa atcaagggcc agcccaaggc cgcccccgac 360
atcgtgctga cacagagccc tgctagcctg gccgtgtctc ctggacagag ggccaccatc 420
acctgtagag ccagcgagag cgtggaatat tacgtgacca gcctgatgca gtggtatcag 480
cagaagcccg gccagccccc caagctgctg attttcgccg ccagcaacgt ggaaagcggc 540
gtgccagcca gattttccgg cagcggctct ggcaccgact tcaccctgac catcaacccc 600
gtggaagcca acgacgtggc caactactac tgccagcaga gccggaaggt gccctacacc 660
tttggccagg gcaccaagct ggaaatcaag accaagggcc ccagccgtac ggtggccgct 720
cccagcgtgt tcatcttccc acctagcgac gagcagctga agtccggcac agcctctgtc 780
gtgtgcctgc tgaacaactt ctaccccgc gaggccaaag tgcagtggaa ggtggacaac 840
gccctgcaga gcggcaacag ccaggaaagc gtgaccgagc aggacagcaa ggactccacc 900

tacagcctga gcagcaccct gacactgagc aaggccgact acgagaagca caaggtgtac 960
gcctgcgaag tgacccacca gggcctgtct agccccgtga ccaagagctt caaccggggc 1020
gagtgt 1026

<210> 13
<211> 451
<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 Ser
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
            20   25   30
Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Gly Arg Ala Thr Leu Thr Ala Asp Glu Ser Thr Ser Thr Ala 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 Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
            100   105   110
Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys
        115   120   125
Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu
    130   135   140
Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145   150   155   160
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
                165   170   175
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
            180   185   190
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn
        195   200   205
Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser
    210   215   220
Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly
225   230   235   240
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245   250   255
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln
            260   265   270
Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275   280   285
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr
    290   295   300
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305   310   315   320
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile
                325   330   335

```
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350
Tyr Thr Leu Pro Pro Cys Gln Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365
Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415
Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445
Leu Gly Lys
    450
```

<210> 14
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 14

```
Asp Leu Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly
 1               5                  10                  15
Gln Arg Ala Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Val Pro Ala
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn
65                  70                  75                  80
Pro Val Glu Ala Asn Asp Thr Ala Asn Tyr Tyr Cys Gln Gln Ser Thr
                85                  90                  95
Glu Asp Pro Trp 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
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
```

<210> 15
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 15
caggtgcagc tggtgcagag cggcgccgaa gtgaagaagc ctggcagcag cgtgaaggtg 60
agctgcaagg ccagcggcta tgccttcagc agctactgga tgaactgggt gaggcaggca 120
cctggccagg gcctggagtg gataggccaa atatggcctg gcgatggcga caccaactac 180
aaccagaagt tcaagggcag agcgaccttg accgccgacg agagcaccag caccgcgtac 240
atggagctga gcagcctgag gagcgaggac accgccgtgt actattgcgc cagaagggag 300
accaccaccg tgggcaggta ctactacgcc atggactact ggggccaggg aaccaccgtg 360
accgtgagca gcgcctcgac caagggccca tcggtgttcc ctctggcccc ttgcagcaga 420
agcaccagcg aatctacagc cgccctgggc tgcctcgtga aggactactt tcccgagccc 480
gtgaccgtgt cctggaactc tggcgctctg acaagcggcg tgcacacctt tccagccgtg 540
ctccagagca gcggcctgta ctctctgagc agcgtcgtga cagtgcccag cagcagcctg 600
ggcaccaaga cctacacctg taacgtggac cacaagccca gcaacaccaa ggtggacaag 660
cgggtggaat ctaagtacgg ccctccctgc cctccttgcc cagcccctga atttctgggc 720
ggaccctccg tgttcctgtt ccccccaaag cccaaggaca ccctgatgat cagccggacc 780
cccgaagtga cctgcgtggt ggtggatgtg tcccaggaag atcccgaggt gcagttcaat 840
tggtacgtgg acggcgtgga agtgcacaac gccaagacca agcccagaga ggaacagttc 900
aacagcacct accgggtggt gtccgtgctg accgtgctgc accaggactg gctgaacggc 960
aaagagtaca agtgcaaggt gtccaacaag ggcctgccca gctccatcga gaaaaccatc 1020
agcaaggcca agggccagcc ccgcgagcct caagtgtata ccctgccccc ttgccaggaa 1080
gagatgacca agaaccaggt gtccctgtgg tgtctcgtga aaggcttcta ccccagcgac 1140
attgccgtgg aatgggagag caacggccag cccgagaaca actacaagac cacccccct 1200
gtgctggaca gcgacggctc attcttcctg tactccaagc tgaccgtgga caagagccgg 1260
tggcaggaag gcaacgtgtt cagctgctcc gtgatgcacg aggccctgca caaccactac 1320
acccagaagt ccctgtctct gtccctgggc aag 1353

<210> 16
<211> 654
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16
gacctcgtgc tgacccagag ccctgcgagc ctggctgtga gccctggcca gagagccacc 60
atcacctgca aagccagcca gagcgtggac tacgacggcg acagctacct caactggtac 120
cagcagaagc ctggccagcc ccccaagctg ctgatttacg atgccagcaa cctggtgagc 180
ggcgtgcctg ctagattcag cggctccggc agcggcaccg acttcaccct gaccatcaac 240
cccgtggagg ccaacgacac cgccaactac tactgccagc agagcacgga ggacccctgg 300
accttcggcc agggcacaaa gctggagatc aagcgtacgg tggccgctcc cagcgtgttc 360
atcttcccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt gtgcctgctg 420
aacaacttct accccgcga ggccaaagtg cagtggaagg tggacaacgc cctgcagagc 480
ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 540
agcaccctga cactgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaagtg 600
acccaccagg gcctgtctag ccccgtgacc aagagcttca accggggcga gtgt 654

<210> 17
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 17
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Ala Lys Pro Gly Thr
 1   5   10   15
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20   25   30
Trp Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Thr Ile Tyr Pro Gly Asp Gly Asp Thr Gly Tyr Ala Gln Lys Phe
    50   55   60
Gln Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Lys Thr Val Tyr
65   70   75   80
Met His Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Gly Asp Tyr Tyr Gly Ser Asn Ser Leu Asp Tyr Trp Gly Gln
            100   105   110
Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115   120   125
Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
    130   135   140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145   150   155   160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165   170   175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180   185   190
Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
        195   200   205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
    210   215   220
Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
225   230   235   240
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245   250   255
Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
            260   265   270
Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275   280   285
Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
    290   295   300
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305   310   315   320
Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
                325   330   335
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340   345   350
Pro Cys Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu

```
        355                 360                 365
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415
Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445


<210> 18
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 18
Asp Ile Val Met Thr Gln Ser His Leu Ser Met Ser Thr Ser Leu Gly
 1               5                  10                  15
Asp Pro Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Thr Val
            20                  25                  30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Arg Arg Leu Ile
        35                  40                  45
Tyr Ser Ala Ser Tyr Arg Tyr Ile Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60
Ser Gly Ala Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Ala
65                  70                  75                  80
Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Ser Pro Pro Tyr
                85                  90                  95
Thr Phe Gly Gly 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
    210


<210> 19
<211> 1341
<212> DNA
```

<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 19
caggtgcagc tggtgcagtc tggcgccgaa gtggccaagc ctggcacaag cgtgaagctg 60
agctgcaagg ccagcggcta caccttcacc gactactgga tgcagtgggt caagcagagg 120
ccaggccagg gcctggaatg gatcggcaca atctatcccg gcgacggcga taccggctac 180
gcccagaagt ttcagggcaa ggccaccctg accgccgaca agagcagcaa gaccgtgtac 240
atgcacctga gcagcctggc cagcgaggac agcgccgtgt actattgcgc cagaggcgac 300
tactacggca gcaacagcct ggactattgg ggccagggca ccagcgtgac agtgtctagt 360
gcgtcgacca agggcccatc ggtgttccct ctggcccctt gcagcagaag caccagcgaa 420
tctacagccg ccctgggctg cctcgtgaag gactactttc ccgagcccgt gaccgtgtcc 480
tggaactctg gcgctctgac aagcggcgtg cacacctttc cagccgtgct ccagagcagc 540
ggcctgtact ctctgagcag cgtcgtgaca gtgcccagca gcagcctggg caccaagacc 600
tacacctgta acgtggacca caagcccagc aacaccaagg tggacaagcg ggtggaatct 660
aagtacggcc ctccctgccc tccttgccca gcccctgaat ttctgggcgg accctccgtg 720
ttcctgttcc ccccaaagcc caaggacacc ctgatgatca gccggacccc cgaagtgacc 780
tgcgtggtgg tggatgtgtc ccaggaagat cccgaggtgc agttcaattg gtacgtggac 840
ggcgtggaag tgcacaacgc caagaccaag cccagagagg aacagttcaa cagcacctac 900
cgggtggtgt ccgtgctgac cgtgctgcac caggactggc tgaacggcaa agagtacaag 960
tgcaaggtgt ccaacaaggg cctgcccagc tccatcgaga aaaccatcag caaggccaag 1020
ggccagcccc gcgagcctca agtgtatacc ctgccccctt gccaggaaga gatgaccaag 1080
aaccaggtgt ccctgtggtg tctcgtgaaa ggcttctacc ccagcgacat tgccgtggaa 1140
tgggagagca acggccagcc cgagaacaac tacaagacca ccccccctgt gctggacagc 1200
gacggctcat tcttcctgta ctccaagctg accgtggaca agagccggtg gcaggaaggc 1260
aacgtgttca gctgctccgt gatgcacgag gccctgcaca accactacac ccagaagtcc 1320
ctgtctctgt ccctgggcaa g 1341

<210> 20
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 20
gacatcgtga tgacccagag ccacctgagc atgagcacca gcctgggcga ccccgtgtcc 60
atcacctgta aagccagcca ggacgtgtcc accgtggtgg cctggtatca gcagaagcct 120
ggccagagcc ccagacggct gatctacagc gccagctatc ggtacatcgg cgtgcccgac 180
agattcaccg gaagcggagc cggcaccgac ttcaccttca ccatcagctc tgtgcaggcc 240
gaggacctgg ccgtgtacta ctgccagcag cactacagcc ccccctacac ctttggcgga 300
ggcaccaagc tggaaatcaa gcgtacggtg gccgctccca gcgtgttcat cttcccacct 360
agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 420
ccccgcgagg ccaaagtgca gtggaaggtg gacaacgccc tgcagagcgg caacagccag 480
gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgaca 540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600
ctgtctagcc ccgtgaccaa gagcttcaac cggggcgagt gt 642

<210> 21
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 21
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asn Tyr
            20   25   30
Asn Ile His Trp Val Lys Lys Ser Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Ala Pro Tyr Ser Gln Lys Phe
    50   55   60
Gln Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Thr Ser Thr Thr Tyr
65   70   75   80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Val Arg Ala Asn Trp Asp Val Ala Phe Ala Tyr Trp Gly Gln Gly Thr
            100   105   110
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115   120   125
Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130   135   140
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145   150   155   160
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165   170   175
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180   185   190
Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195   200   205
Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
    210   215   220
Pro Pro Cys Pro Ala Pro Glu Phe 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 Gln Glu Asp Pro Glu Val Gln
            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 Phe 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 Gly Leu Pro Ser Ser 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 Cys
            340   345   350
Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp 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

```
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415
Glu 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 Leu Gly Lys
        435                 440                 445
```

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

<220>
<223> Synthetic Construct

<400> 22

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asp Arg Tyr
            20                  25                  30
Met Ala Trp Tyr Gln Asp Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35                  40                  45
His Asp Thr Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Arg Asp Tyr Thr Leu Thr Ile Ser Asn Leu Glu Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asn Leu Trp Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
            100                 105                 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205
Asn Arg Gly Glu Cys
    210
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<210> 23
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 23
caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ccggcagcag cgtgaaggtg 60
tcctgcaagg ccagcggcta catcttcacc aactacaaca tccactgggt caagaagtcc 120
ccaggccagg gcctggaatg gatcggcgcc atctatcccg gaaacggcga cgccccttac 180
agccagaagt tccagggcaa ggccaccctg accgccgata ccagcacctc caccacctac 240
atggaactga gcagcctgcg gagcgaggac accgccgtgt actattgcgt gcgggccaac 300
tgggatgtgg ccttcgccta ttggggccag ggcacactcg tgaccgtgtc ctctgcgtcg 360
accaagggcc catcggtgtt ccctctggcc ccttgcagca gaagcaccag cgaatctaca 420
gccgccctgg gctgcctcgt gaaggactac tttcccgagc ccgtgaccgt gtcctggaac 480
tctggcgctc tgacaagcgg cgtgcacacc tttccagccg tgctccagag cagcggcctg 540
tactctctga gcagcgtcgt gacagtgccc agcagcagcc tgggcaccaa gacctacacc 600
tgtaacgtgg accacaagcc cagcaacacc aaggtggaca agcgggtgga atctaagtac 660
ggccctccct gccctccttg cccagccccc gaatttctgg gcggaccctc cgtgttcctg 720
ttcccccaa agcccaagga caccctgatg atcagccgga cccccgaagt gacctgcgtg 780
gtggtggatg tgtcccagga agatcccgag gtgcagttca attggtacgt ggacggcgtg 840
gaagtgcaca acgccaagac caagcccaga gaggaacagt tcaacagcac ctaccgggtg 900
gtgtccgtgc tgaccgtgct gcaccaggac tggctgaacg gcaaagagta caagtgcaag 960
gtgtccaaca agggcctgcc cagctccatc gagaaaacca tcagcaaggc caagggccag 1020
ccccgcgagc ctcaagtgta taccctgccc ccttgccagg aagagatgac caagaaccag 1080
gtgtccctgt ggtgtctcgt gaaaggcttc taccccagcg acattgccgt ggaatgggag 1140
agcaacggcc agcccgagaa caactacaag accacccccc ctgtgctgga cagcgacggc 1200
tcattcttcc tgtactccaa gctgaccgtg gacaagagcc ggtggcagga aggcaacgtg 1260
ttcagctgct ccgtgatgca cgaggccctg cacaaccact acacccagaa gtccctgtct 1320
ctgtccctgg gcaag 1335

<210> 24
<211> 639
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 24
gacatccaga tgacccagag ccccagcagc ctgtctgcca gcgtgggcga cagagtgacc 60
atcacatgca aggccagcca ggacatcgat cggtacatgg cctggtatca ggacaagccc 120
ggcaaggccc ccagactgct gatccacgat accagcacac tgcagagcgg cgtgcccagc 180
agattttccg gctctggcag cggcagagac tacaccctga ccatcagcaa cctggaaccc 240
gaggacttcg ccacctacta ctgcctgcag tacgacaacc tgtggacctt cggcggaggc 300
accaaggtgg aaatcaagcg tacggtggcc gctcccagcg tgttcatctt cccacctagc 360
gacgagcagc tgaagtccgg cacagcctct gtcgtgtgcc tgctgaacaa cttctacccc 420
cgcgaggcca aagtgcagtg gaaggtggac aacgccctgc agagcggcaa cagccaggaa 480
agcgtgaccg agcaggacag caaggactcc acctacagcc tgagcagcac cctgacactg 540
agcaaggccg actacgagaa gcacaaggtg tacgcctgcg aagtgaccca ccagggcctg 600
tctagccccg tgaccaagag cttcaaccgg ggcgagtgt 639

<210> 25
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 25

Gly Phe Asn Ile Lys Asp Thr Tyr
 1   5

<210> 26
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 26
Ile Tyr Pro Thr Asn Gly Tyr Thr
 1   5

<210> 27
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 27
Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr
 1   5   10

<210> 28
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 28
Gly Tyr Thr Phe Thr Ser Tyr Tyr
 1   5

<210> 29
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 29
Ile Tyr Pro Gly Asn Val Asn Thr
 1   5

<210> 30
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 30
Thr Arg Ser His Tyr Gly Leu Asp Trp Asn Phe Asp Val
 1   5   10

<210> 31
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 31
Gly Phe Ser Leu Ser Asp Tyr Gly
 1   5

<210> 32
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 32
Ile Trp Ala Gly Gly Gly Thr
 1   5

<210> 33
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 33
Ala Arg Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp
 1   5   10

<210> 34
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 34
Gly Phe Thr Phe Thr Lys Ala Trp
 1   5

<210> 35
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 35
Ile Lys Asp Lys Ser Asn Ser
 1   5

<210> 36
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 36
Arg Gly Val Tyr Tyr Ala Leu Ser Pro Phe Asp Tyr
 1   5   10

<210> 37
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 37
Gly Tyr Ala Phe Ser Ser Tyr Trp
 1   5

<210> 38
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 38
Ile Trp Pro Gly Asp Gly Asp Thr
 1   5

<210> 39
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 39
Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
 1   5   10   15

<210> 40
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 40
Gly Tyr Thr Phe Thr Asp Tyr Trp
 1   5

<210> 41
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 41
Ile Tyr Pro Gly Asp Gly Asp Thr
 1   5

<210> 42
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 42
Ala Arg Gly Asp Tyr Tyr Gly Ser Asn Ser Leu Asp Tyr
 1   5   10

<210> 43
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 43
Gln Asp Val Asn Thr Ala
 1   5

<210> 44
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 44
Ser Ala Ser
 1

<210> 45
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 45
Gln Gln His Tyr Thr Thr Pro Pro Thr
 1   5

<210> 46
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 46
Gln Asn Ile Tyr Val Trp
 1   5

<210> 47
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 47
Lys Ala Ser
 1

<210> 48
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 48
Gln Gln Gly Gln Thr Tyr Pro Tyr Thr
 1   5

<210> 49
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 49
Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu
 1   5   10

<210> 50
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 50
Ala Ala Ser
 1

<210> 51

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

<220>
<223> Synthetic Construct

<400> 51
Gln Gln Ser Arg Lys Val Pro Tyr Thr
 1   5

<210> 52
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 52
Gln Ser Leu Val His Asn Asn Ala Asn Thr Tyr
 1   5   10

<210> 53
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 53
Lys Val Ser
 1

<210> 54
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 54
Gly Gln Gly Thr Gln Tyr Pro
 1   5

<210> 55
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 55
Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr
 1   5   10

<210> 56
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 56
Asp Ala Ser
 1

<210> 57
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 57
Gln Gln Ser Thr Glu Asp Pro Trp Thr
 1   5

<210> 58
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 58
Gln Asp Val Ser Thr Val
 1   5

<210> 59
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 59
Gln Gln His Tyr Ser Pro Pro Tyr Thr
 1   5

<210> 60
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 60
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20   25   30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
    50   55   60
Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115   120   125
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130   135   140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145   150   155   160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165   170   175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180   185   190
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195   200   205
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210   215   220
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225   230   235   240
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245   250   255
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260   265   270
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275   280   285
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290   295   300
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305   310   315   320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325   330   335
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340   345   350
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355   360   365
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370   375   380
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385   390   395   400
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
                405   410   415
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420   425   430
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435   440   445
Pro Gly
    450

<210> 61
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 61
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gln Pro Lys Ala
            100   105   110
Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala
        115   120   125
Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala
    130   135   140
Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val
145   150   155   160
Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser
                165   170   175
Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
            180   185   190
Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala
        195   200   205

Pro Thr Glu Cys Ser
    210

<210> 62
<211> 570
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 62
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
            20   25   30
Trp Ile His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Met Ile Asp Pro Ser Asp Gly Glu Thr Arg Leu Asn Gln Arg Phe
    50   55   60
Gln Gly Arg Ala Thr Leu Thr Val Asp Glu Ser Thr Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Arg Ser Pro Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Thr Arg Leu Lys Glu Tyr Gly Asn Tyr Asp Ser Phe Tyr Phe Asp Val
            100   105   110
Trp Gly Ala Gly Thr Leu Val Thr Val Ser Ser Glu Val Gln Leu Lys
        115   120   125
Glu Ser Gly Pro Gly Leu Val Ala Pro Gly Gly Ser Leu Ser Ile Thr
    130   135   140
Cys Thr Val Ser Gly Phe Ser Leu Thr Asp Ser Ser Ile Asn Trp Val
145   150   155   160
Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile Trp Gly
                165   170   175
Asp Gly Arg Ile Asp Tyr Ala Asp Ala Leu Lys Ser Arg Leu Ser Ile
            180   185   190
Ser Lys Asp Ser Ser Lys Ser Gln Val Phe Leu Glu Met Thr Ser Leu
        195   200   205
Arg Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Asp Gly Tyr Phe
    210   215   220
Pro Tyr Ala Met Asp Phe Trp Gly Gln Gly Thr Ser Val Thr Val Ser
225   230   235   240
Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
                245   250   255
Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
            260   265   270
Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
        275   280   285
Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
    290   295   300
Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
305   310   315   320
Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
                325   330   335

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Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
            340                 345                 350
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
        355                 360                 365
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    370                 375                 380
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
385                 390                 395                 400
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                405                 410                 415
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            420                 425                 430
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
        435                 440                 445
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    450                 455                 460
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp
465                 470                 475                 480
Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
                485                 490                 495
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            500                 505                 510
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        515                 520                 525
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    530                 535                 540
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe
545                 550                 555                 560
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                565                 570
```

<210> 63
<211> 345
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 63

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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 Glu Ser Val Asp Ser Tyr
            20                  25                  30
Gly Gln Ser Tyr Met His Trp Tyr Gln Gln Lys Ala 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 Arg Thr Asp Phe Thr Leu Thr Ile Asp
65                  70                  75                  80
Pro Val Gln Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Ala
                85                  90                  95
Glu Asp Ser Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
```

```
Gly Ser Gly Ser Ser Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
        115                 120                 125
Pro Ala Ser Leu Ser Val Ser Val Gly Asp Thr Ile Thr Leu Thr Cys
    130                 135                 140
His Ala Ser Gln Asn Ile Asp Val Trp Leu Ser Trp Phe Gln Gln Lys
145                 150                 155                 160
Pro Gly Asn Ile Pro Lys Leu Leu Ile Tyr Lys Ala Ser Asn Leu His
                165                 170                 175
Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Gly Phe
            180                 185                 190
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
        195                 200                 205
Cys Gln Gln Ala His Ser Tyr Pro Phe Thr Phe Gly Gly Gly Thr Lys
    210                 215                 220
Leu Glu Ile Lys Gly Gly Ser Gly Ser Ser Gly Ser Gly Gly Arg Thr
225                 230                 235                 240
Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
                245                 250                 255
Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
            260                 265                 270
Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
        275                 280                 285
Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
    290                 295                 300
Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
305                 310                 315                 320
Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
                325                 330                 335
Thr Lys Ser Phe Asn Arg Gly Glu Cys
            340                 345
```

<210> 64
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 64
gaggtgcagc tggtggaaag cggcggagga ctggtgcagc ccggcagaag cctgagactg 60
agctgcgccg ccagcggctt caccttcgac gactacgcca tgcactgggt ccgccaggcc 120
cctggcaagg gcctggaatg ggtgtccgcc atcacctgga acagcggcca catcgactac 180
gccgacagcg tggaaggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caaggtgtcc 300
tacctgagca ccgccagcag cctggactac tggggccagg gcaccctggt gacagtgtcc 360
agcgcttcca ccaagggccc cagcgtgttc cccctggccc ctagcagcaa gagcacatct 420
ggcggcacag ccgccctggg ctgcctggtc aaggactact tccccgagcc cgtgacagtg 480
tcctggaact ctggcgccct gaccagcgga gtgcatacct tccctgccgt gctgcagtcc 540
agcggcctgt acagcctgag cagcgtggtc acagtgccca gcagcagcct gggcacccag 600
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa 660
cccaagagct gcgacaagac ccacacctgt cccccctgcc ctgcccctga actgctgggc 720
ggaccctccg tgttcctgtt cccccaaag cccaaggaca ccctgatgat cagccggacc 780
cccgaagtga cctgcgtggt ggtggacgtg tcccacgagg accctgaagt gaagttcaat 840

tggtacgtgg acggcgtgga agtgcataac gccaagacca agcccagaga ggaacagtac 900
aacagcacct accgggtggt gtccgtgctg accgtgctgc accaggactg gctgaacggc 960
aaagagtaca agtgcaaggt gtccaacaag gccctgcctg cccccatcga gaaaaccatc 1020
agcaaggcca aggggccagcc tagagagccc caagtctgca ccctgccccc cagcagagat 1080
gagctgacca agaaccaggt gtccctgagc tgcgccgtga agggcttcta ccccagcgat 1140
atcgccgtgg aatgggagag caacggccag cccgagaaca actacaagac cacccccct 1200
gtgctggaca gcgacggctc attcttcctg gtgtccaagc tgacagtgga caagagccgg 1260
tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccattac 1320
acccagaagt ccctgagcct gagccccggc 1350

<210> 65
<211> 639
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 65
gacatccaga tgacccagag ccccagcagc ctgagcgcca gcgtgggcga cagagtgacc 60
atcacctgtc gggccagcca gggcatccgg aactacctgg cctggtatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacgcc gccagcacac tgcagagcgg cgtgcccagc 180
agattcagcg gcagcggctc cggcaccgac ttcaccctga ccatcagcag cctgcagccc 240
gaggacgtgg ccacctacta ctgccagcgg tacaacagag ccccctacac cttcggccag 300
ggcaccaagg tggaaatcaa gggacagccc aaggctgccc cctcggtcac cctgttcccc 360
ccaagcagcg aggaactgca ggccaacaag gccaccctcg tgtgcctgat cagcgacttc 420
taccctggcg ccgtgaccgt ggcctggaag gccgatagct ctcccgtgaa ggccggcgtg 480
gaaaccacca cccccagcaa gcagagcaac aacaaatacg ccgcctccag ctacctgagc 540
ctgaccccg agcagtggaa gtcccaccgg tcctacagct gccaggtcac acacgagggc 600
agcaccgtgg aaaagaccgt ggcccccacc gagtgcagc 639

<210> 66
<211> 1710
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 66
caggtgcagc tgcagcagag cggccctgag ctggtcaagc ctggcgccag cgtgaagatc 60
agctgcaagg ccagcggcta cagcttcacc agctactgga tccactggat caagcagcgg 120
cctggccagg gcctggaatg gatcggcatg atcgacccca gcgacggcga gacacggctg 180
aaccagagat tccagggcag agccaccctg accgtggacg agagcaccag caccgcctac 240
atgcagctgc ggagccccac cagcgaggac agcgccgtgt actactgcac ccggctgaaa 300
gagtacggca actacgacag cttctacttc gacgtgtggg gagccggcac cctggtcacc 360
gtgtccagcg aagtgcagct gaaagaaagc ggccctggcc tggtggcccc tggcggcagc 420
ctgagcatca cctgtaccgt gtccggcttc agcctgaccg acagcagcat caactgggtc 480
cgacagcccc ctggcaaggg cctcgagtgg ctgggaatga tctggggcga cggccggatc 540
gactacgccg acgccctgaa gtcccggctg agcatcagca aggacagcag caagagccag 600
gtgttcctgg aaatgaccag cctgcggacc gacgacaccg ccacctacta ctgcgccagg 660
gacggctact tcccctacgc catggatttc tggggccagg gcaccagcgt gaccgtgtcc 720
tctgcttcca ccaagggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 780
ggcggaacag ccgccctggg ctgcctggtc aaggactact ttcccgagcc cgtgaccgtg 840
tcctggaact ctggtgccct gacaagcgga gtgcatacct tccctgccgt gctgcagagc 900

agcggcctgt actctctgag cagcgtggtc accgtgccaa gcagcagcct gggcacccag 960
acctacatct gcaacgtgaa ccacaagccc tccaacacca aggtggacaa gaaggtggaa 1020
cccaagagct gcgacaagac ccacacctgt cctccctgtc ctgcccctga actgctgggc 1080
ggaccctccg tgttcctgtt ccctccaaag cccaaggata ccctgatgat cagccggacc 1140
cctgaagtga cctgcgtggt ggtggacgtg tcccacgagg atcccgaagt gaagttcaat 1200
tggtacgtgg acggcgtgga agtgcataac gccaagacca agcccagaga ggaacagtac 1260
aacagcacct accgggtggt gtccgtgctg acagtgctgc accaggactg gctgaacggc 1320
aaagagtaca agtgcaaggt gtccaacaag gccctgccag cccctatcga gaaaaccatc 1380
agcaaggcca agggccagcc ccgcgagcct caggtgtaca cactgcctcc atgccgggac 1440
gagctgacca agaaccaggt gtccctgtgg tgcctcgtga agggcttcta cccctccgat 1500
atcgccgtgg aatgggagag caacggccag cccgagaaca actacaagac cacccctccc 1560
gtgctggaca gcgacggctc attcttcctg tacagcaagc tgaccgtgga caagtcccgg 1620
tggcagcagg gcaacgtgtt cagctgctct gtgatgcacg aggccctgca caaccggttc 1680
acccagaagt ccctgagcct gagccctggc 1710

<210> 67
<211> 1035
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 67
gacatcgtgc tgacccagag ccctgccagc ctggccgtgt ctctgggcca gagagccacc 60
atcagctgcc gggccagcga gagcgtggac agctacggcc agagctacat gcactggtat 120
cagcagaagg ccggccagcc ccccaagctg ctgatctacc tggccagcaa cctggaaagc 180
ggcgtgcccg ccagattcag cggcagcggc agcagaaccg acttcaccct gaccatcgac 240
cccgtgcagg ccgaggacgc cgccacctac tactgccagc agaacgccga ggacagccgg 300
accttcggcg gaggcaccaa gctggaaatc aagggcggct ccggcagcag cggctctggc 360
ggcgatatcc agatgaccca gtcccccgcc tccctgagcg tgtccgtggg cgacaccatc 420
accctgacat gccacgccag ccagaacatc gacgtgtggc tgagctggtt ccagcagaag 480
cctggcaaca tccctaagct gctcatctat aaggcctcca acctgcacac cggcgtgccc 540
agcaggtttt ccggctctgg cagcggcacc ggctttaccc tgacaatcag cagcctgcag 600
cccgaggata tcgccacata ttactgtcag caggcccaca gctacccctt cacctttggc 660
ggcggaacaa agctcgagat taagggcggc agcggaagct ccggctccgg cggacgtacg 720
gtggccgctc cttccgtgtt catcttccct ccctccgacg agcagctgaa gtccggcacc 780
gcctccgtgg tgtgtctgct gaacaacttc taccctcggg aggccaaggt gcagtggaag 840
gtggacaacg ccctgcagtc cggcaactcc caggagtccg tcaccgagca ggactccaag 900
gacagcacct actccctgtc ctccaccctg accctgtcca aggccgacta cgagaagcac 960
aaggtgtacg cctgtgaggt gacccaccag ggcctgtcca gccctgtgac caagtccttc 1020
aaccggggcg agtgc 1035

<210> 68
<211> 570
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 68
Glu Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Gly Gly
 1   5   10   15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asp Ser

```
            20                  25                  30
Ser Ile Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Met Ile Trp Gly Asp Gly Arg Ile Asp Tyr Ala Asp Ala Leu Lys
    50                  55                  60
Ser Arg Leu Ser Ile Ser Lys Asp Ser Ser Lys Ser Gln Val Phe Leu
65                  70                  75                  80
Glu Met Thr Ser Leu Arg Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala
                85                  90                  95
Arg Asp Gly Tyr Phe Pro Tyr Ala Met Asp Phe Trp Gly Gln Gly Thr
            100                 105                 110
Ser Val Thr Val Ser Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu
        115                 120                 125
Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
    130                 135                 140
Tyr Ser Phe Thr Ser Tyr Trp Ile His Trp Ile Lys Gln Arg Pro Gly
145                 150                 155                 160
Gln Gly Leu Glu Trp Ile Gly Met Ile Asp Pro Ser Asp Gly Glu Thr
                165                 170                 175
Arg Leu Asn Gln Arg Phe Gln Gly Arg Ala Thr Leu Thr Val Asp Glu
            180                 185                 190
Ser Thr Ser Thr Ala Tyr Met Gln Leu Arg Ser Pro Thr Ser Glu Asp
        195                 200                 205
Ser Ala Val Tyr Tyr Cys Thr Arg Leu Lys Glu Tyr Gly Asn Tyr Asp
    210                 215                 220
Ser Phe Tyr Phe Asp Val Trp Gly Ala Gly Thr Leu Val Thr Val Ser
225                 230                 235                 240
Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
                245                 250                 255
Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
            260                 265                 270
Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
        275                 280                 285
Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
    290                 295                 300
Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
305                 310                 315                 320
Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
                325                 330                 335
Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
            340                 345                 350
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
        355                 360                 365
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    370                 375                 380
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
385                 390                 395                 400
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                405                 410                 415
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            420                 425                 430
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
        435                 440                 445
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    450                 455                 460
```

```
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp
465                 470                 475                 480
Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
                485                 490                 495
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            500                 505                 510
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        515                 520                 525
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    530                 535                 540
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe
545                 550                 555                 560
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                565                 570


<210> 69
<211> 345
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 69
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Val Ser Val Gly
 1               5                  10                  15
Asp Thr Ile Thr Leu Thr Cys His Ala Ser Gln Asn Ile Asp Val Trp
            20                  25                  30
Leu Ser Trp Phe Gln Gln Lys Pro Gly Asn Ile Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Ala His Ser Tyr Pro Phe
                85                  90                  95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Ser Gly Ser
            100                 105                 110
Ser Gly Ser Gly Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu
        115                 120                 125
Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu
    130                 135                 140
Ser Val Asp Ser Tyr Gly Gln Ser Tyr Met His Trp Tyr Gln Gln Lys
145                 150                 155                 160
Ala Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu
                165                 170                 175
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe
            180                 185                 190
Thr Leu Thr Ile Asp Pro Val Gln Ala Glu Asp Ala Ala Thr Tyr Tyr
        195                 200                 205
Cys Gln Gln Asn Ala Glu Asp Ser Arg Thr Phe Gly Gly Gly Thr Lys
    210                 215                 220
Leu Glu Ile Lys Gly Gly Ser Gly Ser Ser Gly Ser Gly Gly Arg Thr
225                 230                 235                 240
```

```
Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
                245                 250                 255
Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
            260                 265                 270
Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
        275                 280                 285
Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
    290                 295                 300
Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
305                 310                 315                 320
Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
                325                 330                 335
Thr Lys Ser Phe Asn Arg Gly Glu Cys
            340                 345


<210> 70
<211> 1035
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 70
gacatccaga tgacccagag ccccgccagc ctgagcgtgt ccgtgggcga taccatcacc 60
ctgacctgcc acgccagcca gaacatcgac gtgtggctga gctggttcca gcagaagccc 120
ggcaacatcc ccaagctgct gatctacaag gccagcaacc tgcacaccgg cgtgcccagc 180
agattcagcg gctctggcag cggcaccggc tttaccctga ccatcagcag cctgcagccc 240
gaggatatcg ccacctacta ctgccagcag gcccacagct acccccttcac cttcggcgga 300
ggcaccaagc tggaaatcaa gggcggcagc ggcagctccg gctctggcgg cgatatcgtg 360
ctgacccagt ctcccgcctc cctggccgtg tctctgggcc agagagccac catcagctgc 420
cgggccagcg agagcgtgga cagctacggc cagagctaca tgcactggta tcagcagaag 480
gccggacagc cccctaaact gctcatctac ctggcctcca acctggaaag cggcgtgccc 540
gccaggtttt ccggcagcgg ctccagaacc gacttcaccc tgacaatcga ccccgtgcag 600
gccgaggacg ccgccacata ttactgtcag cagaacgccg aggacagcag aacctttggc 660
ggcggaacaa agctcgagat taagggcggc tccggctcca gcggatctgg cggacgtacg 720
gtggccgctc cttccgtgtt catcttccct ccctccgacg agcagctgaa gtccggcacc 780
gcctccgtgg tgtgtctgct gaacaacttc taccctcggg aggccaaggt gcagtggaag 840
gtggacaacg ccctgcagtc cggcaactcc caggagtccg tcaccgagca ggactccaag 900
gacagcacct actccctgtc ctccaccctg accctgtcca aggccgacta cgagaagcac 960
aaggtgtacg cctgtgaggt gacccaccag ggcctgtcca gccctgtgac caagtccttc 1020
aaccggggcg agtgc                                                  1035

<210> 71
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 71
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15
```

```
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205
Phe Asn Arg Gly Glu Cys
    210
```

<210> 72
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 72
gacatccaga tgacccagag ccccagcagc ctgagcgcca gcgtgggcga cagagtgacc 60
atcacctgtc gggccagcca gggcatccgg aactacctgg cctggtatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacgcc gccagcacac tgcagagcgg cgtgcccagc 180
agattcagcg gcagcggctc cggcaccgac ttcaccctga ccatcagcag cctgcagccc 240
gaggacgtgg ccacctacta ctgccagcgg tacaacagag ccccctacac cttcggccag 300
ggcaccaagg tggaaatcaa gcgtacggtg gccgctcctt ccgtgttcat cttccctccc 360
tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gtctgctgaa caacttctac 420
cctcgggagg ccaaggtgca gtggaaggtg gacaacgccc tgcagtccgg caactcccag 480
gagtccgtca ccgagcagga ctccaaggac agcacctact ccctgtcctc caccctgacc 540
ctgtccaagg ccgactacga gaagcacaag gtgtacgcct gtgaggtgac ccaccagggc 600
ctgtccagcc ctgtgaccaa gtccttcaac cggggcgagt gc   642

<210> 73
<211> 447
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 73
Glu Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Gly Gly
 1   5   10   15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asp Ser
            20   25   30
Ser Ile Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
        35   40   45
Gly Met Ile Trp Gly Asp Gly Arg Ile Asp Tyr Ala Asp Ala Leu Lys
    50   55   60
Ser Arg Leu Ser Ile Ser Lys Asp Ser Ser Lys Ser Gln Val Phe Leu
65   70   75   80
Glu Met Thr Ser Leu Arg Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala
                85   90   95
Arg Asp Gly Tyr Phe Pro Tyr Ala Met Asp Phe Trp Gly Gln Gly Thr
            100   105   110
Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115   120   125
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130   135   140
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145   150   155   160
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165   170   175
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180   185   190
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195   200   205
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210   215   220
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225   230   235   240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245   250   255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260   265   270
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275   280   285
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290   295   300
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305   310   315   320
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                325   330   335
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
            340   345   350
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys
        355   360   365
Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370   375   380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385   390   395   400
Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser
                405   410   415

```
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445


<210> 74
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 74
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 Glu Ser Val Asp Ser Tyr
            20                  25                  30
Gly Gln Ser Tyr Met His Trp Tyr Gln Gln Lys Ala 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 Arg Thr Asp Phe Thr Leu Thr Ile Asp
65                  70                  75                  80
Pro Val Gln Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Ala
                85                  90                  95
Glu Asp Ser Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
        115                 120                 125
Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
    130                 135                 140
Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
145                 150                 155                 160
Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175
Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
            180                 185                 190
His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
        195                 200                 205
Lys Thr Val Ala Pro Thr Glu Cys Ser
    210                 215


<210> 75
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 75
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
```

```
 1               5                  10                  15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
            20                  25                  30
Trp Ile His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Met Ile Asp Pro Ser Asp Gly Glu Thr Arg Leu Asn Gln Arg Phe
    50                  55                  60
Gln Gly Arg Ala Thr Leu Thr Val Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Arg Ser Pro Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Thr Arg Leu Lys Glu Tyr Gly Asn Tyr Asp Ser Phe Tyr Phe Asp Val
            100                 105                 110
Trp Gly Ala Gly Thr Leu Val Thr Val Ser Ser Glu Val Gln Leu Val
        115                 120                 125
Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser
    130                 135                 140
Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val
145                 150                 155                 160
Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp
                165                 170                 175
Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr
            180                 185                 190
Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser
        195                 200                 205
Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr
    210                 215                 220
Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val
225                 230                 235                 240
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
                245                 250                 255
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
            260                 265                 270
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
        275                 280                 285
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
    290                 295                 300
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
305                 310                 315                 320
Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
                325                 330                 335
Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
            340                 345                 350
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
        355                 360                 365
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
    370                 375                 380
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
385                 390                 395                 400
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
                405                 410                 415
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
            420                 425                 430
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
        435                 440                 445
```

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
    450   455   460
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
465   470   475   480
Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
                485   490   495
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            500   505   510
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
        515   520   525
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
    530   535   540
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
545   550   555   560
Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                565   570

<210> 76
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 76
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly Ser Gly Ser
            100   105   110
Ser Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu
        115   120   125
Ser Val Ser Val Gly Asp Thr Ile Thr Leu Thr Cys His Ala Ser Gln
    130   135   140
Asn Ile Asp Val Trp Leu Ser Trp Phe Gln Gln Lys Pro Gly Asn Ile
145   150   155   160
Pro Lys Leu Leu Ile Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro
                165   170   175
Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile
            180   185   190
Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Ala
        195   200   205
His Ser Tyr Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
    210   215   220

```
Gly Gly Ser Gly Ser Ser Gly Ser Gly Gly Arg Thr Val Ala Ala Pro
225                 230                 235                 240
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
                245                 250                 255
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            260                 265                 270
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
        275                 280                 285
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    290                 295                 300
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
305                 310                 315                 320
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
                325                 330                 335
Asn Arg Gly Glu Cys
            340
```

<210> 77
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 77
```
gaggtgcagc tgaaggagag cggccccggc ctggtggccc ccggcggcag cctgagcatc 60
acctgcaccg tgagcggctt cagcctgacc gacagcagca tcaactgggt gcgccagccc 120
cccggcaagg gcctggagtg gctgggcatg atctggggcg acggccgcat cgactacgcc 180
gacgccctga agagccgcct gagcatcagc aaggacagca gcaagagcca ggtgttcctg 240
gagatgacca gcctgcgcac cgacgacacc gccacctact actgcgcccg cgacggctac 300
ttcccctacg ccatggactt ctggggccag ggcaccagcg tgaccgtgag cagcgccagc 360
accaagggcc ccagcgtgtt ccccctggcc cctagcagca agagcacatc tggcggcaca 420
gccgccctgg gctgcctggt caaggactac ttccccgagc ccgtgacagt gtcctggaac 480
tctggcgccc tgaccagcgg agtgcatacc ttccctgccg tgctgcagtc cagcggcctg 540
tacagcctga gcagcgtggt cacagtgccc agcagcagcc tgggcaccca gacctacatc 600
tgcaacgtga accacaagcc cagcaacacc aaggtggaca agaaggtgga acccaagagc 660
tgcgacaaga cccacacctg tccccctgc cctgccctg aactgctggg cggaccctcc 720
gtgttcctgt tccccccaaa gcccaaggac accctgatga tcagccggac ccccgaagtg 780
acctgcgtgg tggtggacgt gtcccacgag gaccctgaag tgaagttcaa ttggtacgtg 840
gacggcgtgg aagtgcataa cgccaagacc aagcccagag aggaacagta caacagcacc 900
taccgggtgg tgtccgtgct gaccgtgctg caccaggact ggctgaacgg caaagagtac 960
aagtgcaagg tgtccaacaa ggccctgcct gcccccatcg agaaaaccat cagcaaggcc 1020
aagggccagc ctagagagcc ccaagtctgc accctgcccc ccagcagaga tgagctgacc 1080
aagaaccagg tgtccctgag ctgcgccgtg aagggcttct accccagcga tatcgccgtg 1140
gaatgggaga gcaacggcca gcccgagaac aactacaaga ccacccccc tgtgctggac 1200
agcgacggct cattcttcct ggtgtccaag ctgacagtgg acaagagccg gtggcagcag 1260
ggcaacgtgt tcagctgcag cgtgatgcac gaggccctgc acaaccatta cacccagaag 1320
tccctgagcc tgagccccgg c                                          1341
```

<210> 78
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 78
gacatcgtgc tgacccagag ccctgccagc ctggccgtgt ctctgggcca gagagccacc 60
atcagctgcc gggccagcga gagcgtggac agctacggcc agagctacat gcactggtat 120
cagcagaagg ccggccagcc ccccaagctg ctgatctacc tggccagcaa cctggaaagc 180
ggcgtgcccg ccagattcag cggcagcggc agcagaaccg acttcaccct gaccatcgac 240
cccgtgcagg ccgaggacgc cgccacctac tactgccagc agaacgccga ggacagccgg 300
accttcggcg gaggcaccaa gctggaaatc aagggacagc ccaaggctgc cccctcggtc 360
accctgttcc ccccaagcag cgaggaactg caggccaaca aggccaccct cgtgtgcctg 420
atcagcgact tctaccctgg cgccgtgacc gtggcctgga aggccgatag ctctcccgtg 480
aaggccggcg tggaaaccac cacccccagc aagcagagca acaacaaata cgccgccagc 540
agctacctga gcctgacccc cgagcagtgg aagtcccacc ggtcctacag ctgccaggtc 600
acacacgagg gcagcaccgt ggaaaagacc gtggccccca ccgagtgcag c   651

<210> 79
<211> 1719
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 79
caggtgcagc tgcagcagag cggccctgag ctggtcaagc ctggcgccag cgtgaagatc 60
agctgcaagg ccagcggcta cagcttcacc agctactgga tccactggat caagcagcgg 120
cctggccagg gcctggaatg gatcggcatg atcgacccca gcgacggcga gacacggctg 180
aaccagagat tccagggcag agccaccctg accgtggacg agagcaccag caccgcctac 240
atgcagctgc ggagccccac cagcgaggac agcgccgtgt actactgcac ccggctgaaa 300
gagtacggca actacgacag cttctacttc gacgtgtggg gagccggcac cctggtcacc 360
gtgtccagcg aagtgcagct ggtggaaagc ggcggaggcc tggtgcagcc cggcagaagc 420
ctgagactga gctgcgccgc cagcggcttc accttcgacg actacgccat gcactgggtc 480
cgacaggccc ctggcaaagg actggaatgg gtgtccgcca tcacctggaa cagcggccac 540
atcgactacg ccgacagcgt ggaaggccgg ttcaccatca gccgggacaa cgccaagaac 600
agcctgtacc tgcagatgaa cagcctgcgg gccgaggata ccgccgtgta ttattgcgcc 660
aaggtgtcct acctgagcac cgccagcagc ctggactact ggggccaggg caccctcgtg 720
acagtgtcct ccgcttccac caagggcccc agcgtgttcc ctctggcccc tagcagcaag 780
agcacatctg gcggaacagc cgccctgggc tgcctggtca aggactactt tcccgagccc 840
gtgaccgtgt cctggaactc tggtgccctg acaagcggag tgcatacctt ccctgccgtg 900
ctgcagagca gcggcctgta ctctctgagc agcgtggtca ccgtgccaag cagcagcctg 960
ggcacccaga cctacatctg caacgtgaac cacaagccct ccaacaccaa ggtggacaag 1020
aaggtggaac ccaagagctg cgacaagacc cacacctgtc ctccctgtcc tgcccctgaa 1080
ctgctgggcg gaccctccgt gttcctgttc cctccaaagc ccaaggatac cctgatgatc 1140
agccggaccc ctgaagtgac ctgcgtggtg gtggacgtgt cccacgagga tcccgaagtg 1200
aagttcaatt ggtacgtgga cggcgtggaa gtgcataacg ccaagaccaa gcccagagag 1260
gaacagtaca acagcaccta ccgggtggtg tccgtgctga cagtgctgca ccaggactgg 1320
ctgaacggca aagagtacaa gtgcaaggtg tccaacaagg ccctgccagc ccctatcgag 1380
aaaaccatca gcaaggccaa gggccagccc cgcgagcctc aggtgtacac actgcctcca 1440
tgccgggacg agctgaccaa gaaccaggtg tccctgtggt gcctcgtgaa gggcttctac 1500
ccctccgata tcgccgtgga atgggagagc aacggccagc ccgagaacaa ctacaagacc 1560
acccctcccg tgctggacag cgacggctca ttcttcctgt acagcaagct gaccgtggac 1620
aagtcccggt ggcagcaggg caacgtgttc agctgctctg tgatgcacga ggccctgcac 1680
aaccggttca cccagaagtc cctgagcctg agccctggc   1719

<210> 80
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 80
gacatccaga tgacccagag ccccagcagc ctgagcgcca gcgtgggcga cagagtgacc 60
atcacctgtc gggccagcca gggcatccgg aactacctgg cctggtatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacgcc gccagcacac tgcagagcgg cgtgcccagc 180
agattcagcg gcagcggctc cggcaccgac ttcaccctga ccatcagcag cctgcagccc 240
gaggacgtgg ccacctacta ctgccagcgg tacaacagag ccccctacac cttcggccag 300
ggcaccaagg tggaaatcaa gggcggctct ggcagctccg gcagcggcgg agacattcag 360
atgacacagt ccccgccag cctgtccgtg tccgtgggcg ataccatcac cctgacatgc 420
cacgccagcc agaacatcga cgtgtggctg agctggttcc agcagaaacc tggcaacatc 480
cctaagctgc tcatctataa ggccagcaac ctgcacacag gcgtgccctc cagattctcc 540
ggctctggct ctggcaccgg ctttacactg acaatcagtt ctctgcagcc tgaggatatc 600
gccacatatt actgtcagca ggcccacagc tacccttca ccttcggagg cggcaccaag 660
ctcgagatta agggcggaag cggctcctcc ggctccggcg gacgtacggt ggccgctcct 720
tccgtgttca tcttccctcc ctccgacgag cagctgaagt ccggcaccgc ctccgtggtg 780
tgtctgctga acaacttcta ccctcgggag gccaaggtgc agtggaaggt ggacaacgcc 840
ctgcagtccg gcaactccca ggagtccgtc accgagcagg actccaagga cagcacctac 900
tccctgtcct ccaccctgac cctgtccaag gccgactacg agaagcacaa ggtgtacgcc 960
tgtgaggtga cccaccaggg cctgtccagc cctgtgacca agtccttcaa ccggggcgag 1020
tgc 1023

<210> 81
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 81
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20   25   30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
    50   55   60
Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser Gln Val Gln Leu Gln Gln Ser
        115   120   125
Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys

```
    130                 135                 140
Ala Ser Gly Tyr Ser Phe Thr Ser Tyr Trp Ile His Trp Ile Lys Gln
145                 150                 155                 160
Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Met Ile Asp Pro Ser Asp
                165                 170                 175
Gly Glu Thr Arg Leu Asn Gln Arg Phe Gln Gly Arg Ala Thr Leu Thr
            180                 185                 190
Val Asp Glu Ser Thr Ser Thr Ala Tyr Met Gln Leu Arg Ser Pro Thr
        195                 200                 205
Ser Glu Asp Ser Ala Val Tyr Tyr Cys Thr Arg Leu Lys Glu Tyr Gly
    210                 215                 220
Asn Tyr Asp Ser Phe Tyr Phe Asp Val Trp Gly Ala Gly Thr Leu Val
225                 230                 235                 240
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
                245                 250                 255
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
            260                 265                 270
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
        275                 280                 285
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
    290                 295                 300
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
305                 310                 315                 320
Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
                325                 330                 335
Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
            340                 345                 350
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
        355                 360                 365
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
    370                 375                 380
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
385                 390                 395                 400
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
                405                 410                 415
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
            420                 425                 430
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
        435                 440                 445
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
    450                 455                 460
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
465                 470                 475                 480
Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
                485                 490                 495
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            500                 505                 510
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
        515                 520                 525
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
    530                 535                 540
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
545                 550                 555                 560
Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                565                 570
```

<210> 82
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 82
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Val Ser Val Gly
 1   5   10   15
Asp Thr Ile Thr Leu Thr Cys His Ala Ser Gln Asn Ile Asp Val Trp
            20   25   30
Leu Ser Trp Phe Gln Gln Lys Pro Gly Asn Ile Pro Lys Leu Leu Ile
        35   40   45
Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Ala His Ser Tyr Pro Phe
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Ser Gly Ser
            100   105   110
Ser Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
        115   120   125
Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
    130   135   140
Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
145   150   155   160
Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro
                165   170   175
Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
            180   185   190
Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr
        195   200   205
Asn Arg Ala Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
    210   215   220
Gly Gly Ser Gly Ser Ser Gly Ser Gly Gly Arg Thr Val Ala Ala Pro
225   230   235   240
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
                245   250   255
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            260   265   270
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
        275   280   285
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    290   295   300
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
305   310   315   320
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
                325   330   335
Asn Arg Gly Glu Cys
            340

<210> 83
<211> 1719
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 83
gaggtgcagc tggtggaaag cggcggagga ctggtgcagc ccggcagaag cctgagactg 60
agctgcgccg ccagcggctt caccttcgac gactacgcca tgcactgggt ccgacaggcc 120
cctggcaagg gcctggaatg ggtgtccgcc atcacctgga acagcggcca catcgactac 180
gccgacagcg tggaaggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caaggtgtcc 300
tacctgagca ccgccagcag cctggactac tggggccagg gcaccctggt caccgtgtcc 360
agtcaggtcc agctgcagca gagcggccct gagctggtca agcctggcgc cagcgtgaag 420
atcagctgca aggccagcgg ctacagcttc accagctact ggatccactg gatcaagcag 480
cggcctggcc agggcctcga gtggatcggc atgatcgacc ccagcgacgg cgagacacgg 540
ctgaaccaga gattccaggg cagagccacc ctgaccgtgg acgagagcac cagcaccgcc 600
tacatgcagc tgcggagccc caccagcgag gatagcgccg tgtattattg cacccggctg 660
aaagagtacg gcaactacga cagcttctac ttcgacgtgt ggggagccgg caccctcgtg 720
acagtgtcct ccgcttccac caagggcccc agcgtgttcc ctctggcccc tagcagcaag 780
agcacatctg gcggaacagc cgccctgggc tgcctggtca aggactactt tcccgagccc 840
gtgaccgtgt cctggaactc tggtgccctg acaagcggag tgcatacctt ccctgccgtg 900
ctgcagagca gcggcctgta ctctctgagc agcgtggtca ccgtgccaag cagcagcctg 960
ggcacccaga cctacatctg caacgtgaac cacaagccct ccaacaccaa ggtggacaag 1020
aaggtggaac ccaagagctg cgacaagacc cacacctgtc ctccctgtcc tgcccctgaa 1080
ctgctgggcg gaccctccgt gttcctgttc cctccaaagc ccaaggatac cctgatgatc 1140
agccggaccc ctgaagtgac ctgcgtggtg gtggacgtgt cccacgagga tcccgaagtg 1200
aagttcaatt ggtacgtgga cggcgtggaa gtgcataacg ccaagaccaa gcccagagag 1260
gaacagtaca acagcaccta ccgggtggtg tccgtgctga cagtgctgca ccaggactgg 1320
ctgaacggca aagagtacaa gtgcaaggtg tccaacaagg ccctgccagc ccctatcgag 1380
aaaaccatca gcaaggccaa gggccagccc cgcgagcctc aggtgtacac actgcctcca 1440
tgccgggacg agctgaccaa gaaccaggtg tccctgtggt gcctcgtgaa gggcttctac 1500
ccctccgata tcgccgtgga atgggagagc aacggccagc ccgagaacaa ctacaagacc 1560
acccctcccg tgctggacag cgacggctca ttcttcctgt acagcaagct gaccgtggac 1620
aagtcccggt ggcagcaggg caacgtgttc agctgctctg tgatgcacga ggccctgcac 1680
aaccggttca cccagaagtc cctgagcctg agccctggc 1719

<210> 84
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 84
gacatccaga tgacccagag ccccgccagc ctgagcgtgt ccgtgggcga taccatcacc 60
ctgacctgcc acgccagcca gaacatcgac gtgtggctga gctggttcca gcagaagccc 120
ggcaacatcc ccaagctgct gatctacaag gccagcaacc tgcacaccgg cgtgcccagc 180
agattcagcg gctctggcag cggcaccggc tttaccctga ccatcagcag cctgcagccc 240
gaggatatcg ccacctacta ctgccagcag gcccacagct acccccttcac cttcggcgga 300

ggcaccaagc tggaaatcaa gggcggcagc ggcagctccg gcagcggcgg agacattcag 360
atgacacagt cccccagcag cctgtccgcc agcgtgggcg acagagtgac catcacctgt 420
cgggccagcc agggcatccg gaactacctg gcctggtatc agcagaaacc tggcaaggcc 480
cctaaactgc tcatctacgc cgccagcaca ctgcagtctg gcgtgccctc cagattctcc 540
ggaagcggct ccggcaccga tttcaccctg acaatctcat ctctgcagcc tgaggacgtg 600
gccacatatt actgccagag atacaacaga gccccctaca cctttggcca gggcaccaag 660
gtcgagatta agggcggatc cggctccagc ggcagcggag gacgtacggt ggccgctcct 720
tccgtgttca tcttccctcc ctccgacgag cagctgaagt ccggcaccgc ctccgtggtg 780
tgtctgctga acaacttcta ccctcgggag gccaaggtgc agtggaaggt ggacaacgcc 840
ctgcagtccg gcaactccca ggagtccgtc accgagcagg actccaagga cagcacctac 900
tccctgtcct ccaccctgac cctgtccaag gccgactacg agaagcacaa ggtgtacgcc 960
tgtgaggtga cccaccaggg cctgtccagc cctgtgacca agtccttcaa ccggggcgag 1020
tgc 1023

<210> 85
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 85
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
            20   25   30
Trp Ile His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Met Ile Asp Pro Ser Asp Gly Glu Thr Arg Leu Asn Gln Arg Phe
    50   55   60
Gln Gly Arg Ala Thr Leu Thr Val Asp Glu Ser Thr Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Arg Ser Pro Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Thr Arg Leu Lys Glu Tyr Gly Asn Tyr Asp Ser Phe Tyr Phe Asp Val
            100   105   110
Trp Gly Ala Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115   120   125
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130   135   140
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145   150   155   160
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165   170   175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180   185   190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195   200   205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210   215   220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225   230   235   240
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245   250   255

```
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350
Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365
Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu
                405                 410                 415
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445
Leu Ser Pro Gly
    450


<210> 86
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 86
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Val Ser Val Gly
 1               5                  10                  15
Asp Thr Ile Thr Leu Thr Cys His Ala Ser Gln Asn Ile Asp Val Trp
            20                  25                  30
Leu Ser Trp Phe Gln Gln Lys Pro Gly Asn Ile Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Ala His Ser Tyr Pro Phe
                85                  90                  95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gln Pro Lys Ala
            100                 105                 110
Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala
        115                 120                 125
Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala
    130                 135                 140
```

```
Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val
145                 150                 155                 160
Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser
                165                 170                 175
Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
            180                 185                 190
Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala
        195                 200                 205
Pro Thr Glu Cys Ser
    210
```

<210> 87
<211> 568
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 87

```
Glu Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Gly Gly
 1               5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asp Ser
            20                  25                  30
Ser Ile Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Met Ile Trp Gly Asp Gly Arg Ile Asp Tyr Ala Asp Ala Leu Lys
    50                  55                  60
Ser Arg Leu Ser Ile Ser Lys Asp Ser Ser Lys Ser Gln Val Phe Leu
65                  70                  75                  80
Glu Met Thr Ser Leu Arg Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala
                85                  90                  95
Arg Asp Gly Tyr Phe Pro Tyr Ala Met Asp Phe Trp Gly Gln Gly Thr
            100                 105                 110
Ser Val Thr Val Ser Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
        115                 120                 125
Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
    130                 135                 140
Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly
145                 150                 155                 160
Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp Asn Ser Gly His Ile
                165                 170                 175
Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn
            180                 185                 190
Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
        195                 200                 205
Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser
    210                 215                 220
Ser Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
225                 230                 235                 240
Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
                245                 250                 255
Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
            260                 265                 270
```

```
Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
        275                 280                 285
Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
    290                 295                 300
Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
305                 310                 315                 320
Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
                325                 330                 335
Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
            340                 345                 350
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        355                 360                 365
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    370                 375                 380
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
385                 390                 395                 400
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
                405                 410                 415
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
            420                 425                 430
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        435                 440                 445
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    450                 455                 460
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu
465                 470                 475                 480
Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro
                485                 490                 495
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            500                 505                 510
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        515                 520                 525
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    530                 535                 540
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
545                 550                 555                 560
Lys Ser Leu Ser Leu Ser Pro Gly
                565
```

<210> 88
<211> 344
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 88

```
Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 1               5                  10                  15
Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr Leu
            20                  25                  30
Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
        35                  40                  45
```

```
Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65                  70                  75                  80
Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr Thr
                85                  90                  95
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly Ser Gly Ser Ser
            100                 105                 110
Gly Ser Gly Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
        115                 120                 125
Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser
    130                 135                 140
Val Asp Ser Tyr Gly Gln Ser Tyr Met His Trp Tyr Gln Gln Lys Ala
145                 150                 155                 160
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser
                165                 170                 175
Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr
            180                 185                 190
Leu Thr Ile Asp Pro Val Gln Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
        195                 200                 205
Gln Gln Asn Ala Glu Asp Ser Arg Thr Phe Gly Gly Gly Thr Lys Leu
    210                 215                 220
Glu Ile Lys Gly Gly Ser Gly Ser Ser Gly Ser Gly Gly Arg Thr Val
225                 230                 235                 240
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
                245                 250                 255
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
            260                 265                 270
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
        275                 280                 285
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
    290                 295                 300
Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
305                 310                 315                 320
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
                325                 330                 335
Lys Ser Phe Asn Arg Gly Glu Cys
            340
```

<210> 89
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 89
caggtgcagc tgcagcagag cggccccgag ctggtgaagc ccggcgccag cgtgaagatc 60
agctgcaagg ccagcggcta cagcttcacc agctactgga ttcactggat caagcagcgc 120
cccggccagg gcctggagtg gatcggcatg atcgacccca gcgacggcga gacccgcctg 180
aaccagcgct tccagggccg cgccaccctg accgtggacg agagcaccag caccgcctac 240
atgcagctgc gcagccccac cagcgaggac agcgccgtgt actactgcac ccgcctgaag 300
gagtacggca actacgacag cttctacttc gacgtgtggg gcgccggcac cctggtgacc 360

gtgagcagcg ccagcaccaa gggccccagc gtgttccccc tggcccctag cagcaagagc 420
acatctggcg gcacagccgc cctgggctgc ctggtcaagg actacttccc cgagcccgtg 480
acagtgtcct ggaactctgg cgccctgacc agcggagtgc ataccttccc tgccgtgctg 540
cagtccagcg gcctgtacag cctgagcagc gtggtcacag tgcccagcag cagcctgggc 600
acccagacct acatctgcaa cgtgaaccac aagcccagca acaccaaggt ggacaagaag 660
gtggaaccca agagctgcga caagacccac acctgtcccc cctgccctgc ccctgaactg 720
ctgggcggac cctccgtgtt cctgttcccc ccaaagccca aggacaccct gatgatcagc 780
cggacccccg aagtgacctg cgtggtggtg gacgtgtccc acgaggaccc tgaagtgaag 840
ttcaattggt acgtggacgg cgtggaagtg cataacgcca agaccaagcc cagagaggaa 900
cagtacaaca gcacctaccg ggtggtgtcc gtgctgaccg tgctgcacca ggactggctg 960
aacggcaaag agtacaagtg caaggtgtcc aacaaggccc tgcctgcccc catcgagaaa 1020
accatcagca aggccaaggg ccagcctaga gagccccaag tctgcaccct gccccccagc 1080
agagatgagc tgaccaagaa ccaggtgtcc ctgagctgcg ccgtgaaggg cttctacccc 1140
agcgatatcg ccgtggaatg ggagagcaac ggccagcccg agaacaacta caagaccacc 1200
ccccctgtgc tggacagcga cggctcattc ttcctggtgt ccaagctgac agtggacaag 1260
agccggtggc agcagggcaa cgtgttcagc tgcagcgtga tgcacgaggc cctgcacaac 1320
cattacaccc agaagtccct gagcctgagc cccggc 1356

<210> 90
<211> 639
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 90
gacatccaga tgacccagag ccccgccagc ctgagcgtgt ccgtgggcga taccatcacc 60
ctgacctgcc acgccagcca gaacatcgac gtgtggctga gctggttcca gcagaagccc 120
ggcaacatcc ccaagctgct gatctacaag gccagcaacc tgcacaccgg cgtgcccagc 180
agattcagcg gctctggcag cggcaccggc tttaccctga ccatcagcag cctgcagccc 240
gaggatatcg ccacctacta ctgccagcag gcccacagct acccccttcac cttcggcgga 300
ggcaccaagc tggaaatcaa gggacagccc aaggctgccc cctcggtcac cctgttcccc 360
ccaagctctg aggaactgca ggccaacaag gccaccctcg tgtgcctgat cagcgacttc 420
taccctggcg ccgtgaccgt ggcctggaag gccgatagct ctcccgtgaa ggccggcgtg 480
gaaaccacca cccccagcaa gcagagcaac aacaaatacg ccgccagcag ctacctgagc 540
ctgacccccg agcagtggaa gtcccaccgg tcctacagct gccaggtcac acacgagggc 600
agcaccgtgg aaaagaccgt ggcccccacc gagtgcagc 639

<210> 91
<211> 1704
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 91
gaggtgcagc tgaaagagtc cggccctgga ctggtggccc ctggcggcag cctgagcatc 60
acctgtaccg tgtccggctt cagcctgacc gacagcagca tcaactgggt ccgacagccc 120
cctggcaagg gcctggaatg gctgggcatg atctggggcg acggccggat cgactacgcc 180
gacgccctga agtcccggct gagcatcagc aaggacagca gcaagagcca ggtgttcctg 240
gaaatgacca gcctgcggac cgacgacacc gccacctact actgcgccag ggacggctac 300
ttcccctacg ccatggattt ctggggccag ggcaccagcg tgaccgtgtc ctccgaagtg 360
cagctggtgg aaagcggcgg aggcctggtg cagcccggca gaagcctgag actgagctgc 420

gccgccagcg gcttcacctt cgacgactac gccatgcact gggtccgcca ggctcccgga 480
aagggactcg agtgggtgtc cgccatcacc tggaacagcg gccacatcga ttacgccgat 540
agcgtggaag gccggttcac catcagccgg gacaacgcca agaacagcct gtacctgcag 600
atgaacagcc tgagagccga ggataccgcc gtgtactact gtgccaaggt gtcctacctg 660
agcaccgcca gcagcctgga ctactgggga cagggaaccc tggtcaccgt gtccagcgct 720
tccaccaagg gccccagcgt gttccctctg gcccctagca gcaagagcac atctggcgga 780
acagccgccc tgggctgcct ggtcaaggac tactttcccg agcccgtgac cgtgtcctgg 840
aactctggtg ccctgacaag cggagtgcat accttccctg ccgtgctgca gagcagcggc 900
ctgtactctc tgagcagcgt ggtcaccgtg ccaagcagca gcctgggcac ccagacctac 960
atctgcaacg tgaaccacaa gccctccaac accaaggtgg acaagaaggt ggaacccaag 1020
agctgcgaca agacccacac ctgtcctccc tgtcctgccc ctgaactgct gggcggaccc 1080
tccgtgttcc tgttccctcc aaagcccaag gataccctga tgatcagccg gacccctgaa 1140
gtgacctgcg tggtggtgga cgtgtcccac gaggatcccg aagtgaagtt caattggtac 1200
gtggacggcg tggaagtgca taacgccaag accaagccca gagaggaaca gtacaacagc 1260
acctaccggg tggtgtccgt gctgacagtg ctgcaccagg actggctgaa cggcaaagag 1320
tacaagtgca aggtgtccaa caaggccctg ccagccccta tcgagaaaac catcagcaag 1380
gccaagggcc agccccgcga gcctcaggtg tacacactgc ctccatgccg ggacgagctg 1440
accaagaacc aggtgtccct gtggtgcctc gtgaagggct tctacccctc cgatatcgcc 1500
gtggaatggg agagcaacgg ccagcccgag aacaactaca agaccacccc tcccgtgctg 1560
gacagcgacg gctcattctt cctgtacagc aagctgaccg tggacaagtc ccggtggcag 1620
cagggcaacg tgttcagctg ctctgtgatg cacgaggccc tgcacaaccg gttcacccag 1680
aagtccctga gcctgagccc tggc 1704

<210> 92
<211> 1035
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 92
gacatccaga tgacccagag ccccagcagc ctgagcgcca gcgtgggcga cagagtgacc 60
atcacctgtc gggccagcca gggcatccgg aactacctgg cctggtatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacgcc gccagcacac tgcagagcgg cgtgcccagc 180
agattcagcg gcagcggctc cggcaccgac ttcaccctga ccatcagcag cctgcagccc 240
gaggacgtgg ccacctacta ctgccagcgg tacaacagag ccccctacac cttcggccag 300
ggcaccaagg tggaaatcaa gggcggctct ggcagctccg gctctggcgg cgatatcgtg 360
ctgacccagt ctcccgccag cctggccgtg tctctgggcc agagagccac catcagctgc 420
agagccagcg agagcgtgga cagctacggc cagagctaca tgcattggta tcagcagaaa 480
gccggccagc ctcctaaact gctcatctac ctggccagca acctggaatc cggcgtgccc 540
gccaggtttt ccggcagcgg cagcagaacc gatttcacac tgacaatcga ccccgtgcag 600
gccgaggatg ccgccacata ttactgtcag cagaacgccg aggacagccg gaccttcggc 660
ggaggcacca agctcgagat taagggcgga agcggctcca gcggcagtgg cggacgtacg 720
gtggccgctc cttccgtgtt catcttccct ccctccgacg agcagctgaa gtccggcacc 780
gcctccgtgg tgtgtctgct gaacaacttc taccctcggg aggccaaggt gcagtggaag 840
gtggacaacg ccctgcagtc cggcaactcc caggagtccg tcaccgagca ggactccaag 900
gacagcacct actccctgtc ctccaccctg accctgtcca aggccgacta cgagaagcac 960
aaggtgtacg cctgtgaggt gacccaccag ggcctgtcca gccctgtgac caagtccttc 1020
aaccggggcg agtgc 1035

<210> 93
<211> 568
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 93
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20   25   30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
    50   55   60
Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser Glu Val Gln Leu Lys Glu Ser
        115   120   125
Gly Pro Gly Leu Val Ala Pro Gly Gly Ser Leu Ser Ile Thr Cys Thr
    130   135   140
Val Ser Gly Phe Ser Leu Thr Asp Ser Ser Ile Asn Trp Val Arg Gln
145   150   155   160
Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile Trp Gly Asp Gly
                165   170   175
Arg Ile Asp Tyr Ala Asp Ala Leu Lys Ser Arg Leu Ser Ile Ser Lys
            180   185   190
Asp Ser Ser Lys Ser Gln Val Phe Leu Glu Met Thr Ser Leu Arg Thr
        195   200   205
Asp Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Asp Gly Tyr Phe Pro Tyr
    210   215   220
Ala Met Asp Phe Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
225   230   235   240
Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
                245   250   255
Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
            260   265   270
Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
        275   280   285
Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
    290   295   300
Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
305   310   315   320
Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
                325   330   335
Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
            340   345   350
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        355   360   365
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    370   375   380
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
385   390   395   400

```
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
                405                 410                 415
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
            420                 425                 430
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        435                 440                 445
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    450                 455                 460
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu
465                 470                 475                 480
Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro
                485                 490                 495
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            500                 505                 510
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        515                 520                 525
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    530                 535                 540
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
545                 550                 555                 560
Lys Ser Leu Ser Leu Ser Pro Gly
                565
```

<210> 94
<211> 345
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 94

```
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 Glu Ser Val Asp Ser Tyr
            20                  25                  30
Gly Gln Ser Tyr Met His Trp Tyr Gln Gln Lys Ala 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 Arg Thr Asp Phe Thr Leu Thr Ile Asp
65                  70                  75                  80
Pro Val Gln Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Ala
                85                  90                  95
Glu Asp Ser Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
Gly Ser Gly Ser Ser Gly Ser Gly Gly Asp Ile Gln Met Thr Gln Ser
        115                 120                 125
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
    130                 135                 140
Arg Ala Ser Gln Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
145                 150                 155                 160
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln
                165                 170                 175
```

```
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            180                 185                 190
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr
        195                 200                 205
Cys Gln Arg Tyr Asn Arg Ala Pro Tyr Thr Phe Gly Gln Gly Thr Lys
    210                 215                 220
Val Glu Ile Lys Gly Gly Ser Gly Ser Ser Gly Ser Gly Gly Arg Thr
225                 230                 235                 240
Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
                245                 250                 255
Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
            260                 265                 270
Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
        275                 280                 285
Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
    290                 295                 300
Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
305                 310                 315                 320
Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
                325                 330                 335
Thr Lys Ser Phe Asn Arg Gly Glu Cys
            340                 345
```

<210> 95
<211> 1704
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 95
```
gaggtgcagc tggtggaaag cggcggagga ctggtgcagc ccggcagaag cctgagactg 60
agctgcgccg ccagcggctt caccttcgac gactacgcca tgcactgggt ccgacaggcc 120
cctggcaagg gcctggaatg ggtgtccgcc atcacctgga acagcggcca catcgactac 180
gccgacagcg tggaaggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caaggtgtcc 300
tacctgagca ccgccagcag cctggactac tggggccagg gcaccctggt caccgtgtcc 360
tccgaagtgc agctgaaaga gtccggccct ggcctggtgg cccctggcgg cagcctgagc 420
atcacctgta ccgtgtccgg cttcagcctg accgacagca gcatcaactg ggtccgccag 480
cctcccggaa agggactcga gtggctgggc atgatctggg gcgacggccg gatcgattac 540
gccgatgccc tgaagtcccg gctgagcatc agcaaggaca gcagcaagag ccaggtgttc 600
ctggaaatga ccagcctgag aaccgacgac accgccacct actactgtgc ccgggacggc 660
tacttccccc acgccatgga tttctgggga cagggaacca gcgtgaccgt gtccagcgct 720
tccaccaagg gccccagcgt gttccctctg gcccctagca gcaagagcac atctggcgga 780
acagccgccc tgggctgcct ggtcaaggac tactttcccg agcccgtgac cgtgtcctgg 840
aactctggtg ccctgacaag cggagtgcat accttccctg ccgtgctgca gagcagcggc 900
ctgtactctc tgagcagcgt ggtcaccgtg ccaagcagca gcctgggcac ccagacctac 960
atctgcaacg tgaaccacaa gccctccaac accaaggtgg acaagaaggt ggaacccaag 1020
agctgcgaca agacccacac ctgtcctccc tgtcctgccc ctgaactgct gggcggaccc 1080
tccgtgttcc tgttccctcc aaagcccaag gataccctga tgatcagccg gacccctgaa 1140
gtgacctgcg tggtggtgga cgtgtcccac gaggatcccg aagtgaagtt caattggtac 1200
gtggacggcg tggaagtgca taacgccaag accaagccca gagaggaaca gtacaacagc 1260
acctaccggg tggtgtccgt gctgacagtg ctgcaccagg actggctgaa cggcaaagag 1320
```

tacaagtgca aggtgtccaa caaggccctg ccagccccta tcgagaaaac catcagcaag 1380
gccaagggcc agccccgcga gcctcaggtg tacacactgc ctccatgccg ggacgagctg 1440
accaagaacc aggtgtccct gtggtgcctc gtgaagggct tctacccctc cgatatcgcc 1500
gtggaatggg agagcaacgg ccagcccgag aacaactaca agaccacccc tcccgtgctg 1560
gacagcgacg gctcattctt cctgtacagc aagctgaccg tggacaagtc ccggtggcag 1620
cagggcaacg tgttcagctg ctctgtgatg cacgaggccc tgcacaaccg gttcacccag 1680
aagtccctga gcctgagccc tggc 1704

<210> 96
<211> 1035
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 96
gacatcgtgc tgacccagag ccctgccagc ctggccgtgt ctctgggcca gagagccacc 60
atcagctgcc gggccagcga gagcgtggac agctacggcc agagctacat gcactggtat 120
cagcagaagg ccggccagcc ccccaagctg ctgatctacc tggccagcaa cctggaaagc 180
ggcgtgcccg ccagattcag cggcagcggc agcagaaccg acttcaccct gaccatcgac 240
cccgtgcagg ccgaggacgc cgccacctac tactgccagc agaacgccga ggacagccgg 300
accttcggcg gaggcaccaa gctggaaatc aagggcggct ccggcagcag cggctctggc 360
ggcgatatcc agatgaccca gtcccccagc agcctgagcg ccagcgtggg cgacagagtg 420
accatcacct gtagagccag ccagggcatc cggaactacc tggcttggta tcagcagaaa 480
cccggaaagg cccctaaact gctcatctac gccgccagca ccctgcagtc cggcgtgcca 540
agcagattct ccggctctgg cagcggcacc gatttcacac tgacaatcag cagcctgcag 600
cccgaggatg tggccaccta ttattgccag agatacaaca gagccccta caccttcggc 660
cagggcacca aggtcgagat taagggcgga agcggcagct ccggctccgg cggacgtacg 720
gtggccgctc cttccgtgtt catcttccct ccctccgacg agcagctgaa gtccggcacc 780
gcctccgtgg tgtgtctgct gaacaacttc taccctcggg aggccaaggt gcagtggaag 840
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gacagcacct actccctgtc ctccaccctg accctgtcca aggccgacta cgagaagcac 960
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<210> 97
<211> 1710
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<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 97
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cctggcaagg gcctggaatg gctgggcatg atctggggcg acggccggat cgactacgcc 180
gacgccctga agtcccggct gagcatcagc aaggacagca gcaagagcca ggtgttcctg 240
gaaatgacca gcctgcggac cgacgacacc gccacctact actgcgccag ggacggctac 300
ttcccctacg ccatggattt ctggggccag ggcaccagcg tgaccgtgtc cagtcaggtc 360
cagctgcagc agagcggccc tgagctggtc aagcctggcg ccagcgtgaa gatcagctgc 420
aaggccagcg gctacagctt caccagctac tggatccact ggatcaagca gcggcctggc 480
cagggcctcg agtggatcgg aatgatcgac cccagcgacg gcgagacacg gctgaaccag 540
agattccagg gcagagccac cctgaccgtg gacgagagca ccagcaccgc ctacatgcag 600

ctgcggagcc ccaccagcga ggacagcgcc gtgtactact gcacccggct gaaagaatac 660
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<210> 98
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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 98
Gly Gly Gly Gly
 1

<210> 99
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 99
Gly Gly Gly Gly Gly
 1   5

<210> 100
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 100

Gly Gly Gly Gly Gly Gly
 1   5

<210> 101
<211> 7
<212> PRT
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<220>
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<400> 101
Gly Gly Gly Gly Gly Gly Gly
 1   5

<210> 102
<211> 8
<212> PRT
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<220>
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<400> 102
Gly Gly Gly Gly Gly Gly Gly Gly
 1   5

<210> 103
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 103
Gly Gly Gly Gly Ser
 1   5

<210> 104
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 104
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5   10

<210> 105
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 105
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5   10   15

<210> 106
<211> 5
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<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 106
Thr Lys Gly Pro Ser
 1   5

<210> 107
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 107
Thr Val Ala Ala Pro
 1   5

<210> 108
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 108
Gln Pro Lys Ala Ala
 1   5

<210> 109
<211> 5

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 109
Gln Arg Ile Glu Gly
 1   5

<210> 110
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 110
Ala Ser Thr Lys Gly Pro Ser
 1   5

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

<220>
<223> Synthetic Construct

<400> 111
Arg Thr Val Ala Ala Pro Ser
 1   5

<210> 112
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 112
Gly Gln Pro Lys Ala Ala Pro
 1   5

<210> 113
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 113
His Ile Asp Ser Pro Asn Lys
 1   5

<210> 114
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 114
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30
Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile
        35   40   45
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
    50   55   60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly
            100   105   110
Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser
        115   120   125
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
    130   135   140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145   150   155   160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165   170   175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180   185   190
Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His
        195   200   205
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
    210   215   220
Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser
225   230   235   240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245   250   255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
            260   265   270
Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275   280   285
Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
    290   295   300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320
Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
325 330 335
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350
Pro Pro Cys Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys
355 360 365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415
Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

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

<220>
<223> Synthetic Construct

<400> 115
Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
1 5 10 15
Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile
20 25 30
His Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45
Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65 70 75 80
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn Pro Pro Thr
85 90 95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 116
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 116
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cccggcagag gcctggaatg gatcggcgcc atctaccccg gcaacggcga cacctcctac 180
aaccagaagt tcaagggcaa ggccaccctg accgccgaca agagcagcag cacagcctac 240
atgcagctgt ccagcctgac cagcgaggac agcgccgtgt actactgcgc cagaagcacc 300
tactacggcg gcgactggta cttcaacgtg tggggagccg gcaccaccgt gacagtgtct 360
gctgcttcga ccaagggccc atcggtgttc cctctggccc cttgcagcag aagcaccagc 420
gaatctacag ccgccctggg ctgcctcgtg aaggactact ttcccgagcc cgtgaccgtg 480
tcctggaact ctggcgctct gacaagcggc gtgcacacct ttccagccgt gctccagagc 540
agcggcctgt actctctgag cagcgtcgtg acagtgccca gcagcagcct gggcaccaag 600
acctacacct gtaacgtgga ccacaagccc agcaacacca aggtggacaa gcgggtggaa 660
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gtgttcctgt tccccccaaa gcccaaggac accctgatga tcagccggac ccccgaagtg 780
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taccgggtgg tgtccgtgct gaccgtgctg caccaggact ggctgaacgg caaagagtac 960
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tccctgtctc tgtccctggg caag 1344

<210> 117
<211> 639
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 117
cagatcgtgc tgagccagag ccctgccatc ctgagcgctt ccccaggcga gaaagtgacc 60
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agcagcccca agccttggat ctacgccacc agcaatctgg ccagcggagt gcctgtgcgg 180
tttagcggct ctggcagcgg cacaagctac agcctgacca tcagccgggt ggaagccgaa 240
gatgccgcca cctactactg ccagcagtgg accagcaacc cccccacatt tggcggaggc 300
accaagctgg aaatcaagcg tacggtggcc gctcccagcg tgttcatctt cccacctagc 360
gacgagcagc tgaagtccgg cacagcctct gtcgtgtgcc tgctgaacaa cttctacccc 420
cgcgaggcca aagtgcagtg gaaggtggac aacgccctgc agagcggcaa cagccaggaa 480
agcgtgaccg agcaggacag caaggactcc acctacagcc tgagcagcac cctgacactg 540

agcaaggccg actacgagaa gcacaaggtg tacgcctgcg aagtgaccca ccagggcctg 600
tctagccccg tgaccaagag cttcaaccgg ggcgagtgt 639

<210> 118
<211> 1713
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 118
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cccagcctga agtccagaaa gaccatcagc aaggacacca gcaagaacca ggtgtccctg 240
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tacagctact actacagcat ggactactgg ggccagggca ccaccgtgac cgtgtcatcc 360
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acccagaagt ccctgtctct gtccctgggc aag 1713

<210> 119
<211> 1026
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 119
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tatctgcaga agcccggcca gagcccccag tccctgatct acaaggtgtc caacagattc 180
agcggcgtgc ccgacagatt ctccggcagc ggctctggca ccgacttcac cctgaagatc 240

agccgggtgg aagccgagga cgtgggcgtg tactattgtg gccagggcac ccagtacccc 300
ttcacctttg gcagcggcac caaggtggaa atcaagggcc agcccaaggc cgcccccgac 360
atcgtgctga cacagagccc tgctagcctg gccgtgtctc ctggacagag ggccaccatc 420
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gtggaagcca acgacgtggc caactactac tgccagcaga gccggaaggt gccctacacc 660
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gagtgt 1026

<210> 120
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 120
Gly Tyr Thr Phe Thr Ser Tyr Asn
 1   5

<210> 121
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 121
Ile Tyr Pro Gly Asn Gly Asp Thr
 1   5

<210> 122
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 122
Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val
 1   5   10

<210> 123

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

<220>
<223> Synthetic Construct

<400> 123
Ser Ser Val Ser Tyr
 1   5

<210> 124
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 124
Ala Thr Ser
 1

<210> 125
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 125
Gln Gln Trp Thr Ser Asn Pro
 1   5

<210> 126
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 126
Gly Tyr Ile Phe Thr Asn Tyr Asn Ile His
 1   5   10

<210> 127
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 127
Ala Ile Tyr Pro Gly Asn Gly Asp Ala Pro
 1   5   10

<210> 128
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 128
Ala Asn Trp Asp Val Ala Phe Ala Tyr
 1   5

<210> 129
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 129
Gly Phe Thr Phe Asp Asp Tyr Ala Met His
 1   5   10

<210> 130
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<400> 130
Ala Ile Thr Trp Asn Ser Gly His Ile Asp
 1   5   10

<210> 131
<211> 12
<212> PRT
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<220>
<223> Synthetic Construct

<400> 131
Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr
 1   5   10

<210> 132
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<400> 132
Gly Tyr Ser Phe Thr Ser Tyr Trp Ile His
 1   5   10

<210> 133
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<400> 133
Met Ile Asp Pro Ser Asp Gly Glu Thr
 1   5

<210> 134
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 134
Leu Lys Glu Tyr Gly Asn Tyr Asp Ser Phe Tyr Phe Asp Val
 1   5   10

<210> 135
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 135
Gly Phe Ser Leu Thr Asp Ser Ser Ile Asn

1 5 10

<210> 136
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 136
Met Ile Trp Gly Asp Gly Arg Ile Asp
1 5

<210> 137
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 137
Asp Gly Tyr Phe Pro Tyr Ala Met Asp Phe
1 5 10

<210> 138
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 138
Lys Ala Ser Gln Asp Ile Asp Arg Tyr Met Ala
1 5 10

<210> 139
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 139
Asp Thr Ser Thr Leu Gln Ser
1 5

<210> 140
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 140
Leu Gln Tyr Asp Asn Leu Trp Thr
 1   5

<210> 141
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 141
Arg Ala Ser Gln Gly Ile Arg Asn Tyr Leu Ala
 1   5   10

<210> 142
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 142
Gln Arg Tyr Asn Arg Ala Pro Tyr Thr
 1   5

<210> 143
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<400> 143
His Ala Ser Gln Asn Ile Asp Val Trp Leu Ser
 1   5   10

<210> 144
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 144
Gln Gln Ala His Ser Tyr Pro Phe Thr
 1   5

<210> 145
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 145
Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Gln Ser Tyr Met His
 1   5   10   15

<210> 146
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 146
Leu Ala Ser Asn Leu Glu Ser
 1   5

<210> 147
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 147
Gln Gln Asn Ala Glu Asp Ser Arg Thr
 1   5

<210> 148
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 148
Gly Gly Ser Gly Ser Ser Gly Ser Gly Gly
 1   5   10

<210> 149
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 149
Gln Ser Leu Val His Asn Asn Gly Asn Thr Tyr
 1   5   10

<210> 150
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 150
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
            20   25   30
Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 151
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 151
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
            20   25   30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 152
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 152
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Lys Ala
            20   25   30
Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gln Leu Glu Trp Val
        35   40   45
Ala Gln Ile Lys Asp Lys Ser Asn Ser Tyr Ala Thr Tyr Tyr Ala Asp
    50   55   60
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65   70   75   80
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85   90   95
Tyr Cys Arg Gly Val Tyr Tyr Ala Leu Ser Pro Phe Asp Tyr Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 153
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 153
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1   5   10   15

```
Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Val His Asn
            20                  25                  30
Asn Ala Asn Thr Tyr Leu Ser Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45
Pro Gln Ser Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gly Gln Gly
                85                  90                  95
Thr Gln Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 154
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 154
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Lys Ala
            20                  25                  30
Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ala Gln Ile Lys Asp Lys Ser Asn Ser Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65                  70                  75                  80
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95
Tyr Cys Arg Gly Val Tyr Tyr Ala Leu Ser Pro Phe Asp Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 155
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 155
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1               5                  10                  15
Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Val His Asn
            20                  25                  30
Asn Gly Asn Thr Tyr Leu Ser Trp Tyr Leu Gln Lys Pro Gly Gln Ser
```

```
        35                  40                  45
Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gly Gln Gly
                85                  90                  95
Thr Gln Tyr Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 156
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 156
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
            20                  25                  30
Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Gly Arg Ala Thr Leu Thr Ala Asp Glu Ser Thr Ser Thr Ala 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 Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
            100                 105                 110
Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 157
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 157
Asp Leu Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly
 1               5                  10                  15
Gln Arg Ala Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Val Pro Ala
    50                  55                  60
```

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn
65 70 75 80
Pro Val Glu Ala Asn Asp Thr Ala Asn Tyr Tyr Cys Gln Gln Ser Thr
85 90 95
Glu Asp Pro Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 158
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 158
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly
100 105 110
Ala Gly Thr Thr Val Thr Val Ser Ala
115 120

<210> 159
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 159
Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
1 5 10 15
Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile
20 25 30
His Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45
Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65 70 75 80
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn Pro Pro Thr

```
                85                  90                  95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 160
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 160
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Val 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
Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Ser Ile Tyr Pro Gly Asn Val Asn Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60
Gln Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Thr Arg Ser His Tyr Gly Leu Asp Trp Asn Phe Asp Val Trp Gly Lys
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 161
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 161
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asn Ile Tyr Val Trp
            20                  25                  30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Gln Thr Tyr Pro Tyr
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 162
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 162
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1   5   10   15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp 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 Ala Gly Gly Gly Thr Asn Tyr Asn Pro Ser Leu Lys
    50   55   60
Ser Arg Lys Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val 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 Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
            100   105   110
Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 163
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 163
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly
 1   5   10   15
Gln Arg Ala Thr Ile Thr Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
            20   25   30
Val Thr Ser Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Lys Leu Leu Ile Phe Ala Ala Ser Asn Val Glu Ser Gly Val Pro Ala
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn
65   70   75   80
Pro Val Glu Ala Asn Asp Val Ala Asn Tyr Tyr Cys Gln Gln Ser Arg
                85   90   95
Lys Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 164

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

<220>
<223> Synthetic Construct

<400> 164
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Ala Lys Pro Gly Thr
 1   5   10   15
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20   25   30
Trp Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Thr Ile Tyr Pro Gly Asp Gly Asp Thr Gly Tyr Ala Gln Lys Phe
    50   55   60
Gln Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Lys Thr Val Tyr
65   70   75   80
Met His Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Gly Asp Tyr Tyr Gly Ser Asn Ser Leu Asp Tyr Trp Gly Gln
            100   105   110
Gly Thr Ser Val Thr Val Ser Ser
        115   120

<210> 165
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 165
Asp Ile Val Met Thr Gln Ser His Leu Ser Met Ser Thr Ser Leu Gly
 1   5   10   15
Asp Pro Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Thr Val
            20   25   30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Arg Arg Leu Ile
        35   40   45
Tyr Ser Ala Ser Tyr Arg Tyr Ile Gly Val Pro Asp Arg Phe Thr Gly
    50   55   60
Ser Gly Ala Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Ala
65   70   75   80
Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Ser Pro Pro Tyr
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 166
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 166
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asn Tyr
            20   25   30
Asn Ile His Trp Val Lys Lys Ser Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Ala Pro Tyr Ser Gln Lys Phe
    50   55   60
Gln Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Thr Ser Thr Thr Tyr
65   70   75   80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Val Arg Ala Asn Trp Asp Val Ala Phe Ala Tyr Trp Gly Gln Gly Thr
            100   105   110
Leu Val Thr Val Ser Ser
        115

<210> 167
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 167
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asp Arg Tyr
            20   25   30
Met Ala Trp Tyr Gln Asp Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
        35   40   45
His Asp Thr Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Arg Asp Tyr Thr Leu Thr Ile Ser Asn Leu Glu Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asn Leu Trp Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 168
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 168
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20   25   30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
    50   55   60
Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 169
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 169
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 170
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 170
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala

```
 1               5                  10                  15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
            20                  25                  30
Trp Ile His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Met Ile Asp Pro Ser Asp Gly Glu Thr Arg Leu Asn Gln Arg Phe
    50                  55                  60
Gln Gly Arg Ala Thr Leu Thr Val Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Arg Ser Pro Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Thr Arg Leu Lys Glu Tyr Gly Asn Tyr Asp Ser Phe Tyr Phe Asp Val
            100                 105                 110
Trp Gly Ala Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 171
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 171

```
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Val Ser Val Gly
 1               5                  10                  15
Asp Thr Ile Thr Leu Thr Cys His Ala Ser Gln Asn Ile Asp Val Trp
            20                  25                  30
Leu Ser Trp Phe Gln Gln Lys Pro Gly Asn Ile Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Ala His Ser Tyr Pro Phe
                85                  90                  95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 172
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 172

```
Glu Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Gly Gly
 1               5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asp Ser
            20                  25                  30
```

```
Ser Ile Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Met Ile Trp Gly Asp Gly Arg Ile Asp Tyr Ala Asp Ala Leu Lys
    50                  55                  60
Ser Arg Leu Ser Ile Ser Lys Asp Ser Ser Lys Ser Gln Val Phe Leu
65                  70                  75                  80
Glu Met Thr Ser Leu Arg Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala
                85                  90                  95
Arg Asp Gly Tyr Phe Pro Tyr Ala Met Asp Phe Trp Gly Gln Gly Thr
            100                 105                 110
Ser Val Thr Val Ser Ser
        115
```

<210> 173
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 173

```
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 Glu Ser Val Asp Ser Tyr
            20                  25                  30
Gly Gln Ser Tyr Met His Trp Tyr Gln Gln Lys Ala 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 Arg Thr Asp Phe Thr Leu Thr Ile Asp
65                  70                  75                  80
Pro Val Gln Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Ala
                85                  90                  95
Glu Asp Ser Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
```

<210> 174
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> VARIANT
<222> (1)...(5)
<223> Can be absent or present, or present in repeats
of up to 5 times

<400> 174

```
Gly Gly Gly Gly Ser
```

1 5

<210> 175
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 175
Gly Gln Pro Lys Ala Ala Pro
1 5

<210> 176
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 176
Asp Lys Thr His Thr
1 5

<210> 177
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 177
Thr Lys Gly Pro Ser Arg
1 5

<210> 178
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 178
Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 179
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 179
Lys Ala Ser Asn Leu His Thr
 1   5