SEQUENCE LISTING

<110> INTREXON CORPORATION

<120> CD33 SPECIFIC CHIMERIC ANTIGEN RECEPTORS

<130> 50471-709.601

<140>
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<150> 62/347,503
<151> 2016-06-08

<160> 62

<170> PatentIn version 3.5

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

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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

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

Gly Ile Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

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

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

Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Lys

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                85                  90                  95

Glu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 2
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 2
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atcacatgca gagccagcga aagtgtcgac aattatggca ttagctttat gaactggttc      120

caacagaaac ccgggaaggc tcctaagctt ctgatttacg ctgcatccaa ccaaggctcc      180

ggggtaccct ctcgcttctc aggcagtgga tctgggacag acttcactct caccatttca      240

tctctgcagc ctgatgactt cgcaacctat tactgtcagc aaagtaagga ggttccgtgg      300

acgttcggtc aagggaccaa ggtggagatc aaa                                   333


<210> 3
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 3
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 Thr Phe Thr Asp Tyr
            20                  25                  30
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Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Pro Tyr Asn Gly Gly Thr Gly Tyr Asn Gln Lys Phe
50 55 60

Lys Ser Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn 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 Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 4
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 4
caggttcagc tggtgcagtc tggagctgag gtgaagaagc ctgggagctc agtgaaggtt 60

tcctgcaaag cttctggcta caccttcact gactacaaca tgcactgggt gaggcaggct 120

cctggccaag gcctggaatg gattggatat atttatcctt acaatggtgg taccggctac 180

aaccagaagt tcaagagcaa ggccacaatt acagcagacg agagtactaa cacagcctac 240

atggaactct ccagcctgag gtctgaggac actgcagtct attactgcgc aagagggcgc 300

cccgctatgg actactgggg ccaagggact ctggtcactg tctcttca 348

<210> 5
<211> 45

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 5
ggtggcggtg gctcgggcgg tggtgggtcg ggtggcggcg gatct 45

<210> 6
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 6
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 7
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 7
gacattcaga tgacccagtc tccgagctct ctgtccgcat cagtaggaga cagggtcacc 60

atcacatgca gagccagcga aagtgtcgac aattatggca ttagctttat gaactggttc 120

caacagaaac ccgggaaggc tcctaagctt ctgatttacg ctgcatccaa ccaaggctcc 180

ggggtaccct ctcgcttctc aggcagtgga tctgggacag acttcactct caccatttca 240

tctctgcagc ctgatgactt cgcaacctat tactgtcagc aaagtaagga ggttccgtgg 300

acgttcggtc aagggaccaa ggtggagatc aaaggtggcg gtggctcggg cggtggtggg 360

tcgggtggcg gcggatctca ggttcagctg gtgcagtctg gagctgaggt gaagaagcct 420

gggagctcag tgaaggtttc ctgcaaagct tctggctaca ccttcactga ctacaacatg 480

cactgggtga ggcaggctcc tggccaaggc ctggaatgga ttggatatat ttatccttac 540

aatggtggta ccggctacaa ccagaagttc aagagcaagg ccacaattac agcagacgag 600

agtactaaca cagcctacat ggaactctcc agcctgaggt ctgaggacac tgcagtctat 660

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tcttca 726

<210> 8
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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

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

Gly Ile Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

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

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

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

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Glu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
            100                 105                 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
        115                 120                 125

Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val
    130                 135                 140

Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Asn Met
145                 150                 155                 160

His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
                165                 170                 175

Ile Tyr Pro Tyr Asn Gly Gly Thr Gly Tyr Asn Gln Lys Phe Lys Ser
            180                 185                 190

Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr Met Glu
        195                 200                 205

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
    210                 215                 220

Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
225                 230                 235                 240

Ser Ser
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<210> 9
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 9
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Thr
1   5   10   15

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

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

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

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

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

Ala Ser Gly Tyr Glu Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
            100   105   110

Val Thr Val Ser Ser
        115

<210> 10
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

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

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

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Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
        35                  40                  45

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

Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Tyr
65                  70                  75                  80

Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Glu Phe Pro Leu
                85                  90                  95

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


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

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 11
Glu Val Lys Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15

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

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

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

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

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

Ala Arg Asp Tyr Arg Tyr Glu Val Tyr Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 12
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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

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

His Trp Tyr Gln Gln Lys Ser Gly Asp Ser Pro Leu Arg Trp Ile Phe
35 40 45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Thr Met Glu Ala Glu
65 70 75 80

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

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

Thr Val Ser
115

<210> 13
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 13
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Val 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

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

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

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

Thr Val Thr Val Ser Ser
115

<210> 14
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 14
Asn Ile Met Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Phe Phe Ser
20 25 30

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

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

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

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

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

Arg

<210> 15
<211> 66
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 15
atgctgctgc tggtgaccag cctgctgctg tgtgagctgc cccaccccgc ctttctgctg 60

atcccc 66

<210> 16
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 16
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro
20

<210> 17
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 17
atctacatct gggcccctct ggccggcacc tgtggcgtgc tgctgctgag cctggtcatc 60

accctgtact gcaaccaccg gaat 84

<210> 18
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 18
Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
1 5 10 15

Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn
20 25

<210> 19
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 19
ttttgggtgc tggtggtggt tggtggagtc ctggcttgct atagcttgct agtaacagtg 60

gcctttatta ttttctgggt g 81

<210> 20
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 20
Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
20 25

<210> 21

<211> 141
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 21
aagcccacca ccacccctgc ccctagacct ccaaccccag cccctacaat cgccagccag 60

cccctgagcc tgaggcccga agcctgtaga cctgccgctg gcggagccgt gcacaccaga 120

ggcctggatt tcgcctgcga c 141

<210> 22
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 22
Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
1 5 10 15

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

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
35 40 45

<210> 23
<211> 126
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 23
aagagaggcc ggaagaaact gctgtacatc ttcaagcagc ccttcatgcg gcccgtgcag 60

accacccagg aagaggacgg ctgcagctgc cggttccccg aggaagagga aggcggctgc 120

gaactg 126

<210> 24
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 24
Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1 5 10 15

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
20 25 30

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
35 40

<210> 25
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 25
cgggtgaagt tcagccggag cgccgacgcc cctgcctacc agcagggcca gaaccagctg 60

tacaacgagc tgaacctggg ccggagggag gagtacgacg tgctggacaa gcggagaggc 120

cgggaccctg agatgggcgg caagccccgg agaaagaacc ctcaggaggg cctgtataac 180

gaactgcaga aagacaagat ggccgaggcc tacagcgaga tcggcatgaa gggcgagcgg 240

cggaggggca agggccacga cggcctgtac cagggcctga gcaccgccac caaggatacc 300

tacgacgccc tgcacatgca ggccctgccc cccaga 336

<210> 26
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 26
Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 27
<211> 123
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 27
aggagcaagc ggagcagagg cggccacagc gactacatga acatgacccc ccggaggcct 60

ggccccaccc ggaagcacta ccagccctac gcccctccca gggacttcgc cgcctaccgg 120

agc 123

<210> 28
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 28
Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 29
<211> 54
<212> DNA
<213> Thosea asigna virus

<400> 29
gagggcagag gaagtcttct aacatgcggt gacgtggagg agaatcccgg ccct 54

<210> 30
<211> 18
<212> PRT
<213> Thosea asigna virus

<400> 30

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
1   5   10   15

Gly Pro

<210> 31
<211> 1005
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 31
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 300

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 360

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 420

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 480

agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag 540

ggctgctggg gcccggagcc cagggactgc gtctcttgcc ggaatgtcag ccgaggcagg 600

gaatgcgtgg acaagtgcaa ccttctggag ggtgagccaa gggagtttgt ggagaactct 660

gagtgcatac agtgccaccc agagtgcctg cctcaggcca tgaacatcac ctgcacagga 720

cggggaccag acaactgtat ccagtgtgcc cactacattg acggccccca ctgcgtcaag 780

acctgcccgg caggagtcat gggagaaaac aacaccctgg tctggaagta cgcagacgcc 840

ggccatgtgt gccacctgtg ccatccaaac tgcacctacg gatgcactgg gccaggtctt 900

gaaggctgtc caacgaatgg gcctaagatc ccgtccatcg ccactgggat ggtgggggcc 960

ctcctcttgc tgctggtggt ggccctgggg atcggcctct tcatg 1005

<210> 32
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 32
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
100 105 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

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Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145                 150                 155                 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
                165                 170                 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
            180                 185                 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
        195                 200                 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
    210                 215                 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
225                 230                 235                 240

Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro
                245                 250                 255

His Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr
            260                 265                 270

Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His
        275                 280                 285

Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro
    290                 295                 300

Thr Asn Gly Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala
305                 310                 315                 320

Leu Leu Leu Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met
                325                 330                 335
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<210> 33

<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 33
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<210> 34
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 34
Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Pro
1 5 10 15

Gly Ser Ser Gly
20

<210> 35
<211> 891
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 35
atgacaacac ccagaaattc agtaaatggg actttcccgg cagagccaat gaaaggccct 60

attgctatgc aatctggtcc aaaaccactc ttcaggagga tgtcttcact ggtgggcccc 120

acgcaaagct tcttcatgag ggaatctaag actttggggg ctgtccagat tatgaatggg 180

ctcttccaca ttgccctggg gggtcttctg atgatcccag cagggatcta tgcacccatc 240

tgtgtgactg tgtggtaccc tctctgggga ggcattatgt atattatttc cggatcactc 300

ctggcagcaa cggagaaaaa ctccaggaag tgtttggtca aaggaaaaat gataatgaat 360

tcattgagcc tctttgctgc catttctgga atgattcttt caatcatgga catacttaat 420

attaaaattt cccatttttt aaaaatggag agtctgaatt ttattagagc tcacacacca 480

tatattaaca tatacaactg tgaaccagct aatccctctg agaaaaactc cccatctacc 540

caatactgtt acagcataca atctctgttc ttgggcattt tgtcagtgat gctgatcttt 600

gccttcttcc aggaacttgt aatagctggc atcgttgaga atgaatggaa aagaacgtgc 660

tccagaccca aatctaacat agttctcctg tcagcagaag aaaaaaaaga acagactatt 720

gaaataaaag aagaagtggt tgggctaact gaaacatctt cccaaccaaa gaatgaagaa 780

gacattgaaa ttattccaat ccaagaagag gaagaagaag aaacagagac gaactttcca 840

gaacctcccc aagatcagga atcctcacca atagaaaatg acagctctcc t 891

<210> 36
<211> 297
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 36
Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
1 5 10 15

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
20 25 30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
35 40 45

Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile
50 55 60

```
Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile
65                  70                  75                  80

Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
                85                  90                  95

Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
            100                 105                 110

Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile
        115                 120                 125

Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
    130                 135                 140

His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
145                 150                 155                 160

Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
                165                 170                 175

Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
            180                 185                 190

Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
        195                 200                 205

Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
    210                 215                 220

Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
225                 230                 235                 240

Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro
                245                 250                 255

Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu
```

260 265 270

Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser
275 280 285

Ser Pro Ile Glu Asn Asp Ser Ser Pro
290 295

<210> 37
<211> 395
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 37
Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp
20 25 30

Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp
35 40 45

Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu
50 55 60

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

Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly
85 90 95

Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys
100 105 110

```
Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe
        115                 120                 125

Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    130                 135                 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Ile Thr
145                 150                 155                 160

Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser
                165                 170                 175

Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys
            180                 185                 190

Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala
        195                 200                 205

Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg Asp
    210                 215                 220

Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val Thr Thr
225                 230                 235                 240

Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly Lys Glu
                245                 250                 255

Pro Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala Thr Thr Ala
            260                 265                 270

Ala Ile Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser Pro Ser Thr
        275                 280                 285

Gly Thr Thr Glu Ile Ser Ser His Glu Ser Ser His Gly Thr Pro Ser
    290                 295                 300

Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala Ser His Gln
305                 310                 315                 320
```

Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp Thr Thr Val Ala Ile
325 330 335

Ser Thr Ser Thr Val Leu Leu Cys Gly Leu Ser Ala Val Ser Leu Leu
340 345 350

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

Met Glu Ala Met Glu Ala Leu Pro Val Thr Trp Gly Thr Ser Ser Arg
370 375 380

Asp Glu Asp Leu Glu Asn Cys Ser His His Leu
385 390 395

<210> 38
<211> 1476
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 38
atgctgctgc tggtgaccag cctgctgctg tgtgagctgc cccaccccgc ctttctgctg 60

atccccgaca ttcagatgac ccagtctccg agctctctgt ccgcatcagt aggagacagg 120

gtcaccatca catgcagagc cagcgaaagt gtcgacaatt atggcattag ctttatgaac 180

tggttccaac agaaacccgg gaaggctcct aagcttctga tttacgctgc atccaaccaa 240

ggctccgggg taccctctcg cttctcaggc agtggatctg ggacagactt cactctcacc 300

atttcatctc tgcagcctga tgacttcgca acctattact gtcagcaaag taaggaggtt 360

ccgtggacgt tcggtcaagg gaccaaggtg gagatcaaag gtggcggtgg ctcgggcggt 420

ggtgggtcgg gtggcggcgg atctcaggtt cagctggtgc agtctggagc tgaggtgaag 480

aagcctggga gctcagtgaa ggtttcctgc aaagcttctg gctacacctt cactgactac 540

aacatgcact gggtgaggca ggctcctggc caaggcctgg aatggattgg atatatttat 600

ccttacaatg gtggtaccgg ctacaaccag aagttcaaga gcaaggccac aattacagca 660

gacgagagta ctaacacagc ctacatggaa ctctccagcc tgaggtctga ggacactgca 720

gtctattact gcgcaagagg gcgccccgct atggactact ggggccaagg gactctggtc 780

actgtctctt caaagcccac caccaccct gcccctagac ctccaacccc agcccctaca 840

atcgccagcc agcccctgag cctgaggccc gaagcctgta gacctgccgc tggcggagcc 900

gtgcacacca gaggcctgga tttcgcctgc gacatctaca tctgggcccc tctggccggc 960

acctgtggcg tgctgctgct gagcctggtc atcaccctgt actgcaacca ccggaatagg 1020

agcaagcgga gcagaggcgg ccacagcgac tacatgaaca tgaccccccg gaggcctggc 1080

cccacccgga agcactacca gccctacgcc cctcccaggg acttcgccgc ctaccggagc 1140

cgggtgaagt tcagccggag cgccgacgcc cctgcctacc agcagggcca gaaccagctg 1200

tacaacgagc tgaacctggg ccggagggag gagtacgacg tgctggacaa gcggagaggc 1260

cgggaccctg agatgggcgg caagccccgg agaaagaacc ctcaggaggg cctgtataac 1320

gaactgcaga aagacaagat ggccgaggcc tacagcgaga tcggcatgaa gggcgagcgg 1380

cggaggggca agggccacga cggcctgtac cagggcctga gcaccgccac caaggatacc 1440

tacgacgccc tgcacatgca ggccctgccc cccaga 1476

<210> 39
<211> 492
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 39
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser

```
            20                  25                  30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
        35                  40                  45

Glu Ser Val Asp Asn Tyr Gly Ile Ser Phe Met Asn Trp Phe Gln Gln
    50                  55                  60

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

Gly Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
                85                  90                  95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr
            100                 105                 110

Tyr Cys Gln Gln Ser Lys Glu Val Pro Trp Thr Phe Gly Gln Gly Thr
        115                 120                 125

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140

Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
145                 150                 155                 160

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
                165                 170                 175

Phe Thr Asp Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
            180                 185                 190

Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Gly Thr Gly Tyr
        195                 200                 205

Asn Gln Lys Phe Lys Ser Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr
    210                 215                 220
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Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
225                 230                 235                 240

Val Tyr Tyr Cys Ala Arg Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln
                245                 250                 255

Gly Thr Leu Val Thr Val Ser Ser Lys Pro Thr Thr Thr Pro Ala Pro
            260                 265                 270

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
        275                 280                 285

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
    290                 295                 300

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
305                 310                 315                 320

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn
                325                 330                 335

His Arg Asn Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met
            340                 345                 350

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
        355                 360                 365

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe
    370                 375                 380

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
385                 390                 395                 400

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
                405                 410                 415

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
```

420 425 430

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
435 440 445

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
450 455 460

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
465 470 475 480

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 40
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 40
atgctgctgc tggtgaccag cctgctgctg tgtgagctgc cccaccccgc ctttctgctg 60

atccccgaca ttcagatgac ccagtctccg agctctctgt ccgcatcagt aggagacagg 120

gtcaccatca catgcagagc cagcgaaagt gtcgacaatt atggcattag ctttatgaac 180

tggttccaac agaaacccgg gaaggctcct aagcttctga tttacgctgc atccaaccaa 240

ggctccgggg taccctctcg cttctcaggc agtggatctg ggacagactt cactctcacc 300

atttcatctc tgcagcctga tgacttcgca acctattact gtcagcaaag taaggaggtt 360

ccgtggacgt tcggtcaagg gaccaaggtg gagatcaaag gtggcggtgg ctcgggcggt 420

ggtgggtcgg gtggcggcgg atctcaggtt cagctggtgc agtctggagc tgaggtgaag 480

aagcctggga gctcagtgaa ggtttcctgc aaagcttctg gctacacctt cactgactac 540

aacatgcact gggtgaggca ggctcctggc caaggcctgg aatggattgg atatatttat 600

ccttacaatg gtggtaccgg ctacaaccag aagttcaaga gcaaggccac aattacagca 660

gacgagagta ctaacacagc ctacatggaa ctctccagcc tgaggtctga ggacactgca 720

gtctattact gcgcaagagg gcgccccgct atggactact ggggccaagg gactctggtc 780

actgtctctt caaagcccac caccaccccct gcccctagac ctccaacccc agcccctaca 840

atcgccagcc agcccctgag cctgaggccc gaagcctgta gacctgccgc tggcggagcc 900

gtgcacacca gaggcctgga tttcgcctgc gacatctaca tctgggcccc tctggccggc 960

acctgtggcg tgctgctgct gagcctggtc atcaccctgt actgcaacca ccggaatcgg 1020

gtgaagttca gccggagcgc cgacgcccct gcctaccagc agggccagaa ccagctgtac 1080

aacgagctga acctgggccg gagggaggag tacgacgtgc tggacaagcg gagaggccgg 1140

gaccctgaga tgggcggcaa gccccggaga aagaaccctc aggagggcct gtataacgaa 1200

ctgcagaaag acaagatggc cgaggcctac agcgagatcg gcatgaaggg cgagcggcgg 1260

aggggcaagg gccacgacgg cctgtaccag ggcctgagca ccgccaccaa ggatacctac 1320

gacgccctgc acatgcaggc cctgcccccc aga 1353

<210> 41
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 41
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
35 40 45

```
Glu Ser Val Asp Asn Tyr Gly Ile Ser Phe Met Asn Trp Phe Gln Gln
    50                  55                  60

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

Gly Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
                85                  90                  95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr
            100                 105                 110

Tyr Cys Gln Gln Ser Lys Glu Val Pro Trp Thr Phe Gly Gln Gly Thr
        115                 120                 125

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140

Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
145                 150                 155                 160

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
                165                 170                 175

Phe Thr Asp Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
            180                 185                 190

Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Gly Thr Gly Tyr
        195                 200                 205

Asn Gln Lys Phe Lys Ser Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr
    210                 215                 220

Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
225                 230                 235                 240

Val Tyr Tyr Cys Ala Arg Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln
                245                 250                 255
```

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Gly Thr Leu Val Thr Val Ser Ser Lys Pro Thr Thr Thr Pro Ala Pro
            260                 265                 270

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
        275                 280                 285

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
    290                 295                 300

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
305                 310                 315                 320

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn
                325                 330                 335

His Arg Asn Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
            340                 345                 350

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
        355                 360                 365

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
    370                 375                 380

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
385                 390                 395                 400

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
                405                 410                 415

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
            420                 425                 430

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
        435                 440                 445
```

Pro Pro Arg
    450

<210> 42
<211> 2619
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 42
atgctgctgc tggtgaccag cctgctgctg tgtgagctgc cccaccccgc ctttctgctg 60

atccccgaca ttcagatgac ccagtctccg agctctctgt ccgcatcagt aggagacagg 120

gtcaccatca catgcagagc cagcgaaagt gtcgacaatt atggcattag ctttatgaac 180

tggttccaac agaaacccgg gaaggctcct aagcttctga tttacgctgc atccaaccaa 240

ggctccgggg taccctctcg cttctcaggc agtggatctg ggacagactt cactctcacc 300

atttcatctc tgcagcctga tgacttcgca acctattact gtcagcaaag taaggaggtt 360

ccgtggacgt tcggtcaagg gaccaaggtg gagatcaaag gtggcggtgg ctcgggcggt 420

ggtgggtcgg gtggcggcgg atctcaggtt cagctggtgc agtctggagc tgaggtgaag 480

aagcctggga gctcagtgaa ggtttcctgc aaagcttctg gctacacctt cactgactac 540

aacatgcact gggtgaggca ggctcctggc caaggcctgg aatggattgg atatatttat 600

ccttacaatg gtggtaccgg ctacaaccag aagttcaaga gcaaggccac aattacagca 660

gacgagagta ctaacacagc ctacatggaa ctctccagcc tgaggtctga ggacactgca 720

gtctattact gcgcaagagg gcgccccgct atggactact ggggccaagg gactctggtc 780

actgtctctt caaagcccac caccaccct gcccctagac ctccaacccc agcccctaca 840

atcgccagcc agcccctgag cctgaggccc gaagcctgta gacctgccgc tggcggagcc 900

gtgcacacca gaggcctgga tttcgcctgc gacatctaca tctgggcccc tctggccggc 960

acctgtggcg tgctgctgct gagcctggtc atcaccctgt actgcaacca ccggaatagg 1020

agcaagcgga gcagaggcgg ccacagcgac tacatgaaca tgaccccccg gaggcctggc 1080

cccacccgga agcactacca gccctacgcc cctcccaggg acttcgccgc ctaccggagc 1140

cgggtgaagt tcagccggag cgccgacgcc cctgcctacc agcagggcca gaaccagctg 1200

tacaacgagc tgaacctggg ccggagggag gagtacgacg tgctggacaa gcggagaggc 1260

cgggaccctg agatgggcgg caagccccgg agaaagaacc ctcaggaggg cctgtataac 1320

gaactgcaga aagacaagat ggccgaggcc tacagcgaga tcggcatgaa gggcgagcgg 1380

cggaggggca agggccacga cggcctgtac cagggcctga gcaccgccac caaggatacc 1440

tacgacgccc tgcacatgca ggccctgccc cccagactcg agggcggcgg agagggcaga 1500

ggaagtcttc taacatgcgg tgacgtggag gagaatcccg gccctaggat gcttctcctg 1560

gtgacaagcc ttctgctctg tgagttacca cacccagcat tcctcctgat cccacgcaaa 1620

gtgtgtaacg gaataggtat tggtgaattt aaagactcac tctccataaa tgctacgaat 1680

attaaacact tcaaaaactg cacctccatc agtggcgatc tccacatcct gccggtggca 1740

tttaggggtg actccttcac acatactcct cctctggatc cacaggaact ggatattctg 1800

aaaaccgtaa aggaaatcac agggtttttg ctgattcagg cttggcctga aaacaggacg 1860

gacctccatg cctttgagaa cctagaaatc atacgcggca ggaccaagca acatggtcag 1920

ttttctcttg cagtcgtcag cctgaacata acatccttgg gattacgctc cctcaaggag 1980

ataagtgatg gagatgtgat aatttcagga aacaaaaatt tgtgctatgc aaatacaata 2040

aactggaaaa aactgtttgg gacctccggt cagaaaacca aaattataag caacagaggt 2100

gaaaacagct gcaaggccac aggccaggtc tgccatgcct tgtgctcccc cgagggctgc 2160

tggggcccgg agcccaggga ctgcgtctct tgccggaatg tcagccgagg cagggaatgc 2220

gtggacaagt gcaaccttct ggagggtgag ccaagggagt ttgtggagaa ctctgagtgc 2280

atacagtgcc acccagagtg cctgcctcag gccatgaaca tcacctgcac aggacgggga 2340

ccagacaact gtatccagtg tgcccactac attgacggcc cccactgcgt caagacctgc 2400

ccggcaggag tcatgggaga aaacaacacc ctggtctgga agtacgcaga cgccggccat 2460

gtgtgccacc tgtgccatcc aaactgcacc tacggatgca ctgggccagg tcttgaaggc 2520

tgtccaacga atgggcctaa gatcccgtcc atcgccactg ggatggtggg ggccctcctc 2580

ttgctgctgg tggtggccct ggggatcggc ctcttcatg 2619

<210> 43
<211> 873
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 43
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
35 40 45

Glu Ser Val Asp Asn Tyr Gly Ile Ser Phe Met Asn Trp Phe Gln Gln
50 55 60

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

Gly Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr
100 105 110

Tyr Cys Gln Gln Ser Lys Glu Val Pro Trp Thr Phe Gly Gln Gly Thr
115 120 125

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

```
Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
145                 150                 155                 160

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
                165                 170                 175

Phe Thr Asp Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
            180                 185                 190

Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Gly Thr Gly Tyr
        195                 200                 205

Asn Gln Lys Phe Lys Ser Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr
    210                 215                 220

Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
225                 230                 235                 240

Val Tyr Tyr Cys Ala Arg Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln
                245                 250                 255

Gly Thr Leu Val Thr Val Ser Ser Lys Pro Thr Thr Thr Pro Ala Pro
            260                 265                 270

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
        275                 280                 285

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
    290                 295                 300

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
305                 310                 315                 320

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn
                325                 330                 335

His Arg Asn Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met
```

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            340                 345                 350

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
        355                 360                 365

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe
    370                 375                 380

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
385                 390                 395                 400

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
                405                 410                 415

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
            420                 425                 430

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
        435                 440                 445

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
    450                 455                 460

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
465                 470                 475                 480

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Leu Glu Gly Gly
                485                 490                 495

Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn
            500                 505                 510

Pro Gly Pro Arg Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu
        515                 520                 525

Leu Pro His Pro Ala Phe Leu Leu Ile Pro Arg Lys Val Cys Asn Gly
    530                 535                 540
```

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Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn
545                 550                 555                 560

Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile
                565                 570                 575

Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu
            580                 585                 590

Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly
        595                 600                 605

Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala
    610                 615                 620

Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln
625                 630                 635                 640

Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg
                645                 650                 655

Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys
            660                 665                 670

Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr
        675                 680                 685

Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys
    690                 695                 700

Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys
705                 710                 715                 720

Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg
                725                 730                 735

Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg
```

740 745 750

Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu
755 760 765

Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys
770 775 780

Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys
785 790 795 800

Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala
805 810 815

Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly
820 825 830

Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly Pro Lys Ile
835 840 845

Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu Leu Leu Val
850 855 860

Val Ala Leu Gly Ile Gly Leu Phe Met
865 870

<210> 44
<211> 792
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 44
atgctgctgc tggtgaccag cctgctgctg tgtgagctgc cccaccccgc ctttctgctg 60

atccccgaca ttcagatgac ccagtctccg agctctctgt ccgcatcagt aggagacagg 120

gtcaccatca catgcagagc cagcgaaagt gtcgacaatt atggcattag ctttatgaac 180

tggttccaac agaaacccgg gaaggctcct aagcttctga tttacgctgc atccaaccaa 240

ggctccgggg taccctctcg cttctcaggc agtggatctg ggacagactt cactctcacc 300

atttcatctc tgcagcctga tgacttcgca acctattact gtcagcaaag taaggaggtt 360

ccgtggacgt tcggtcaagg gaccaaggtg gagatcaaag gtggcggtgg ctcgggcggt 420

ggtgggtcgg gtggcggcgg atctcaggtt cagctggtgc agtctggagc tgaggtgaag 480

aagcctggga gctcagtgaa ggtttcctgc aaagcttctg gctacacctt cactgactac 540

aacatgcact gggtgaggca ggctcctggc caaggcctgg aatggattgg atatatttat 600

ccttacaatg gtggtaccgg ctacaaccag aagttcaaga gcaaggccac aattacagca 660

gacgagagta ctaacacagc ctacatggaa ctctccagcc tgaggtctga ggacactgca 720

gtctattact gcgcaagagg gcgccccgct atggactact ggggccaagg gactctggtc 780

actgtctctt ca 792

<210> 45
<211> 264
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 45
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
35 40 45

Glu Ser Val Asp Asn Tyr Gly Ile Ser Phe Met Asn Trp Phe Gln Gln
50 55 60

```
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Gln
65                  70                  75                  80

Gly Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
                85                  90                  95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr
            100                 105                 110

Tyr Cys Gln Gln Ser Lys Glu Val Pro Trp Thr Phe Gly Gln Gly Thr
        115                 120                 125

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140

Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
145                 150                 155                 160

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
                165                 170                 175

Phe Thr Asp Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
            180                 185                 190

Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Gly Thr Gly Tyr
        195                 200                 205

Asn Gln Lys Phe Lys Ser Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr
    210                 215                 220

Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
225                 230                 235                 240

Val Tyr Tyr Cys Ala Arg Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln
                245                 250                 255
```

Gly Thr Leu Val Thr Val Ser Ser
260

<210> 46
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 46
atgctgctgc tggtgaccag cctgctgctg tgtgagctgc cccaccccgc ctttctgctg 60

atccccgaca ttcagatgac ccagtctccg agctctctgt ccgcatcagt aggagacagg 120

gtcaccatca catgcagagc cagcgaaagt gtcgacaatt atggcattag ctttatgaac 180

tggttccaac agaaacccgg gaaggctcct aagcttctga tttacgctgc atccaaccaa 240

ggctccgggg taccctctcg cttctcaggc agtggatctg ggacagactt cactctcacc 300

atttcatctc tgcagcctga tgacttcgca acctattact gtcagcaaag taaggaggtt 360

ccgtggacgt tcggtcaagg gaccaaggtg gagatcaaag gtggcggtgg ctcgggcggt 420

ggtgggtcgg gtggcggcgg atctcaggtt cagctggtgc agtctggagc tgaggtgaag 480

aagcctggga gctcagtgaa ggtttcctgc aaagcttctg gctacacctt cactgactac 540

aacatgcact gggtgaggca ggctcctggc caaggcctgg aatggattgg atatatttat 600

ccttacaatg gtggtaccgg ctacaaccag aagttcaaga gcaaggccac aattacagca 660

gacgagagta ctaacacagc ctacatggaa ctctccagcc tgaggtctga ggacactgca 720

gtctattact gcgcaagagg gcgccccgct atggactact ggggccaagg gactctggtc 780

actgtctctt caaagcccac caccaccct gcccctagac ctccaacccc agcccctaca 840

atcgccagcc agcccctgag cctgaggccc gaagcctgta gacctgccgc tggcggagcc 900

gtgcacacca gaggcctgga tttcgcctgc gacatctaca tctgggcccc tctggccggc 960

acctgtggcg tgctgctgct gagcctggtc atcaccctgt actgcaacca ccggaataag 1020

agaggccgga agaaactgct gtacatcttc aagcagccct tcatgcggcc cgtgcagacc 1080

acccaggaag aggacggctg cagctgccgg ttccccgagg aagaggaagg cggctgcgaa 1140

ctgcgggtga agttcagccg gagcgccgac gcccctgcct accagcaggg ccagaaccag 1200

ctgtacaacg agctgaacct gggccggagg gaggagtacg acgtgctgga caagcggaga 1260

ggccgggacc ctgagatggg cggcaagccc cggagaaaga accctcagga gggcctgtat 1320

aacgaactgc agaaagacaa gatggccgag gcctacagcg agatcggcat gaagggcgag 1380

cggcggaggg gcaagggcca cgacggcctg taccagggcc tgagcaccgc caccaaggat 1440

acctacgacg ccctgcacat gcaggccctg ccccccaga 1479

<210> 47
<211> 493
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 47
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
35 40 45

Glu Ser Val Asp Asn Tyr Gly Ile Ser Phe Met Asn Trp Phe Gln Gln
50 55 60

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

Gly Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

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Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr
            100                 105                 110

Tyr Cys Gln Gln Ser Lys Glu Val Pro Trp Thr Phe Gly Gln Gly Thr
        115                 120                 125

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140

Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
145                 150                 155                 160

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
                165                 170                 175

Phe Thr Asp Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
            180                 185                 190

Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Gly Thr Gly Tyr
        195                 200                 205

Asn Gln Lys Phe Lys Ser Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr
    210                 215                 220

Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
225                 230                 235                 240

Val Tyr Tyr Cys Ala Arg Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln
                245                 250                 255

Gly Thr Leu Val Thr Val Ser Ser Lys Pro Thr Thr Thr Pro Ala Pro
            260                 265                 270

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
        275                 280                 285

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
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    290                 295                 300

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
305                 310                 315                 320

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn
                325                 330                 335

His Arg Asn Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
            340                 345                 350

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
        355                 360                 365

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
    370                 375                 380

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
385                 390                 395                 400

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
                405                 410                 415

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
            420                 425                 430

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
        435                 440                 445

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
    450                 455                 460

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
465                 470                 475                 480

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490
```

<210> 48
<211> 2622
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 48
atgctgctgc tggtgaccag cctgctgctg tgtgagctgc cccaccccgc ctttctgctg 60

atccccgaca ttcagatgac ccagtctccg agctctctgt ccgcatcagt aggagacagg 120

gtcaccatca catgcagagc cagcgaaagt gtcgacaatt atggcattag ctttatgaac 180

tggttccaac agaaacccgg gaaggctcct aagcttctga tttacgctgc atccaaccaa 240

ggctccgggg taccctctcg cttctcaggc agtggatctg ggacagactt cactctcacc 300

atttcatctc tgcagcctga tgacttcgca acctattact gtcagcaaag taaggaggtt 360

ccgtggacgt tcggtcaagg gaccaaggtg gagatcaaag gtggcggtgg ctcgggcggt 420

ggtgggtcgg gtggcggcgg atctcaggtt cagctggtgc agtctggagc tgaggtgaag 480

aagcctggga gctcagtgaa ggtttcctgc aaagcttctg gctacacctt cactgactac 540

aacatgcact gggtgaggca ggctcctggc caaggcctgg aatggattgg atatatttat 600

ccttacaatg gtggtaccgg ctacaaccag aagttcaaga gcaaggccac aattacagca 660

gacgagagta ctaacacagc ctacatggaa ctctccagcc tgaggtctga ggacactgca 720

gtctattact gcgcaagagg gcgccccgct atggactact ggggccaagg gactctggtc 780

actgtctctt caaagcccac caccacccct gcccctagac ctccaacccc agcccctaca 840

atcgccagcc agcccctgag cctgaggccc gaagcctgta gacctgccgc tggcggagcc 900

gtgcacacca gaggcctgga tttcgcctgc gacatctaca tctgggcccc tctggccggc 960

acctgtggcg tgctgctgct gagcctggtc atcaccctgt actgcaacca ccggaataag 1020

agaggccgga agaaactgct gtacatcttc aagcagccct tcatgcggcc cgtgcagacc 1080

acccaggaag aggacggctg cagctgccgg ttccccgagg aagaggaagg cggctgcgaa 1140

ctgcgggtga agttcagccg gagcgccgac gcccctgcct accagcaggg ccagaaccag 1200

ctgtacaacg agctgaacct gggccggagg gaggagtacg acgtgctgga caagcggaga 1260

ggccgggacc ctgagatggg cggcaagccc cggagaaaga accctcagga gggcctgtat 1320

aacgaactgc agaaagacaa gatggccgag gcctacagcg agatcggcat gaagggcgag 1380

cggcggaggg gcaagggcca cgacggcctg taccagggcc tgagcaccgc caccaaggat 1440

acctacgacg ccctgcacat gcaggccctg ccccccagac tcgagggcgg cggagagggc 1500

agaggaagtc ttctaacatg cggtgacgtg gaggagaatc ccggccctag gatgcttctc 1560

ctggtgacaa gccttctgct ctgtgagtta ccacacccag cattcctcct gatcccacgc 1620

aaagtgtgta acggaatagg tattggtgaa tttaaagact cactctccat aaatgctacg 1680

aatattaaac acttcaaaaa ctgcacctcc atcagtggcg atctccacat cctgccggtg 1740

gcatttaggg gtgactcctt cacacatact cctcctctgg atccacagga actggatatt 1800

ctgaaaaccg taaaggaaat cacagggttt ttgctgattc aggcttggcc tgaaaacagg 1860

acggacctcc atgcctttga gaacctagaa atcatacgcg gcaggaccaa gcaacatggt 1920

cagttttctc ttgcagtcgt cagcctgaac ataacatcct tgggattacg ctccctcaag 1980

gagataagtg atggagatgt gataatttca ggaaacaaaa atttgtgcta tgcaaataca 2040

ataaactgga aaaaactgtt tgggacctcc ggtcagaaaa ccaaaattat aagcaacaga 2100

ggtgaaaaca gctgcaaggc cacaggccag gtctgccatg ccttgtgctc ccccgagggc 2160

tgctggggcc cggagcccag ggactgcgtc tcttgccgga atgtcagccg aggcagggaa 2220

tgcgtggaca agtgcaacct tctggagggt gagccaaggg agtttgtgga gaactctgag 2280

tgcatacagt gccacccaga gtgcctgcct caggccatga acatcacctg cacaggacgg 2340

ggaccagaca actgtatcca gtgtgcccac tacattgacg gcccccactg cgtcaagacc 2400

tgcccggcag gagtcatggg agaaaacaac accctggtct ggaagtacgc agacgccggc 2460

catgtgtgcc acctgtgcca tccaaactgc acctacggat gcactgggcc aggtcttgaa 2520

ggctgtccaa cgaatgggcc taagatcccg tccatcgcca ctgggatggt gggggccctc 2580

ctcttgctgc tggtggtggc cctggggatc ggcctcttca tg 2622

<210> 49
<211> 874
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 49
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
35 40 45

Glu Ser Val Asp Asn Tyr Gly Ile Ser Phe Met Asn Trp Phe Gln Gln
50 55 60

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

Gly Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr
100 105 110

Tyr Cys Gln Gln Ser Lys Glu Val Pro Trp Thr Phe Gly Gln Gly Thr
115 120 125

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
145 150 155 160

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Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
                165                 170                 175

Phe Thr Asp Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
            180                 185                 190

Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Gly Thr Gly Tyr
        195                 200                 205

Asn Gln Lys Phe Lys Ser Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr
    210                 215                 220

Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
225                 230                 235                 240

Val Tyr Tyr Cys Ala Arg Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln
                245                 250                 255

Gly Thr Leu Val Thr Val Ser Ser Lys Pro Thr Thr Thr Pro Ala Pro
            260                 265                 270

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
        275                 280                 285

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
    290                 295                 300

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
305                 310                 315                 320

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn
                325                 330                 335

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

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
    370                 375                 380

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
385                 390                 395                 400

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
                405                 410                 415

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
            420                 425                 430

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
        435                 440                 445

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
    450                 455                 460

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
465                 470                 475                 480

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Leu Glu Gly
                485                 490                 495

Gly Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu
            500                 505                 510

Asn Pro Gly Pro Arg Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys
        515                 520                 525

Glu Leu Pro His Pro Ala Phe Leu Leu Ile Pro Arg Lys Val Cys Asn
    530                 535                 540

Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr
545                 550                 555                 560
```

```
Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His
                565                 570                 575

Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro
            580                 585                 590

Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr
        595                 600                 605

Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His
    610                 615                 620

Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly
625                 630                 635                 640

Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu
                645                 650                 655

Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn
            660                 665                 670

Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly
        675                 680                 685

Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser
    690                 695                 700

Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly
705                 710                 715                 720

Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn Val Ser
                725                 730                 735

Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro
            740                 745                 750
```

```
Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro Glu Cys
        755                 760                 765


Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn
    770                 775                 780


Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val Lys Thr
785                 790                 795                 800


Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr
                805                 810                 815


Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys Thr Tyr
            820                 825                 830


Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly Pro Lys
        835                 840                 845


Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu Leu Leu
    850                 855                 860


Val Val Ala Leu Gly Ile Gly Leu Phe Met
865                 870


<210> 50
<211> 2442
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 50
atgctgctgc tggtgaccag cctgctgctg tgtgagctgc cccaccccgc ctttctgctg       60

atccccgaca ttcagatgac ccagtctccg agctctctgt ccgcatcagt aggagacagg      120

gtcaccatca catgcagagc cagcgaaagt gtcgacaatt atggcattag ctttatgaac      180

tggttccaac agaaacccgg gaaggctcct aagcttctga tttacgctgc atccaaccaa      240
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ggctccgggg taccctctcg cttctcaggc agtggatctg ggacagactt cactctcacc 300

atttcatctc tgcagcctga tgacttcgca acctattact gtcagcaaag taaggaggtt 360

ccgtggacgt tcggtcaagg gaccaaggtg gagatcaaag gtggcggtgg ctcgggcggt 420

ggtgggtcgg gtggcggcgg atctcaggtt cagctggtgc agtctggagc tgaggtgaag 480

aagcctggga gctcagtgaa ggtttcctgc aaagcttctg gctacacctt cactgactac 540

aacatgcact gggtgaggca ggctcctggc caaggcctgg aatggattgg atatatttat 600

ccttacaatg gtggtaccgg ctacaaccag aagttcaaga gcaaggccac aattacagca 660

gacgagagta ctaacacagc ctacatggaa ctctccagcc tgaggtctga ggacactgca 720

gtctattact gcgcaagagg gcgccccgct atggactact ggggccaagg gactctggtc 780

actgtctctt caaagcccac caccaccct gcccctagac ctccaacccc agcccctaca 840

atcgccagcc agcccctgag cctgaggccc gaagcctgta gacctgccgc tggcggagcc 900

gtgcacacca gaggcctgga tttcgcctgc gacatctaca tctgggcccc tctggccggc 960

acctgtggcg tgctgctgct gagcctggtc atcaccctgt actgcaacca ccggaataag 1020

agaggccgga agaaactgct gtacatcttc aagcagccct tcatgcggcc cgtgcagacc 1080

acccaggaag aggacggctg cagctgccgg ttccccgagg aagaggaagg cggctgcgaa 1140

ctgcgggtga agttcagccg gagcgccgac gcccctgcct accagcaggg ccagaaccag 1200

ctgtacaacg agctgaacct gggccggagg gaggagtacg acgtgctgga caagcggaga 1260

ggccgggacc ctgagatggg cggcaagccc cggagaaaga accctcagga gggcctgtat 1320

aacgaactgc agaaagacaa gatggccgag gcctacagcg agatcggcat gaagggcgag 1380

cggcggaggg gcaagggcca cgacggcctg taccagggcc tgagcaccgc caccaaggat 1440

acctacgacg ccctgcacat gcaggccctg ccccccagac tcgagggcgg cggagagggc 1500

agaggaagtc ttctaacatg cggtgacgtg gaggagaatc ccggccctag gatgacaaca 1560

cccagaaatt cagtaaatgg gactttcccg gcagagccaa tgaaaggccc tattgctatg 1620

caatctggtc caaaaccact cttcaggagg atgtcttcac tggtgggccc cacgcaaagc 1680

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gtgtggtacc ctctctgggg aggcattatg tatattattt ccggatcact cctggcagca 1860

acggagaaaa actccaggaa gtgtttggtc aaaggaaaaa tgataatgaa ttcattgagc 1920

ctctttgctg ccatttctgg aatgattctt tcaatcatgg acatacttaa tattaaaatt 1980

tcccattttt taaaaatgga gagtctgaat tttattagag ctcacacacc atatattaac 2040

atatacaact gtgaaccagc taatccctct gagaaaaact ccccatctac ccaatactgt 2100

tacagcatac aatctctgtt cttgggcatt ttgtcagtga tgctgatctt tgccttcttc 2160

caggaacttg taatagctgg catcgttgag aatgaatgga aaagaacgtg ctccagaccc 2220

aaatctaaca tagttctcct gtcagcagaa gaaaaaaaag aacagactat tgaaataaaa 2280

gaagaagtgg ttgggctaac tgaaacatct tcccaaccaa agaatgaaga agacattgaa 2340

attattccaa tccaagaaga ggaagaagaa gaaacagaga cgaactttcc agaacctccc 2400

caagatcagg aatcctcacc aatagaaaat gacagctctc ct 2442

<210> 51
<211> 814
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 51
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
35 40 45

Glu Ser Val Asp Asn Tyr Gly Ile Ser Phe Met Asn Trp Phe Gln Gln

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    50                  55                  60

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

Gly Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
                85                  90                  95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr
            100                 105                 110

Tyr Cys Gln Gln Ser Lys Glu Val Pro Trp Thr Phe Gly Gln Gly Thr
        115                 120                 125

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140

Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
145                 150                 155                 160

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
                165                 170                 175

Phe Thr Asp Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
            180                 185                 190

Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Gly Thr Gly Tyr
        195                 200                 205

Asn Gln Lys Phe Lys Ser Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr
    210                 215                 220

Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
225                 230                 235                 240

Val Tyr Tyr Cys Ala Arg Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln
                245                 250                 255
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Gly Thr Leu Val Thr Val Ser Ser Lys Pro Thr Thr Thr Pro Ala Pro
            260                 265                 270

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
        275                 280                 285

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
    290                 295                 300

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
305                 310                 315                 320

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn
                325                 330                 335

His Arg Asn Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
            340                 345                 350

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
        355                 360                 365

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
    370                 375                 380

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
385                 390                 395                 400

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
                405                 410                 415

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
            420                 425                 430

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
        435                 440                 445

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
```

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    450                 455                 460

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
465                 470                 475                 480

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Leu Glu Gly
                485                 490                 495

Gly Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu
            500                 505                 510

Asn Pro Gly Pro Arg Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr
        515                 520                 525

Phe Pro Ala Glu Pro Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro
    530                 535                 540

Lys Pro Leu Phe Arg Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser
545                 550                 555                 560

Phe Phe Met Arg Glu Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn
                565                 570                 575

Gly Leu Phe His Ile Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly
            580                 585                 590

Ile Tyr Ala Pro Ile Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly
        595                 600                 605

Ile Met Tyr Ile Ile Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn
    610                 615                 620

Ser Arg Lys Cys Leu Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser
625                 630                 635                 640

Leu Phe Ala Ala Ile Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu
                645                 650                 655
```

Asn Ile Lys Ile Ser His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile
660 665 670

Arg Ala His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn
675 680 685

Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln
690 695 700

Ser Leu Phe Leu Gly Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe
705 710 715 720

Gln Glu Leu Val Ile Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr
725 730 735

Cys Ser Arg Pro Lys Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys
740 745 750

Lys Glu Gln Thr Ile Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu
755 760 765

Thr Ser Ser Gln Pro Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile
770 775 780

Gln Glu Glu Glu Glu Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro
785 790 795 800

Gln Asp Gln Glu Ser Ser Pro Ile Glu Asn Asp Ser Ser Pro
805 810

<210> 52
<211> 861
<212> DNA
<213> Homo sapiens

<400> 52
atgccgctgc tgctactgct gcccctgctg tgggcagggg ccctggctat ggatccaaat 60

ttctggctgc aagtgcagga gtcagtgacg gtacaggagg gtttgtgcgt cctcgtgccc 120

tgcactttct tccatcccat accctactac gacaagaact ccccagttca tggttactgg 180

ttccgggaag gagccattat atccagggac tctccagtgg ccacaaacaa gctagatcaa 240

gaagtacagg aggagactca gggcagattc cgcctccttg gggatcccag taggaacaac 300

tgctccctga gcatcgtaga cgccaggagg agggataatg gttcatactt ctttcggatg 360

gagagaggaa gtaccaaata cagttacaaa tctccccagc tctctgtgca tgtgacagac 420

ttgacccaca ggcccaaaat cctcatccct ggcactctag aacccggcca ctccaaaaac 480

ctgacctgct ctgtgtcctg ggcctgtgag cagggaacac ccccgatctt ctcctggttg 540

tcagctgccc ccacctccct gggccccagg actactcact cctcggtgct cataatcacc 600

ccacggcccc aggaccacgg caccaacctg acctgtcagg tgaagttcgc tggagctggt 660

gtgactacgg agagaaccat ccagctcaac gtcacctatg ttccacagaa cccaacaact 720

ggtatctttc caggagatgg ctcagggaaa caagagacca gagcaggagt ggttcatggg 780

gccattggag gagctggtgt tacagccctg ctcgctcttt gtctctgcct catcttcttc 840

atagtgaaga cccacaggag g 861

<210> 53
<211> 287
<212> PRT
<213> Homo sapiens

<400> 53
Met Pro Leu Leu Leu Leu Leu Pro Leu Leu Trp Ala Gly Ala Leu Ala
1 5 10 15

Met Asp Pro Asn Phe Trp Leu Gln Val Gln Glu Ser Val Thr Val Gln
20 25 30

Glu Gly Leu Cys Val Leu Val Pro Cys Thr Phe Phe His Pro Ile Pro
35 40 45

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

```
Ala Ile Ile Ser Arg Asp Ser Pro Val Ala Thr Asn Lys Leu Asp Gln
65                  70                  75                  80

Glu Val Gln Glu Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Pro
                85                  90                  95

Ser Arg Asn Asn Cys Ser Leu Ser Ile Val Asp Ala Arg Arg Arg Asp
            100                 105                 110

Asn Gly Ser Tyr Phe Phe Arg Met Glu Arg Gly Ser Thr Lys Tyr Ser
        115                 120                 125

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

Pro Lys Ile Leu Ile Pro Gly Thr Leu Glu Pro Gly His Ser Lys Asn
145                 150                 155                 160

Leu Thr Cys Ser Val Ser Trp Ala Cys Glu Gln Gly Thr Pro Pro Ile
                165                 170                 175

Phe Ser Trp Leu Ser Ala Ala Pro Thr Ser Leu Gly Pro Arg Thr Thr
            180                 185                 190

His Ser Ser Val Leu Ile Ile Thr Pro Arg Pro Gln Asp His Gly Thr
        195                 200                 205

Asn Leu Thr Cys Gln Val Lys Phe Ala Gly Ala Gly Val Thr Thr Glu
    210                 215                 220

Arg Thr Ile Gln Leu Asn Val Thr Tyr Val Pro Gln Asn Pro Thr Thr
225                 230                 235                 240

Gly Ile Phe Pro Gly Asp Gly Ser Gly Lys Gln Glu Thr Arg Ala Gly
                245                 250                 255

Val Val His Gly Ala Ile Gly Gly Ala Gly Val Thr Ala Leu Leu Ala
            260                 265                 270
```

Leu Cys Leu Cys Leu Ile Phe Phe Ile Val Lys Thr His Arg Arg
        275   280   285

<210> 54
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 54
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1   5   10   15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
            20   25   30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
        35   40   45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
    50   55   60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65   70   75   80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
                85   90   95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
            100   105   110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
        115   120   125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp

```
    130                 135                 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145                 150                 155                 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
                165                 170                 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
            180                 185                 190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        195                 200                 205

Gly Gly Gly Ser Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala
    210                 215                 220

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg
225                 230                 235                 240

Ser Lys Arg Ser
```

<210> 55
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 55
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 300

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 360

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 420

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 480

agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag 540

ggctgctggg gcccggagcc cagggactgc gtctctggtg gcggtggctc gggcggtggt 600

gggtcgggtg gcggcggatc tggtggcggt ggctcgtttt gggtgctggt ggtggttggt 660

ggagtcctgg cttgctatag cttgctagta acagtggcct ttattatttt ctgggtgagg 720

agtaagagga gc 732

<210> 56
<211> 263
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 56
Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
1 5 10 15

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
20 25 30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
35 40 45

Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile
50 55 60

Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile
65 70 75 80

```
Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
                85                  90                  95

Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
            100                 105                 110

Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile
        115                 120                 125

Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
    130                 135                 140

His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
145                 150                 155                 160

Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
                165                 170                 175

Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
            180                 185                 190

Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
        195                 200                 205

Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
    210                 215                 220

Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
225                 230                 235                 240

Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro
                245                 250                 255

Lys Asn Glu Glu Asp Ile Glu
            260
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<210> 57
<211> 789

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 57
atgaccacac cacggaactc tgtgaatggc accttcccag cagagccaat gaagggacca 60

atcgcaatgc agagcggacc caagcctctg tttcggagaa tgagctccct ggtgggccca 120

acccagtcct tctttatgag agagtctaag acactgggcg ccgtgcagat catgaacgga 180

ctgttccaca tcgccctggg aggactgctg atgatcccag ccggcatcta cgcccctatc 240

tgcgtgaccg tgtggtaccc tctgtggggc ggcatcatgt atatcatctc cggctctctg 300

ctggccgcca cagagaagaa cagcaggaag tgtctggtga agggcaagat gatcatgaat 360

agcctgtccc tgtttgccgc catctctggc atgatcctga gcatcatgga catcctgaac 420

atcaagatca gccacttcct gaagatggag agcctgaact tcatcagagc ccacacccct 480

tacatcaaca tctataattg cgagcctgcc aacccatccg agaagaattc tccaagcaca 540

cagtactgtt attccatcca gtctctgttc ctgggcatcc tgtctgtgat gctgatcttt 600

gccttctttc aggagctggt catcgccggc atcgtggaga acgagtggaa gaggacctgc 660

agccgcccca agtccaatat cgtgctgctg tccgccgagg agaagaagga gcagacaatc 720

gagatcaagg aggaggtggt gggcctgacc gagacatcta gccagcctaa gaatgaggag 780

gatatcgag 789

<210> 58
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 58
ctgtgcgcac gcccacgccg cagccccgcc caagaagatg gcaaagtcta catcaacatg 60

ccaggcaggg gc 72

<210> 59
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 59
Leu Cys Ala Arg Pro Arg Arg Ser Pro Ala Gln Glu Asp Gly Lys Val
1 5 10 15

Tyr Ile Asn Met Pro Gly Arg Gly
20

<210> 60
<211> 156
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 60
tacttcctgg gccggctggt ccctcggggg cgaggggctg cggaggcagc gacccggaaa 60

cagcgtatca ctgagaccga gtcgccttat caggagctcc agggtcagag gtcggatgtc 120

tacagcgacc tcaacacaca gaggccgtat tacaaa 156

<210> 61
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 61
Tyr Phe Leu Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala
1   5   10   15

Ala Thr Arg Lys Gln Arg Ile Thr Glu Thr Glu Ser Pro Tyr Gln Glu
            20   25   30

Leu Gln Gly Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Arg
        35   40   45

Pro Tyr Tyr Lys
    50

<210> 62
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 62
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
1   5   10