SEQUENCE LISTING

<110> ENCODED THERAPEUTICS, INC.

<120> COMPOSITIONS AND METHODS FOR SELECTIVE GENE REGULATION

<130> 46482-724.601

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<150> 63/008,569
<151> 2020-04-10

<150> 62/857,727
<151> 2019-06-05

<150> 62/854,238
<151> 2019-05-29

<160> 226

<170> PatentIn version 3.5

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<223> Description of Artificial Sequence: Synthetic
polynucleotide

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tttccaaaat gtcgtaacaa ctccgcccca ttgacgcaaa tgggcggtag gcgtgtacgg 180

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

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gatcaacact atggtttgaa aaggggggaaa ttgtagagca cagatgtgtt cgtgtggcag 180

tgtgctgtct ctagcaatac tcagagaaga gagagaacaa tgaaattctg attggcccca 240

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caaacggtcc tcctgcatca gcctcccaag tagctggaat tacaggagtg gcccaccatg 480

cccagctaat ttttgtattt ttaatagata cgggggtttc accatatcac ccaggctggt 540

ctcgaactcc tggcctcaag tgatccacct gcctcggcct cccaaagtgc tgggattata 600

ggcgtcagcc actatgccca acccgaccaa cctttttaa aataaatatt taaaaaattg 660

gtatttcaca tatatactag tatttacatt tatccacaca aaacggacgg gcctccgctg 720

aaccagtgag gccccagacg tgcgcataaa taacccctgc gtgctgcacc acctggggag 780

agggggagga ccacggtaaa tggagcgagc gcatagcaaa agggacgcgg ggtccttttc 840

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gagctcaagg aagcgtcgca gggtcacaga tctgggggaa ccccggggaa aagcactgag 960

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cctttcctcc ctcttgtctc tccagagccg gatcttcaag gggagcctcc gtgcccccgg 1920

ctgctcagtc cctccggtgt gcaggacccc ggaagtcctc cccgcacagc tctcgcttct 1980

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cgaccgagct g 2051

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<211> 1878
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<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

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cacaggcagg atccagtctg ctggtcccag gaagctaacc gtctcagaca gagcacaaag 180

caccgagaca tgtgccacaa ggcttgtgta gagaggtcag aggacagcgt acaggtccca 240

gagatcaaac tcaacctcac caggcttggc agcaagcctt taccaaccca cccccacccc 300

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cctaaaatgt ttaaggatga cactggctgc tgagtggaaa tgagacagca gaagtcaaca 420

gtagatttta ggaaagccag agaaaaaggc ttgtgctgtt tttagaaagc caagggacaa 480

gctaagatag ggcccaagta atgctagtat ttacatttat ccacacaaaa cggacgggcc 540

tccgctgaac cagtgaggcc ccagacgtgc gcataaataa cccctgcgtg ctgcaccacc 600

tggggagagg gggaggacca cggtaaatgg agcgagcgca tagcaaaagg gacgcggggt 660

ccttttctct gccggtggca ctgggtagct gtggccaggt gtggtacttt gatggggccc 720

agggctggag ctcaaggaag cgtcgcaggg tcacagatct gggggaaccc cggggaaaag 780

cactgaggca aaaccgccgc tcgtctccta caatatatgg gaggggggagg ttgagtacgt 840

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tataatcgcc ctataaagct ccagaggcgg tcaggcacct gcagaggagc cccgccgctc 960

cgccgactag ctgcccccgc gagcaacggc ctcgtgattt ccccgccgat ccggtccccg 1020

cctccccact ctgcccccgc ctaccccgga gccgtgcagc cgcctctccg aatctctctc 1080

ttctcctggc gctcgcgtgc gagagggaac tagcgagaac gaggaagcag ctggaggtga 1140

cgccgggcag attacgcctg tcagggccga gccgagcgga tcgctgggcg ctgtgcagag 1200

gaaaggcggg agtgcccggc tcgctgtcgc agagccgagg tgggtaagct agcgaccacc 1260

tggacttccc agcgcccaac cgtggctttt cagccaggtc ctctcctccc gcggcttctc 1320

aaccaacccc atcccagcgc cggccaccca acctcccgaa atgagtgctt cctgccccag 1380

cagccgaagg cgctactagg aacggtaacc tgttactttt ccaggggccg tagtcgaccc 1440

gctgcccgag ttgctgtgcg actgcgcgcg cggggctaga gtgcaaggtg actgtggttc 1500

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gtctcaccaa agtccctagt ccccggagca gttagcctct ttctttccag ggaattagcc 1620

agacacaaca acgggaacca gacaccgaac cagacatgcc cgccccgtgc gccctccccg 1680

ctcgctgcct ttcctccctc ttgtctctcc agagccggat cttcaagggg agcctccgtg 1740

cccccggctg ctcagtccct ccggtgtgca ggaccccgga agtcctcccc gcacagctct 1800

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cccgggacga ccgagctg 1878

<210> 4
<211> 509
<212> DNA
<213> Artificial Sequence

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

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tgggagccac ctgggcagca ggggccaagg gtgtcctaga agggacctgg agtccacgct 180

gggccaagcc tgccctttct ccctctgtct tccgtccctg cttgcggttc tgctgaatgt 240

ggttatttct ctggctcctt ttacagagaa tgctgctgct aattttatgt ggagctctga 300

ggcagtgtaa ttggaagcca gacaccctgt cagcagtggg ctcccgtcct gagctgccat 360

gcttcctgct ctcctcccgt cccggctcct catttcatgc agccacctgt cccagggaga 420

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cacataccaa gcagccgctg gtgcaatct 509

<210> 5
<211> 1644
<212> DNA
<213> Artificial Sequence

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

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gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc attgacgtca 120

atgggtggag tatttacggt aaactgccca cttggcagta catcaagtgt atcatatgcc 180

aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt atgcccagta 240

catgacctta tgggactttc ctacttggca gtacatctac gtattagtca tcgctattac 300

catgggtcga ggtgagcccc acgttctgct tcactctccc catctccccc ccctccccac 360

ccccaatttt gtatttattt atttttaat tattttgtgc agcgatgggg gcgggggggg 420

gggggcgcgc cgccaggcgg ggcggggcgg ggcgaggggc ggggcggggc gaggcggaga 480

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gctcgggggga ggggcgcggc ggccccggag cgccggcggc tgtcgaggcg cggcgagccg 1260

cagccattgc cttttatggt aatcgtgcga gagggcgcag ggacttcctt tgtcccaaat 1320

ctggcggagc cgaaatctgg gaggcgccgc cgcaccccct ctagcgggcg cgggcgaagc 1380

ggtgcggcgc cggcaggaag gaaatgggcg gggagggcct tcgtgcgtcg ccgcgccgcc 1440

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acggggcagg gcggggttcg gcttctggcg tgtgaccggc ggctctagag cctctgctaa 1560

ccatgttcat gccttcttct ttttcctaca gctcctgggc aacgtgctgg ttgttgtgct 1620

gtctcatcat tttggcaaag aatt 1644

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<211> 1335
<212> DNA
<213> Artificial Sequence

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

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ctcccactaa cgtagaaccc agagatcgct gcgttcccgc cccctcaccc gcccgctctc 120

gtcatcactg aggtggagaa gagcatgcgt gaggctccgg tgcccgtcag tgggcagagc 180

gcacatcgcc cacagtcccc gagaagttgg ggggaggggt cggcaattga accggtgcct 240

agagaaggtg gcgcggggta aactgggaaa gtgatgtcgt gtactggctc cgccttttc 300

ccgagggtgg gggagaaccg tatataagtg cagtagtcgc cgtgaacgtt ctttttcgca 360

acgggtttgc cgccagaaca caggtaagtg ccgtgtgtgg ttcccgcggg cctggcctct 420

ttacgggtta tggcccttgc gtgccttgaa ttacttccac gcccctggct gcagtacgtg 480

attcttgatc ccgagcttcg ggttggaagt gggtgggaga gttcgaggcc ttgcgcttaa 540

ggagcccctt cgcctcgtgc ttgagttgag gcctggcttg ggcgctgggg ccgccgcgtg 600

cgaatctggt ggcaccttcg cgcctgtctc gctgctttcg ataagtctct agccatttaa 660

aatttttgat gacctgctgc gacgcttttt ttctggcaag atagtcttgt aaatgcgggc 720

caagatctgc acactggtat ttcggttttt ggggccgcgg gcggcgacgg ggcccgtgcg 780

tcccagcgca catgttcggc gaggcggggc ctgcgagcgc ggccaccgag aatcggacgg 840

gggtagtctc aagctggccg gcctgctctg gtgcctggcc tcgcgccgcc gtgtatcgcc 900

ccgccctggg cggcaaggct ggcccggtcg gcaccagttg cgtgagcgga aagatggccg 960

cttcccggcc ctgctgcagg gagctcaaaa tggaggacgc ggcgctcggg agagcgggcg 1020

ggtgagtcac ccacacaaag gaaaagggcc tttccgtcct cagccgtcgc ttcatgtgac 1080

tccacggagt accgggcgcc gtccaggcac ctcgattagt tctcgagctt ttggagtacg 1140

tcgtctttag gttgggggga ggggttttat gcgatggagt ttccccacac tgagtgggtg 1200

gagactgaag ttaggccagc ttggcacttg atgtaattct ccttggaatt tgccctttt 1260

gagtttggat cttggttcat tctcaagcct cagacagtgg ttcaaagttt ttttcttcca 1320

tttcaggtgt cgtga 1335

<210> 7
<211> 214
<212> DNA
<213> Artificial Sequence

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

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cggttcactg tgatcggaaa agagaccggt tcactgtgag cggccttgaa acccagcaga 120

caatgtagct cagtagaaac ccagcagaca atgtagctga atggaaaccc agcagacaat 180

gtagcttcgg agaaacccag cagacaatgt agct 214

<210> 8
<211> 21
<212> RNA
<213> Homo sapiens

<400> 8
ucacagugaa ccggucucuu u 21

<210> 9
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 9
aaagagaccg gttcactgtg a 21

<210> 10
<211> 23
<212> RNA
<213> Homo sapiens

<400> 10
agcuacauug ucugcugggu uuc 23

<210> 11
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 11
gaaacccagc agacaatgta gct 23

<210> 12
<211> 23
<212> RNA
<213> Homo sapiens

<400> 12
agcuacaucu ggcuacuggg ucu 23

<210> 13
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 13
agacccagta gccagatgta gct 23

<210> 14
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 14
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actgtga 67

<210> 15
<211> 134
<212> DNA
<213> Artificial Sequence

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

<400> 15
gaaacccagc agacaatgta gctagaccca gtagccagat gtagctaaag agaccggttc 60

actgtgagaa acccagcaga caatgtagct agacccagta gccagatgta gctaaagaga 120

ccggttcact gtga 134

<210> 16
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

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aataaaagat ctttattttc attagatctg tgtgttggtt ttttgtgtgc ggaccgcacg 60

tg 62

<210> 17
<211> 477
<212> DNA
<213> Artificial Sequence

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

<400> 17
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gtgcccacca gccttgtcct aataaaatta agttgcatca ttttgtctga ctaggtgtcc 120

ttctataata ttatggggtg gaggggggtg gtatggagca aggggcaagt tgggaagaca 180

acctgtaggg cctgcggggt ctattgggaa ccaagctgga gtgcagtggc acaatcttgg 240

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ttgggattcc aggcatgcat gaccaggctc agctaatttt tgtttttttg gtagagacgg 360

ggtttcacca tattggccag gctggtctcc aactcctaat ctcaggtgat ctacccacct 420

tggcctccca aattgctggg attacaggcg tgaaccactg ctcccttccc tgtcctt 477

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<211> 18
<212> DNA
<213> Homo sapiens

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<210> 19
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<212> DNA
<213> Homo sapiens

<400> 19
acttgaccta gacagcct 18

<210> 20
<211> 18
<212> DNA
<213> Homo sapiens

<400> 20
tgaataactc attagtga 18

<210> 21
<211> 18
<212> DNA
<213> Homo sapiens

<400> 21
aaagtacatt aggctaat 18

<210> 22
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<212> DNA
<213> Homo sapiens

<400> 22
ccagcactgg tgcttcgt 18

<210> 23
<211> 18
<212> DNA
<213> Homo sapiens

<400> 23
aaggctgtct aggtcaag 18

<210> 24
<211> 24
<212> DNA
<213> Homo sapiens

<400> 24
ctaggtcaag tgtaggagac acac 24

<210> 25
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<400> 25
ggtcaagtgt aggagaca 18

<210> 26
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<400> 26
caagtgtagg agacacac 18

<210> 27
<211> 24
<212> DNA
<213> Homo sapiens

<400> 27
agtgtaggag acacactgct ggcc 24

<210> 28
<211> 18
<212> DNA
<213> Homo sapiens

<400> 28
agtgtaggag acacactg 18

<210> 29
<211> 21
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<213> Homo sapiens

<400> 29
aggagacaca ctgctggcct g 21

<210> 30
<211> 18
<212> DNA
<213> Homo sapiens

<400> 30
taggtaccat agagtgag 18

<210> 31
<211> 18
<212> DNA
<213> Homo sapiens

<400> 31
gaggatactg cagaggtc 18

<210> 32
<211> 27
<212> DNA
<213> Homo sapiens

<400> 32
taggtaccat agagtgaggc gaggatg 27

<210> 33
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<213> Homo sapiens

<400> 33
atagagtgag gcgaggatga agccgag 27

<210> 34
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<400> 34
tgaagccgag aggatactgc agaggtc 27

<210> 35
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<400> 35
aaggctgtct aggtcaagtg t 21

<210> 36
<211> 21
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<213> Homo sapiens

<400> 36
tgttcctcca gattaacact t 21

<210> 37
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<213> Homo sapiens

<400> 37
gatgaagccg agaggatact g 21

<210> 38
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<213> Homo sapiens

<400> 38
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<210> 39
<211> 21
<212> DNA
<213> Homo sapiens

<400> 39
agaaagctga tacagataca a 21

<210> 40
<211> 21
<212> DNA
<213> Homo sapiens

<400> 40
ggtacgggca aagatttctt g 21

<210> 41
<211> 21
<212> DNA
<213> Homo sapiens

<400> 41
agaaagctga tacagataca a 21

<210> 42
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<213> Homo sapiens

<400> 42
acacaatgag ccacctacaa g 21

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<213> Homo sapiens

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<210> 45
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<213> Homo sapiens

<400> 45
agagagagag agagagagag a 21

<210> 46
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ttctcagttt tgaaattaaa a 21

<210> 47
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<213> Homo sapiens

<400> 47
tggattctct tctgaacctg c 21

<210> 48
<211> 21
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<213> Homo sapiens

<400> 48
tgctgaggca ggacacagtg t 21

<210> 49
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<213> Homo sapiens

<400> 49
atcatctgta accatcaagg a 21

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<212> DNA
<213> Homo sapiens

<400> 50
tcctgcctac ttagtttcaa g 21

<210> 51
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<210> 52
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<400> 56
acaaagtaag tgtcagtgtg g 21

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ataatagttg tgtctttata a 21

<210> 58
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<212> DNA
<213> Homo sapiens

<400> 58
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<210> 59
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<212> DNA
<213> Homo sapiens

<400> 59
gttaacaaat acactaaaca c 21

<210> 60
<211> 21
<212> DNA
<213> Homo sapiens

<400> 60
ttcaacaagc tcccaagaag t 21

<210> 61
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<212> DNA
<213> Homo sapiens

<400> 61
atgttcaagg tgcagaagga a 21

<210> 62
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<213> Homo sapiens

<400> 62
tgtttgctca aacgtgcacc a 21

<210> 63
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<212> DNA
<213> Homo sapiens

<400> 63
aaataagaca tgaaaacaag a 21

<210> 64
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<213> Homo sapiens

<400> 64
aaatatgtac cacaagaaat g 21

<210> 65
<211> 21
<212> DNA
<213> Homo sapiens

<400> 65
tatctggttt ctctcactgc t 21

<210> 66
<211> 21
<212> DNA
<213> Homo sapiens

<400> 66
attgcaaagc ataatttgga t 21

<210> 67
<211> 3585
<212> DNA
<213> Artificial Sequence

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

<400> 67
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attttgaagt tctgttgaca taaagaatca tgatattaat gcccatggaa atgaaagggc 120

gatcaacact atggtttgaa aaggggaaa ttgtagagca cagatgtgtt cgtgtggcag 180

tgtgctgtct ctagcaatac tcagagaaga gagagaacaa tgaaattctg attggcccca 240

gtgtgagccc agatgaggtt cagctgccaa ctttctcttt cacatcttat gaaagtcatt 300

taagcacaac taacttttt ttttttttt ttttttgag acagagtctt gctctgttgc 360

ccaggacaga gtgcagtagt gactcaatct cggctcactg cagcctccac ctcctaggct 420

caaacggtcc tcctgcatca gcctcccaag tagctggaat tacaggagtg gcccaccatg 480

cccagctaat ttttgtattt ttaatagata cgggggtttc accatatcac ccaggctggt 540

ctcgaactcc tggcctcaag tgatccacct gcctcggcct cccaaagtgc tgggattata 600

ggcgtcagcc actatgccca acccgaccaa ccttttttaa aataaatatt taaaaaattg 660

gtatttcaca tatatactag tatttacatt tatccacaca aaacggacgg gcctccgctg 720

aaccagtgag gccccagacg tgcgcataaa taacccctgc gtgctgcacc acctggggag 780

agggggagga ccacggtaaa tggagcgagc gcatagcaaa agggacgcgg ggtccttttc 840

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gagctcaagg aagcgtcgca gggtcacaga tctgggggaa ccccggggaa aagcactgag 960

gcaaaaccgc cgctcgtctc ctacaatata tgggaggggg aggttgagta cgttctggat 1020

tactcataag acctttttt tttccttccg ggcgcaaaac cgtgagctgg atttataatc 1080

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tagctgcccc cgcgagcaac ggcctcgtga tttccccgcc gatccggtcc ccgcctcccc 1200

actctgcccc cgcctacccc ggagccgtgc agccgcctct ccgaatctct ctcttctcct 1260

ggcgctcgcg tgcgagaggg aactagcgag aacgaggaag cagctggagg tgacgccggg 1320

cagattacgc ctgtcagggc cgagccgagc ggatcgctgg gcgctgtgca gaggaaaggc 1380

gggagtgccc ggctcgctgt cgcagagccg aggtgggtaa gctagcgacc acctggactt 1440

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aggcgctact aggaacggta acctgttact tttccagggg ccgtagtcga cccgctgccc 1620

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caaagtccct agtccccgga gcagttagcc tctttctttc cagggaatta gccagacaca 1800

acaacgggaa ccagacaccg aaccagacat gcccgccccg tgcgccctcc ccgctcgctg 1860

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ctgctcagtc cctccggtgt gcaggacccc ggaagtcctc cccgcacagc tctcgcttct 1980

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cgaccgagct ggaattcgcc accatggccc caaagaagaa gcggaaggtc ggtatccacg 2100

gagtcccagc agccctcgaa ccaggtgaaa aaccttacaa atgtcctgaa tgtgggaaat 2160

cattcagtcg cagcgacaac ctggtgagac atcaacgcac ccatacagga gaaaaacctt 2220

ataaatgtcc agaatgtgga aagtccttct cacgagagga taacttgcac actcatcaac 2280

gaacacatac tggtgaaaaa ccatacaagt gtcccgaatg tggtaaaagt tttagccgga 2340

gcgatgaact tgtccgacac caacgaaccc atacaggcga gaagccttac aaatgtcccg 2400

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gtttctctca gaatagtacc ctgaccgaac accagcgaac acacactggg aaaaaaacga 2640

gtaaaaggcc ggcggccacg aaaaaggccg gccaggcaaa aaagaaaaag ggatcctacc 2700

catacgacgt accagattac gctctcgagg acgcgctgga cgatttcgat ctcgacatgc 2760

tgggttctga tgccctcgat gactttgacc tggatatgtt gggaagcgac gcattggatg 2820

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aaagagaccg gttcactgtg atcggaaaag agaccggttc actgtgagcg gccttgaaac 3000

ccagcagaca atgtagctca gtagaaaccc agcagacaat gtagctgaat ggaaacccag 3060

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cttgtcctaa taaaattaag ttgcatcatt ttgtctgact aggtgtcctt ctataatatt 3240

atggggtgga ggggggtggt atggagcaag gggcaagttg ggaagacaac ctgtagggcc 3300

tgcggggtct attgggaacc aagctggagt gcagtggcac aatcttggct cactgcaatc 3360

tccgcctcct gggttcaagc gattctcctg cctcagcctc ccgagttgtt gggattccag 3420

gcatgcatga ccaggctcag ctaatttttg ttttttggt agagacgggg tttcaccata 3480

ttggccaggc tggtctccaa ctcctaatct caggtgatct acccaccttg gcctcccaaa 3540

ttgctgggat tacaggcgtg aaccactgct cccttccctg tcctt 3585

<210> 68
<211> 3371
<212> DNA
<213> Artificial Sequence

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

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attttgaagt tctgttgaca taaagaatca tgatattaat gcccatggaa atgaaagggc 120

gatcaacact atggtttgaa aaggggaaa ttgtagagca cagatgtgtt cgtgtggcag 180

tgtgctgtct ctagcaatac tcagagaaga gagagaacaa tgaaattctg attggcccca 240

gtgtgagccc agatgaggtt cagctgccaa ctttctcttt cacatcttat gaaagtcatt 300

taagcacaac taacttttt ttttttttt ttttttgag acagagtctt gctctgttgc 360

ccaggacaga gtgcagtagt gactcaatct cggctcactg cagcctccac ctcctaggct 420

caaacggtcc tcctgcatca gcctcccaag tagctggaat tacaggagtg gcccaccatg 480

cccagctaat ttttgtattt ttaatagata cgggggtttc accatatcac ccaggctggt 540

ctcgaactcc tggcctcaag tgatccacct gcctcggcct cccaaagtgc tgggattata 600

ggcgtcagcc actatgccca acccgaccaa cctttttaa aataaatatt taaaaaattg 660

gtatttcaca tatatactag tatttacatt tatccacaca aaacggacgg gcctccgctg 720

aaccagtgag gccccagacg tgcgcataaa taacccctgc gtgctgcacc acctggggag 780

agggggagga ccacggtaaa tggagcgagc gcatagcaaa agggacgcgg ggtccttttc 840

tctgccggtg gcactgggta gctgtggcca ggtgtggtac tttgatgggg cccagggctg 900

gagctcaagg aagcgtcgca gggtcacaga tctgggggaa ccccggggaa aagcactgag 960

gcaaaaccgc cgctcgtctc ctacaatata tgggaggggg aggttgagta cgttctggat 1020

tactcataag acctttttt tttccttccg ggcgcaaaac cgtgagctgg atttataatc 1080

gccctataaa gctccagagg cggtcaggca cctgcagagg agccccgccg ctccgccgac 1140

tagctgcccc cgcgagcaac ggcctcgtga tttccccgcc gatccggtcc ccgcctcccc 1200

actctgcccc cgcctacccc ggagccgtgc agccgcctct ccgaatctct ctcttctcct 1260

ggcgctcgcg tgcgagaggg aactagcgag aacgaggaag cagctggagg tgacgccggg 1320

cagattacgc ctgtcagggc cgagccgagc ggatcgctgg gcgctgtgca gaggaaaggc 1380

gggagtgccc ggctcgctgt cgcagagccg aggtgggtaa gctagcgacc acctggactt 1440

cccagcgccc aaccgtggct tttcagccag gtcctctcct cccgcggctt ctcaaccaac 1500

cccatcccag cgccggccac ccaacctccc gaaatgagtg cttcctgccc cagcagccga 1560

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caaagtccct agtccccgga gcagttagcc tctttctttc cagggaatta gccagacaca 1800

acaacgggaa ccagacaccg aaccagacat gcccgccccg tgcgccctcc ccgctcgctg 1860

cctttcctcc ctcttgtctc tccagagccg gatcttcaag gggagcctcc gtgcccccgg 1920

ctgctcagtc cctccggtgt gcaggacccc ggaagtcctc cccgcacagc tctcgcttct 1980

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cgaccgagct ggaattcgcc accatggccc caaagaagaa gcggaaggtc ggtatccacg 2100

gagtcccagc agccctcgaa ccaggtgaaa aaccttacaa atgtcctgaa tgtgggaaat 2160

cattcagtcg cagcgacaac ctggtgagac atcaacgcac ccatacagga gaaaaacctt 2220

ataaatgtcc agaatgtgga aagtccttct cacgagagga taacttgcac actcatcaac 2280

gaacacatac tggtgaaaaa ccatacaagt gtcccgaatg tggtaaaagt tttagccgga 2340

gcgatgaact tgtccgacac caacgaaccc atacaggcga gaagccttac aaatgtcccg 2400

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gtaaaaggcc ggcggccacg aaaaaggccg gccaggcaaa aaagaaaaag ggatcctacc 2700

catacgacgt accagattac gctctcgagg acgcgctgga cgatttcgat ctcgacatgc 2760

tgggttctga tgccctcgat gactttgacc tggatatgtt gggaagcgac gcattggatg 2820

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aagttgccac tccagtgccc accagccttg tcctaataaa attaagttgc atcattttgt 3000

ctgactaggt gtccttctat aatattatgg ggtggagggg ggtggtatgg agcaaggggc 3060

aagttgggaa gacaacctgt agggcctgcg gggtctattg ggaaccaagc tggagtgcag 3120

tggcacaatc ttggctcact gcaatctccg cctcctgggt tcaagcgatt ctcctgcctc 3180

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tttggtagag acggggtttc accatattgg ccaggctggt ctccaactcc taatctcagg 3300

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tccctgtcct t 3371

<210> 69
<211> 4380
<212> DNA
<213> Artificial Sequence

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

<400> 69
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attttgaagt tctgttgaca taaagaatca tgatattaat gcccatggaa atgaaagggc 120

gatcaacact atggtttgaa aaggggggaaa ttgtagagca cagatgtgtt cgtgtggcag 180

tgtgctgtct ctagcaatac tcagagaaga gagagaacaa tgaaattctg attggcccca 240

gtgtgagccc agatgaggtt cagctgccaa ctttctcttt cacatcttat gaaagtcatt 300

taagcacaac taacttttt ttttttttt ttttttgag acagagtctt gctctgttgc 360

ccaggacaga gtgcagtagt gactcaatct cggctcactg cagcctccac ctcctaggct 420

caaacggtcc tcctgcatca gcctcccaag tagctggaat tacaggagtg gcccaccatg 480

cccagctaat ttttgtattt ttaatagata cgggggtttc accatatcac ccaggctggt 540

ctcgaactcc tggcctcaag tgatccacct gcctcggcct cccaaagtgc tgggattata 600

ggcgtcagcc actatgccca acccgaccaa cctttttttaa aataaatatt taaaaaattg 660

gtatttcaca tatatactag tatttacatt tatccacaca aaacggacgg gcctccgctg 720

aaccagtgag gccccagacg tgcgcataaa taacccctgc gtgctgcacc acctggggag 780

agggggagga ccacggtaaa tggagcgagc gcatagcaaa agggacgcgg ggtccttttc 840

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gagctcaagg aagcgtcgca gggtcacaga tctgggggaa ccccggggaa aagcactgag 960

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tactcataag acctttttt tttccttccg ggcgcaaaac cgtgagctgg atttataatc 1080

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cagattacgc ctgtcagggc cgagccgagc ggatcgctgg gcgctgtgca gaggaaaggc 1380

gggagtgccc ggctcgctgt cgcagagccg aggtgggtaa gctagcgacc acctggactt 1440

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cccatcccag cgccggccac ccaacctccc gaaatgagtg cttcctgccc cagcagccga 1560

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caaagtccct agtccccgga gcagttagcc tctttctttc cagggaatta gccagacaca 1800

acaacgggaa ccagacaccg aaccagacat gcccgccccg tgcgccctcc ccgctcgctg 1860

cctttcctcc ctcttgtctc tccagagccg gatcttcaag gggagcctcc gtgccccggg 1920

ctgctcagtc cctccggtgt gcaggacccc ggaagtcctc cccgcacagc tctcgcttct 1980

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cgaccgagct ggaattcgcc accatggccc caaagaagaa gcggaaggtc ggtatccacg 2100

gagtcccagc agccctcgaa ccaggtgaaa aaccttacaa atgtcctgaa tgtgggaaat 2160

cattcagtcg cagcgacaac ctggtgagac atcaacgcac ccatacagga gaaaaacctt 2220

ataaatgtcc agaatgtgga aagtccttct cacgagagga taacttgcac actcatcaac 2280

gaacacatac tggtgaaaaa ccatacaagt gtcccgaatg tggtaaaagt tttagccgga 2340

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gcaaagttgg tagccagtac ctgcccgaca ccgacgaccg gcaccggatc gaggaaaagc 3000

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ccgaccctag acctccacct agaagaatcg ccgtgcccag cagatccagc gccagcgtgc 3120

caaaacctgc cccccagcct tacccccttca ccagcagcct gagcaccatc aactacgacg 3180

agttccctac catggtgttc cccagcggcc agatctctca ggcctctgct ctggctccag 3240

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agctgcagtt cgacgacgag gatctgggag ccctgctggg aaacagcacc gatcctgccg 3480

tgttcaccga cctggccagc gtggacaaca gcgagttcca gcagctgctg aaccagggca 3540

tccctgtggc ccctcacacc accgagccca tgctgatgga ataccccgag gccatcaccc 3600

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ccagcctcgc accaacacca accggtccag tacatgagcc agtcgggtca ctgaccccgg 3960

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tggaggatcc cgatgaagag acgagccagg ctgtcaaagc ccttcgggag atggccgata 4080

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ccccaagggg ccatctggat gagctgacaa ccacacttga gtccatgacc gaggatctga 4200

acctggactc acccctgacc ccggaattga acgagattct ggataccttc ctgaacgacg 4260

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<210> 70
<211> 3332
<212> DNA
<213> Artificial Sequence

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

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attttgaagt tctgttgaca taaagaatca tgatattaat gcccatggaa atgaaagggc 120

gatcaacact atggtttgaa aaggggggaaa ttgtagagca cagatgtgtt cgtgtggcag 180

tgtgctgtct ctagcaatac tcagagaaga gagagaacaa tgaaattctg attggcccca 240

gtgtgagccc agatgaggtt cagctgccaa ctttctcttt cacatcttat gaaagtcatt 300

taagcacaac taacttttt ttttttttt ttttttgag acagagtctt gctctgttgc 360

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ctcgaactcc tggcctcaag tgatccacct gcctcggcct cccaaagtgc tgggattata 600

ggcgtcagcc actatgccca acccgaccaa cctttttaa aataaatatt taaaaaattg 660

gtatttcaca tatatactag tatttacatt tatccacaca aaacggacgg gcctccgctg 720

aaccagtgag gccccagacg tgcgcataaa taacccctgc gtgctgcacc acctggggag 780

agggggagga ccacggtaaa tggagcgagc gcatagcaaa agggacgcgg ggtccttttc 840

tctgccggtg gcactgggta gctgtggcca ggtgtggtac tttgatgggg cccagggctg 900

gagctcaagg aagcgtcgca gggtcacaga tctgggggaa ccccggggaa aagcactgag 960

gcaaaaccgc cgctcgtctc ctacaatata tgggaggggg aggttgagta cgttctggat 1020

tactcataag acctttttt tttccttccg ggcgcaaaac cgtgagctgg atttataatc 1080

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cagattacgc ctgtcagggc cgagccgagc ggatcgctgg gcgctgtgca gaggaaaggc 1380

gggagtgccc ggctcgctgt cgcagagccg aggtgggtaa gctagcgacc acctggactt 1440

cccagcgccc aaccgtggct tttcagccag gtcctctcct cccgcggctt ctcaaccaac 1500

cccatcccag cgccggccac ccaacctccc gaaatgagtg cttcctgccc cagcagccga 1560

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cctttcctcc ctcttgtctc tccagagccg gatcttcaag gggagcctcc gtgccccggg 1920

ctgctcagtc cctccggtgt gcaggacccc ggaagtcctc cccgcacagc tctcgcttct 1980

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cgaccgagct ggaattcgcc accatggccc caaagaagaa gcggaaggtc ggtatccacg 2100

gagtcccagc agccctcgaa ccaggtgaaa aaccttacaa atgtcctgaa tgtgggaaat 2160

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ataaatgtcc agaatgtgga aagtccttct cacgagagga taacttgcac actcatcaac 2280

gaacacatac tggtgaaaaa ccatacaagt gtcccgaatg tggtaaaagt tttagccgga 2340

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cgctggacga tttcgatctc gacatgctgg gttctgatgc cctcgatgac tttgacctgg 2760

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<210> 71
<211> 3546
<212> DNA
<213> Artificial Sequence

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

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gatcaacact atggtttgaa aaggggaaa ttgtagagca cagatgtgtt cgtgtggcag 180

tgtgctgtct ctagcaatac tcagagaaga gagagaacaa tgaaattctg attggcccca 240

gtgtgagccc agatgaggtt cagctgccaa ctttctcttt cacatcttat gaaagtcatt 300

taagcacaac taacttttt ttttttttt ttttttgag acagagtctt gctctgttgc 360

ccaggacaga gtgcagtagt gactcaatct cggctcactg cagcctccac ctcctaggct 420

caaacggtcc tcctgcatca gcctcccaag tagctggaat tacaggagtg gcccaccatg 480

cccagctaat ttttgtattt ttaatagata cgggggtttc accatatcac ccaggctggt 540

ctcgaactcc tggcctcaag tgatccacct gcctcggcct cccaaagtgc tgggattata 600

ggcgtcagcc actatgccca acccgaccaa ccttttttaa aataaatatt taaaaaattg 660

gtatttcaca tatatactag tatttacatt tatccacaca aaacggacgg gcctccgctg 720

aaccagtgag gccccagacg tgcgcataaa taacccctgc gtgctgcacc acctggggag 780

agggggagga ccacggtaaa tggagcgagc gcatagcaaa agggacgcgg ggtccttttc 840

tctgccggtg gcactgggta gctgtggcca ggtgtggtac tttgatgggg cccagggctg 900

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gccctataaa gctccagagg cggtcaggca cctgcagagg agccccgccg ctccgccgac 1140

tagctgcccc cgcgagcaac ggcctcgtga tttccccgcc gatccggtcc ccgcctcccc 1200

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cgaccgagct ggaattcgcc accatggccc caaagaagaa gcggaaggtc ggtatccacg 2100

gagtcccagc agccctcgaa ccaggtgaaa aaccttacaa atgtcctgaa tgtgggaaat 2160

cattcagtcg cagcgacaac ctggtgagac atcaacgcac ccatacagga gaaaaacctt 2220

ataaatgtcc agaatgtgga aagtccttct cacgagagga taacttgcac actcatcaac 2280

gaacacatac tggtgaaaaa ccatacaagt gtcccgaatg tggtaaaagt tttagccgga 2340

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gtttctctca gaatagtacc ctgaccgaac accagcgaac acacactggg aaaaaaacga 2640

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gaccggttca ctgtgagaat gaaagagacc ggttcactgt gatcggaaaa gagaccggtt 2940

cactgtgagc ggccttgaaa cccagcagac aatgtagctc agtagaaacc cagcagacaa 3000

tgtagctgaa tggaaaccca gcagacaatg tagcttcgga gaaacccagc agacaatgta 3060

gctaagcttg ggtggcatcc ctgtgacccc tccccagtgc ctctcctggc cctggaagtt 3120

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tagagacggg gtttcaccat attggccagg ctggtctcca actcctaatc tcaggtgatc 3480

tacccacctt ggcctcccaa attgctggga ttacaggcgt gaaccactgc tcccttccct 3540

gtcctt 3546

<210> 72
<211> 1707
<212> DNA
<213> Artificial Sequence

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

<400> 72
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gccgctgccg cccacggccc ccacgccctg agaacactgc ccccctacgc cggccctggt 120

cttgatagcg gactcagacc tagaggcgcc cctctgggcc ctccacctcc aagacagcct 180

ggagccctgg cctacggcgc cttcggccct ccttctagct tccagccctt ccccgccgtg 240

cctcctccag ccgctggcat cgcccacctg cagcctgtgg ccacccctta ccccggaaga 300

gccgccgccc ctccaaacgc ccctggcgga cctcctggcc cccagcctgc tccaagcgcc 360

gctgcccctc cacctcctgc tcatgccctg ggcggcatgg acgccgagct gatcgacgag 420

gaagccctga ccagcctgga actggaactg ggcctgcaca gagtgcggga actgcctgag 480

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cacactcaca tccgcaccca cacaggcgaa aagcccttcg cctgcgacat ctgtggaaga 1380

aagtttgccc ggagcgatga acttgtccga cataccaaga tccacttgcg gcagaaggac 1440

cgcccttacg cttgcccagt ggagtcctgt gatcgccgct tctcccaatc agggaatctg 1500

actgagcaca tccgcatcca cacaggccag aagcccttcc agtgccgcat ctgcatgaga 1560

aacttcagca caagtggaca tctggtacgc cacatccgca cccacacagg cgaaaagccc 1620

ttcgcctgcg acatctgtgg aagaaagttt gcccagaata gtaccctgac cgaacatacc 1680

aagatccact tgcggcagaa ggacaag 1707

<210> 73
<211> 1755
<212> DNA
<213> Artificial Sequence

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

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gccgctgccg cccacggccc ccacgccctg agaacactgc ccccctacgc cggccctggt 120

cttgatagcg gactcagacc tagaggcgcc cctctgggcc ctccacctcc aagacagcct 180

ggagccctgg cctacggcgc cttcggccct ccttctagct tccagccctt ccccgccgtg 240

cctcctccag ctgctggcat cgcccacctg cagcctgtgg ccacccctta ccccggaaga 300

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cgcatccaca caggccagaa gcccttccag tgccgcatct gcatgagaaa cttcagcaca 1620

agtggacatc tggtacgcca catccgcacc cacacaggcg aaaagccctt cgcctgcgac 1680

atctgtggaa gaaagtttgc ccagaatagt accctgaccg aacataccaa gatccacttg 1740

cggcagaagg acaag 1755

<210> 74
<211> 3438
<212> DNA
<213> Artificial Sequence

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

<400> 74
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attttgaagt tctgttgaca taaagaatca tgatattaat gcccatggaa atgaaagggc 120

gatcaacact atggtttgaa aaggggaaa ttgtagagca cagatgtgtt cgtgtggcag 180

tgtgctgtct ctagcaatac tcagagaaga gagagaacaa tgaaattctg attggcccca 240

gtgtgagccc agatgaggtt cagctgccaa ctttctcttt cacatcttat gaaagtcatt 300

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cccagctaat ttttgtattt ttaatagata cgggggtttc accatatcac ccaggctggt 540

ctcgaactcc tggcctcaag tgatccacct gcctcggcct cccaaagtgc tgggattata 600

ggcgtcagcc actatgccca acccgaccaa ccttttttaa aataaatatt taaaaaattg 660

gtatttcaca tatatactag tatttacatt tatccacaca aaacggacgg gcctccgctg 720

aaccagtgag gccccagacg tgcgcataaa taacccctgc gtgctgcacc acctggggag 780

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gggagtgccc ggctcgctgt cgcagagccg aggtgggtaa gctagcgacc acctggactt 1440

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cctttcctcc ctcttgtctc tccagagccg gatcttcaag gggagcctcc gtgccccggg 1920

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ctgcctcagc ctcccgagtt gttgggattc caggcatgca tgaccaggct cagctaattt 3300

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gctcccttcc ctgtcctt 3438

<210> 75
<211> 3505

<212> DNA
<213> Artificial Sequence

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

<400> 75
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attttgaagt tctgttgaca taaagaatca tgatattaat gcccatggaa atgaaagggc 120

gatcaacact atggtttgaa aaggggggaaa ttgtagagca cagatgtgtt cgtgtggcag 180

tgtgctgtct ctagcaatac tcagagaaga gagagaacaa tgaaattctg attggcccca 240

gtgtgagccc agatgaggtt cagctgccaa ctttctcttt cacatcttat gaaagtcatt 300

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ggcgtcagcc actatgccca acccgaccaa cctttttaa aataaatatt taaaaaattg 660

gtatttcaca tatatactag tatttacatt tatccacaca aaacggacgg gcctccgctg 720

aaccagtgag gccccagacg tgcgcataaa taacccctgc gtgctgcacc acctggggag 780

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gattctcctg cctcagcctc ccgagttgtt gggattccag gcatgcatga ccaggctcag 3360

ctaatttttg ttttttggt agagacgggg tttcaccata ttggccaggc tggtctccaa 3420

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<210> 76
<211> 3804
<212> DNA
<213> Artificial Sequence

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

<400> 76
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gatcaacact atggtttgaa aaggggggaaa ttgtagagca cagatgtgtt cgtgtggcag 180

tgtgctgtct ctagcaatac tcagagaaga gagagaacaa tgaaattctg attggcccca 240

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taagcacaac taacttttt ttttttttt ttttttgag acagagtctt gctctgttgc 360

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caaacggtcc tcctgcatca gcctcccaag tagctggaat tacaggagtg gcccaccatg 480

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gtatttcaca tatatactag tatttacatt tatccacaca aaacggacgg gcctccgctg 720

aaccagtgag gccccagacg tgcgcataaa taacccctgc gtgctgcacc acctggggag 780

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accactgctc ccttccctgt cctt 3804

<210> 77
<211> 176
<212> PRT
<213> Artificial Sequence

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

<400> 77
Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
1 5 10 15

Phe Ser Arg Ser Asp Asn Leu Val Arg His Gln Arg Thr His Thr Gly
20 25 30

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Glu
35 40 45

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

Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Ser Asp Glu Leu Val
65 70 75 80

Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu
85 90 95

Cys Gly Lys Ser Phe Ser Gln Ser Gly Asn Leu Thr Glu His Gln Arg
100 105 110

Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
115 120 125

Phe Ser Thr Ser Gly His Leu Val Arg His Gln Arg Thr His Thr Gly
130 135 140

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Asn
145 150 155 160

Ser Thr Leu Thr Glu His Gln Arg Thr His Thr Gly Lys Lys Thr Ser
165 170 175

<210> 78
<211> 176
<212> PRT
<213> Artificial Sequence

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

<400> 78
Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
1 5 10 15

Phe Ser Thr Lys Asn Ser Leu Thr Glu His Gln Arg Thr His Thr Gly
20 25 30

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Ala
35 40 45

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

Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Leu Ala His Leu Arg
65 70 75 80

Ala His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu
85 90 95

Cys Gly Lys Ser Phe Ser Thr Lys Asn Ser Leu Thr Glu His Gln Arg
100 105 110

Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
115 120 125

Phe Ser Gln Ala Gly His Leu Ala Ser His Gln Arg Thr His Thr Gly
130 135 140

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Thr His
145 150 155 160

Leu Asp Leu Ile Arg His Gln Arg Thr His Thr Gly Lys Lys Thr Ser
165 170 175

<210> 79
<211> 176
<212> PRT
<213> Artificial Sequence

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

<400> 79
Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
1 5 10 15

Phe Ser Gln Ala Gly His Leu Ala Ser His Gln Arg Thr His Thr Gly
20 25 30

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Glu
35 40 45

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

Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Thr Ser Gly Asn Leu Thr
65 70 75 80

Glu His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu
85 90 95

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

Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
115 120 125

Phe Ser Gln Lys Ser Ser Leu Ile Ala His Gln Arg Thr His Thr Gly
130 135 140

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Ala
145 150 155 160

Gly His Leu Ala Ser His Gln Arg Thr His Thr Gly Lys Lys Thr Ser
165 170 175

<210> 80
<211> 176
<212> PRT
<213> Artificial Sequence

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

<400> 80
Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
1 5 10 15

Phe Ser Thr Thr Gly Asn Leu Thr Val His Gln Arg Thr His Thr Gly
20 25 30

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Thr Ser
35 40 45

Gly Glu Leu Val Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr
50 55 60

Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Glu Asp Asn Leu His
65 70 75 80

Thr His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu
85 90 95

Cys Gly Lys Ser Phe Ser Thr Ser Gly Asn Leu Thr Glu His Gln Arg
100 105 110

Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
115 120 125

Phe Ser Gln Ser Ser Ser Leu Val Arg His Gln Arg Thr His Thr Gly
130 135 140

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Arg
145 150 155 160

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

<210> 81
<211> 176
<212> PRT
<213> Artificial Sequence

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

<400> 81
Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
1 5 10 15

Phe Ser Ser Arg Arg Thr Cys Arg Ala His Gln Arg Thr His Thr Gly
20 25 30

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Thr Thr
35 40 45

Gly Ala Leu Thr Glu His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr
50 55 60

Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Ser Asp Glu Leu Val
65 70 75 80

Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu
85 90 95

Cys Gly Lys Ser Phe Ser Arg Asn Asp Ala Leu Thr Glu His Gln Arg
100 105 110

Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
115 120 125

Phe Ser Gln Ser Gly Asp Leu Arg Arg His Gln Arg Thr His Thr Gly
130 135 140

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Thr Ser
145 150 155 160

His Ser Leu Thr Glu His Gln Arg Thr His Thr Gly Lys Lys Thr Ser
165 170 175

<210> 82
<211> 176
<212> PRT
<213> Artificial Sequence

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

<400> 82
Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
1 5 10 15

Phe Ser Arg Lys Asp Asn Leu Lys Asn His Gln Arg Thr His Thr Gly
20 25 30

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Asp Pro
35 40 45

Gly Ala Leu Val Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr
50 55 60

Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Glu Asp Asn Leu His
65 70 75 80

Thr His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu
85 90 95

Cys Gly Lys Ser Phe Ser Asp Pro Gly Ala Leu Val Arg His Gln Arg
100 105 110

Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
115 120 125

Phe Ser Thr Ser Gly Glu Leu Val Arg His Gln Arg Thr His Thr Gly
130 135 140

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Lys
145 150 155 160

Asp Asn Leu Lys Asn His Gln Arg Thr His Thr Gly Lys Lys Thr Ser
165 170 175

<210> 83
<211> 232
<212> PRT
<213> Artificial Sequence

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

<400> 83
Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
1 5 10 15

Phe Ser Ser Lys Lys Ala Leu Thr Glu His Gln Arg Thr His Thr Gly
20 25 30

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Ser Pro
35 40 45

Ala Asp Leu Thr Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr
50 55 60

Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Ser Asp Asn Leu Val
65 70 75 80

Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu
85 90 95

Cys Gly Lys Ser Phe Ser Arg Glu Asp Asn Leu His Thr His Gln Arg
100 105 110

Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
115 120 125

Phe Ser Arg Ser Asp Glu Leu Val Arg His Gln Arg Thr His Thr Gly
130 135 140

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Ser
145 150 155 160

Gly Asn Leu Thr Glu His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr
165 170 175

Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Thr Ser Gly His Leu Val
180 185 190

Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu
195 200 205

Cys Gly Lys Ser Phe Ser Gln Asn Ser Thr Leu Thr Glu His Gln Arg
210 215 220

Thr His Thr Gly Lys Lys Thr Ser
225 230

<210> 84
<211> 176
<212> PRT
<213> Artificial Sequence

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

<400> 84
Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
1 5 10 15

Phe Ser Ser Pro Ala Asp Leu Thr Arg His Gln Arg Thr His Thr Gly
20 25 30

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Ser
35 40 45

Asp Asn Leu Val Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr
50 55 60

Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Glu Asp Asn Leu His
65 70 75 80

Thr His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu
85 90 95

Cys Gly Lys Ser Phe Ser Arg Ser Asp Glu Leu Val Arg His Gln Arg
100 105 110

Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
115 120 125

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Phe Ser Gln Ser Gly Asn Leu Thr Glu His Gln Arg Thr His Thr Gly
    130                 135                 140


Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Thr Ser
145                 150                 155                 160


Gly His Leu Val Arg His Gln Arg Thr His Thr Gly Lys Lys Thr Ser
                165                 170                 175


<210> 85
<211> 176
<212> PRT
<213> Artificial Sequence

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

<400> 85
Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
1               5                   10                  15


Phe Ser Ser Lys Lys Ala Leu Thr Glu His Gln Arg Thr His Thr Gly
            20                  25                  30


Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Ser Pro
        35                  40                  45


Ala Asp Leu Thr Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr
    50                  55                  60


Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Ser Asp Asn Leu Val
65                  70                  75                  80


Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu
                85                  90                  95


Cys Gly Lys Ser Phe Ser Arg Glu Asp Asn Leu His Thr His Gln Arg
            100                 105                 110


Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
        115                 120                 125
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Phe Ser Arg Ser Asp Glu Leu Val Arg His Gln Arg Thr His Thr Gly
130 135 140

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Ser
145 150 155 160

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

<210> 86
<211> 232
<212> PRT
<213> Artificial Sequence

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

<400> 86
Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
1 5 10 15

Phe Ser Asp Cys Arg Asp Leu Ala Arg His Gln Arg Thr His Thr Gly
20 25 30

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Asn
35 40 45

Asp Ala Leu Thr Glu His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr
50 55 60

Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Asn Asp Ala Leu Thr
65 70 75 80

Glu His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu
85 90 95

Cys Gly Lys Ser Phe Ser Ser Pro Ala Asp Leu Thr Arg His Gln Arg
100 105 110

Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
115 120 125

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Phe Ser Asp Pro Gly Asn Leu Val Arg His Gln Arg Thr His Thr Gly
    130                 135                 140

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Arg
145                 150                 155                 160

Ala His Leu Glu Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr
                165                 170                 175

Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Ser Ser Ser Leu Val
            180                 185                 190

Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu
        195                 200                 205

Cys Gly Lys Ser Phe Ser His Arg Thr Thr Leu Thr Asn His Gln Arg
    210                 215                 220

Thr His Thr Gly Lys Lys Thr Ser
225                 230
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<210> 87
<211> 176
<212> PRT
<213> Artificial Sequence

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

<400> 87

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Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
1               5                   10                  15

Phe Ser Arg Asn Asp Ala Leu Thr Glu His Gln Arg Thr His Thr Gly
            20                  25                  30

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Ser Pro
        35                  40                  45

Ala Asp Leu Thr Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr
    50                  55                  60
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Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Asp Pro Gly Asn Leu Val
65 70 75 80

Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu
85 90 95

Cys Gly Lys Ser Phe Ser Gln Arg Ala His Leu Glu Arg His Gln Arg
100 105 110

Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
115 120 125

Phe Ser Gln Ser Ser Ser Leu Val Arg His Gln Arg Thr His Thr Gly
130 135 140

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser His Arg
145 150 155 160

Thr Thr Leu Thr Asn His Gln Arg Thr His Thr Gly Lys Lys Thr Ser
165 170 175

<210> 88
<211> 204
<212> PRT
<213> Artificial Sequence

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

<400> 88
Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
1 5 10 15

Phe Ser Arg Asn Asp Ala Leu Thr Glu His Gln Arg Thr His Thr Gly
20 25 30

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Asp Pro
35 40 45

Gly His Leu Val Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr
50 55 60

Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Thr Ser Gly Glu Leu Val
65 70 75 80

Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu
85 90 95

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

Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
115 120 125

Phe Ser Ser Lys Lys Ala Leu Thr Glu His Gln Arg Thr His Thr Gly
130 135 140

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Leu
145 150 155 160

Ala His Leu Arg Ala His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr
165 170 175

Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Ser Asp His Leu Thr
180 185 190

Asn His Gln Arg Thr His Thr Gly Lys Lys Thr Ser
195 200

<210> 89
<211> 176
<212> PRT
<213> Artificial Sequence

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

<400> 89
Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
1 5 10 15

Phe Ser Arg Ser Asp Asn Leu Val Arg His Gln Arg Thr His Thr Gly
20 25 30

```
Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser His Arg
        35                  40                  45

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

Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Glu Asp Asn Leu His
65                  70                  75                  80

Thr His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu
                85                  90                  95

Cys Gly Lys Ser Phe Ser Thr Ser His Ser Leu Thr Glu His Gln Arg
            100                 105                 110

Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
        115                 120                 125

Phe Ser Gln Ser Ser Ser Leu Val Arg His Gln Arg Thr His Thr Gly
    130                 135                 140

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Glu
145                 150                 155                 160

Asp Asn Leu His Thr His Gln Arg Thr His Thr Gly Lys Lys Thr Ser
                165                 170                 175


<210> 90
<211> 176
<212> PRT
<213> Artificial Sequence

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

<400> 90
Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
1               5                   10                  15

Phe Ser Asp Pro Gly Ala Leu Val Arg His Gln Arg Thr His Thr Gly
            20                  25                  30
```

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Ser
35 40 45

Asp Asn Leu Val Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr
50 55 60

Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Ser Gly Asp Leu Arg
65 70 75 80

Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu
85 90 95

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

Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
115 120 125

Phe Ser Thr Ser Gly Asn Leu Val Arg His Gln Arg Thr His Thr Gly
130 135 140

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Ser
145 150 155 160

Asp Asn Leu Val Arg His Gln Arg Thr His Thr Gly Lys Lys Thr Ser
165 170 175

<210> 91
<211> 260
<212> PRT
<213> Artificial Sequence

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

<400> 91
Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
1 5 10 15

Phe Ser Arg Arg Asp Glu Leu Asn Val His Gln Arg Thr His Thr Gly
20 25 30

```
Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Ser
        35                  40                  45

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

Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Ser Asp Asp Leu Val
65                  70                  75                  80

Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu
                85                  90                  95

Cys Gly Lys Ser Phe Ser Arg Ser Asp Asn Leu Val Arg His Gln Arg
            100                 105                 110

Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
        115                 120                 125

Phe Ser His Arg Thr Thr Leu Thr Asn His Gln Arg Thr His Thr Gly
    130                 135                 140

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Glu
145                 150                 155                 160

Asp Asn Leu His Thr His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr
                165                 170                 175

Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Thr Ser His Ser Leu Thr
            180                 185                 190

Glu His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu
        195                 200                 205

Cys Gly Lys Ser Phe Ser Gln Ser Ser Ser Leu Val Arg His Gln Arg
    210                 215                 220

Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
225                 230                 235                 240

Phe Ser Arg Glu Asp Asn Leu His Thr His Gln Arg Thr His Thr Gly
                245                 250                 255
```

Lys Lys Thr Ser
260

<210> 92
<211> 177
<212> PRT
<213> Artificial Sequence

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

<400> 92
Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg
1 5 10 15

Ser Asp Asn Leu Val Arg His Ile Arg Ile His Thr Gly Gln Lys Pro
20 25 30

Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Glu Asp Asn Leu
35 40 45

His Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp
50 55 60

Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Leu Val Arg His Thr
65 70 75 80

Lys Ile His Leu Arg Gln Lys Asp Arg Pro Tyr Ala Cys Pro Val Glu
85 90 95

Ser Cys Asp Arg Arg Phe Ser Gln Ser Gly Asn Leu Thr Glu His Ile
100 105 110

Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg
115 120 125

Asn Phe Ser Thr Ser Gly His Leu Val Arg His Ile Arg Thr His Thr
130 135 140

Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Gln
145 150 155 160

Asn Ser Thr Leu Thr Glu His Thr Lys Ile His Leu Arg Gln Lys Asp
165 170 175

Lys

<210> 93
<211> 177
<212> PRT
<213> Artificial Sequence

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

<400> 93
Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg
1 5 10 15

Ser Asp Asn Leu Val Arg His Ile Arg Ile His Thr Gly Gln Lys Pro
20 25 30

Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser His Arg Thr Thr Leu
35 40 45

Thr Asn His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp
50 55 60

Ile Cys Gly Arg Lys Phe Ala Arg Glu Asp Asn Leu His Thr His Thr
65 70 75 80

Lys Ile His Leu Arg Gln Lys Asp Arg Pro Tyr Ala Cys Pro Val Glu
85 90 95

Ser Cys Asp Arg Arg Phe Ser Thr Ser His Ser Leu Thr Glu His Ile
100 105 110

Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg
115 120 125

Asn Phe Ser Gln Ser Ser Ser Leu Val Arg His Ile Arg Thr His Thr
130 135 140

Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg
145 150 155 160

Glu Asp Asn Leu His Thr His Thr Lys Ile His Leu Arg Gln Lys Asp
165 170 175

Lys

<210> 94
<211> 264
<212> PRT
<213> Artificial Sequence

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

<400> 94
Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg
1 5 10 15

Arg Asp Glu Leu Asn Val His Ile Arg Ile His Thr Gly Gln Lys Pro
20 25 30

Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu
35 40 45

Thr Asn His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp
50 55 60

Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Asp Leu Val Arg His Thr
65 70 75 80

Lys Ile His Leu Arg Gln Lys Asp Arg Pro Tyr Ala Cys Pro Val Glu
85 90 95

Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Asn Leu Val Arg His Ile
100 105 110

Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg
115 120 125

```
Asn Phe Ser His Arg Thr Thr Leu Thr Asn His Ile Arg Thr His Thr
    130                 135                 140


Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg
145                 150                 155                 160


Glu Asp Asn Leu His Thr His Thr Lys Ile His Leu Arg Gln Lys Asp
                165                 170                 175


Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Thr
            180                 185                 190


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


Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Gln Ser Ser Ser Leu
    210                 215                 220


Val Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp
225                 230                 235                 240


Ile Cys Gly Arg Lys Phe Ala Arg Glu Asp Asn Leu His Thr His Thr
                245                 250                 255


Lys Ile His Leu Arg Gln Lys Asp
            260


<210> 95
<211> 264
<212> PRT
<213> Artificial Sequence

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

<400> 95
Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Asp
1               5                   10                  15


Pro Gly Ala Leu Val Arg His Ile Arg Ile His Thr Gly Gln Lys Pro
            20                  25                  30
```

```
Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Asn Leu
        35                  40                  45

Val Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp
    50                  55                  60

Ile Cys Gly Arg Lys Phe Ala Gln Ser Gly Asp Leu Arg Arg His Thr
65                  70                  75                  80

Lys Ile His Leu Arg Gln Lys Asp Arg Pro Tyr Ala Cys Pro Val Glu
                85                  90                  95

Ser Cys Asp Arg Arg Phe Ser Thr His Leu Asp Leu Ile Arg His Ile
            100                 105                 110

Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg
        115                 120                 125

Asn Phe Ser Thr Ser Gly Asn Leu Val Arg His Ile Arg Thr His Thr
    130                 135                 140

Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg
145                 150                 155                 160

Ser Asp Asn Leu Val Arg His Thr Lys Ile His Leu Arg Gln Lys Asp
                165                 170                 175

Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Gln
            180                 185                 190

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

Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Glu Arg Ser His Leu
    210                 215                 220

Arg Glu His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp
225                 230                 235                 240
```

```
Ile Cys Gly Arg Lys Phe Ala Gln Ala Gly His Leu Ala Ser His Thr
                245                 250                 255


Lys Ile His Leu Arg Gln Lys Asp
            260
```

<210> 96
<211> 175
<212> PRT
<213> Artificial Sequence

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

<400> 96

```
Arg Pro His Ala Cys Pro Ala Glu Gly Cys Asp Arg Arg Phe Ser Arg
1               5                   10                  15


Ser Asp Asn Leu Val Arg His Leu Arg Ile His Thr Gly His Lys Pro
            20                  25                  30


Phe Gln Cys Arg Ile Cys Met Arg Ser Phe Ser Arg Glu Asp Asn Leu
        35                  40                  45


His Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Glu
    50                  55                  60


Phe Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Leu Val Arg His Ala
65                  70                  75                  80


Lys Ile His Leu Lys Gln Lys Glu His Ala Cys Pro Ala Glu Gly Cys
                85                  90                  95


Asp Arg Arg Phe Ser Gln Ser Gly Asn Leu Thr Glu His Leu Arg Ile
            100                 105                 110


His Thr Gly His Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Ser Phe
        115                 120                 125


Ser Thr Ser Gly His Leu Val Arg His Ile Arg Thr His Thr Gly Glu
    130                 135                 140
```

Lys Pro Phe Ala Cys Glu Phe Cys Gly Arg Lys Phe Ala Gln Asn Ser
145 150 155 160

Thr Leu Thr Glu His Ala Lys Ile His Leu Lys Gln Lys Glu Lys
165 170 175

<210> 97
<211> 175
<212> PRT
<213> Artificial Sequence

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

<400> 97
Arg Pro His Ala Cys Pro Ala Glu Gly Cys Asp Arg Arg Phe Ser Arg
1 5 10 15

Ser Asp Asn Leu Val Arg His Leu Arg Ile His Thr Gly His Lys Pro
20 25 30

Phe Gln Cys Arg Ile Cys Met Arg Ser Phe Ser His Arg Thr Thr Leu
35 40 45

Thr Asn His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Glu
50 55 60

Phe Cys Gly Arg Lys Phe Ala Arg Glu Asp Asn Leu His Thr His Ala
65 70 75 80

Lys Ile His Leu Lys Gln Lys Glu His Ala Cys Pro Ala Glu Gly Cys
85 90 95

Asp Arg Arg Phe Ser Thr Ser His Ser Leu Thr Glu His Leu Arg Ile
100 105 110

His Thr Gly His Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Ser Phe
115 120 125

Ser Gln Ser Ser Ser Leu Val Arg His Ile Arg Thr His Thr Gly Glu
130 135 140

Lys Pro Phe Ala Cys Glu Phe Cys Gly Arg Lys Phe Ala Arg Glu Asp
145 150 155 160

Asn Leu His Thr His Ala Lys Ile His Leu Lys Gln Lys Glu Lys
165 170 175

<210> 98
<211> 261
<212> PRT
<213> Artificial Sequence

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

<400> 98
Arg Pro His Ala Cys Pro Ala Glu Gly Cys Asp Arg Arg Phe Ser Arg
1 5 10 15

Arg Asp Glu Leu Asn Val His Leu Arg Ile His Thr Gly His Lys Pro
20 25 30

Phe Gln Cys Arg Ile Cys Met Arg Ser Phe Ser Arg Ser Asp His Leu
35 40 45

Thr Asn His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Glu
50 55 60

Phe Cys Gly Arg Lys Phe Ala Arg Ser Asp Asp Leu Val Arg His Ala
65 70 75 80

Lys Ile His Leu Lys Gln Lys Glu His Ala Cys Pro Ala Glu Gly Cys
85 90 95

Asp Arg Arg Phe Ser Arg Ser Asp Asn Leu Val Arg His Leu Arg Ile
100 105 110

His Thr Gly His Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Ser Phe
115 120 125

Ser His Arg Thr Thr Leu Thr Asn His Ile Arg Thr His Thr Gly Glu
130 135 140

```
Lys Pro Phe Ala Cys Glu Phe Cys Gly Arg Lys Phe Ala Arg Glu Asp
145                 150                 155                 160


Asn Leu His Thr His Ala Lys Ile His Leu Lys Gln Lys Glu His Ala
                165                 170                 175


Cys Pro Ala Glu Gly Cys Asp Arg Arg Phe Ser Thr Ser His Ser Leu
            180                 185                 190


Thr Glu His Leu Arg Ile His Thr Gly His Lys Pro Phe Gln Cys Arg
        195                 200                 205


Ile Cys Met Arg Ser Phe Ser Gln Ser Ser Ser Leu Val Arg His Ile
    210                 215                 220


Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Glu Phe Cys Gly Arg
225                 230                 235                 240


Lys Phe Ala Arg Glu Asp Asn Leu His Thr His Ala Lys Ile His Leu
                245                 250                 255


Lys Gln Lys Glu Lys
            260


<210> 99
<211> 753
<212> PRT
<213> Artificial Sequence

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

<400> 99
Met Ala Pro Lys Lys Lys Arg Lys Val Gly Ile His Gly Val Pro Ala
1               5                   10                  15


Ala Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys
            20                  25                  30


Ser Phe Ser Arg Ser Asp Asn Leu Val Arg His Gln Arg Thr His Thr
        35                  40                  45
```

```
Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser His
    50                  55                  60

Arg Thr Thr Leu Thr Asn His Gln Arg Thr His Thr Gly Glu Lys Pro
65                  70                  75                  80

Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Glu Asp Asn Leu
                85                  90                  95

His Thr His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro
            100                 105                 110

Glu Cys Gly Lys Ser Phe Ser Thr Ser His Ser Leu Thr Glu His Gln
        115                 120                 125

Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys
    130                 135                 140

Ser Phe Ser Gln Ser Ser Ser Leu Val Arg His Gln Arg Thr His Thr
145                 150                 155                 160

Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg
                165                 170                 175

Glu Asp Asn Leu His Thr His Gln Arg Thr His Thr Gly Lys Lys Thr
            180                 185                 190

Ser Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys
        195                 200                 205

Lys Gly Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Leu Glu Glu Ala
    210                 215                 220

Ser Gly Ser Gly Arg Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp Met
225                 230                 235                 240

Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser
                245                 250                 255

Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu
            260                 265                 270
```

```
Asp Asp Phe Asp Leu Asp Met Leu Ile Asn Ser Arg Ser Ser Gly Ser
        275                 280                 285

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

Asp Arg His Arg Ile Glu Glu Lys Arg Lys Arg Thr Tyr Glu Thr Phe
305                 310                 315                 320

Lys Ser Ile Met Lys Lys Ser Pro Phe Ser Gly Pro Thr Asp Pro Arg
                325                 330                 335

Pro Pro Pro Arg Arg Ile Ala Val Pro Ser Arg Ser Ser Ala Ser Val
            340                 345                 350

Pro Lys Pro Ala Pro Gln Pro Tyr Pro Phe Thr Ser Ser Leu Ser Thr
        355                 360                 365

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

Ser Gln Ala Ser Ala Leu Ala Pro Ala Pro Pro Gln Val Leu Pro Gln
385                 390                 395                 400

Ala Pro Ala Pro Ala Pro Ala Pro Ala Met Val Ser Ala Leu Ala Gln
                405                 410                 415

Ala Pro Ala Pro Val Pro Val Leu Ala Pro Gly Pro Pro Gln Ala Val
            420                 425                 430

Ala Pro Pro Ala Pro Lys Pro Thr Gln Ala Gly Glu Gly Thr Leu Ser
        435                 440                 445

Glu Ala Leu Leu Gln Leu Gln Phe Asp Asp Glu Asp Leu Gly Ala Leu
    450                 455                 460

Leu Gly Asn Ser Thr Asp Pro Ala Val Phe Thr Asp Leu Ala Ser Val
465                 470                 475                 480
```

```
Asp Asn Ser Glu Phe Gln Gln Leu Leu Asn Gln Gly Ile Pro Val Ala
                485                 490                 495

Pro His Thr Thr Glu Pro Met Leu Met Glu Tyr Pro Glu Ala Ile Thr
            500                 505                 510

Arg Leu Val Thr Gly Ala Gln Arg Pro Pro Asp Pro Ala Pro Ala Pro
        515                 520                 525

Leu Gly Ala Pro Gly Leu Pro Asn Gly Leu Leu Ser Gly Asp Glu Asp
    530                 535                 540

Phe Ser Ser Ile Ala Asp Met Asp Phe Ser Ala Leu Leu Gly Ser Gly
545                 550                 555                 560

Ser Gly Ser Arg Asp Ser Arg Glu Gly Met Phe Leu Pro Lys Pro Glu
                565                 570                 575

Ala Gly Ser Ala Ile Ser Asp Val Phe Glu Gly Arg Glu Val Cys Gln
            580                 585                 590

Pro Lys Arg Ile Arg Pro Phe His Pro Pro Gly Ser Pro Trp Ala Asn
        595                 600                 605

Arg Pro Leu Pro Ala Ser Leu Ala Pro Thr Pro Thr Gly Pro Val His
    610                 615                 620

Glu Pro Val Gly Ser Leu Thr Pro Ala Pro Val Pro Gln Pro Leu Asp
625                 630                 635                 640

Pro Ala Pro Ala Val Thr Pro Glu Ala Ser His Leu Leu Glu Asp Pro
                645                 650                 655

Asp Glu Glu Thr Ser Gln Ala Val Lys Ala Leu Arg Glu Met Ala Asp
            660                 665                 670

Thr Val Ile Pro Gln Lys Glu Glu Ala Ala Ile Cys Gly Gln Met Asp
        675                 680                 685

Leu Ser His Pro Pro Pro Arg Gly His Leu Asp Glu Leu Thr Thr Thr
    690                 695                 700
```

Leu Glu Ser Met Thr Glu Asp Leu Asn Leu Asp Ser Pro Leu Thr Pro
705 710 715 720

Glu Leu Asn Glu Ile Leu Asp Thr Phe Leu Asn Asp Glu Cys Leu Leu
725 730 735

His Ala Met His Ile Ser Thr Gly Leu Ser Ile Phe Asp Thr Ser Leu
740 745 750

Phe

<210> 100
<211> 753
<212> PRT
<213> Artificial Sequence

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

<400> 100
Met Ala Pro Lys Lys Lys Arg Lys Val Gly Ile His Gly Val Pro Ala
1 5 10 15

Ala Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys
20 25 30

Ser Phe Ser Arg Ser Asp Asn Leu Val Arg His Gln Arg Thr His Thr
35 40 45

Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg
50 55 60

Glu Asp Asn Leu His Thr His Gln Arg Thr His Thr Gly Glu Lys Pro
65 70 75 80

Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Ser Asp Glu Leu
85 90 95

Val Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro
100 105 110

```
Glu Cys Gly Lys Ser Phe Ser Gln Ser Gly Asn Leu Thr Glu His Gln
        115                 120                 125

Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys
    130                 135                 140

Ser Phe Ser Thr Ser Gly His Leu Val Arg His Gln Arg Thr His Thr
145                 150                 155                 160

Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln
                165                 170                 175

Asn Ser Thr Leu Thr Glu His Gln Arg Thr His Thr Gly Lys Lys Thr
            180                 185                 190

Ser Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys
        195                 200                 205

Lys Gly Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Leu Glu Glu Ala
    210                 215                 220

Ser Gly Ser Gly Arg Ala Asp Ala Leu Asp Asp Phe Asp Leu Asp Met
225                 230                 235                 240

Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser
                245                 250                 255

Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu
            260                 265                 270

Asp Asp Phe Asp Leu Asp Met Leu Ile Asn Ser Arg Ser Ser Gly Ser
        275                 280                 285

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

Asp Arg His Arg Ile Glu Glu Lys Arg Lys Arg Thr Tyr Glu Thr Phe
305                 310                 315                 320
```

```
Lys Ser Ile Met Lys Lys Ser Pro Phe Ser Gly Pro Thr Asp Pro Arg
                325                 330                 335

Pro Pro Pro Arg Arg Ile Ala Val Pro Ser Arg Ser Ser Ala Ser Val
            340                 345                 350

Pro Lys Pro Ala Pro Gln Pro Tyr Pro Phe Thr Ser Ser Leu Ser Thr
        355                 360                 365

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

Ser Gln Ala Ser Ala Leu Ala Pro Ala Pro Pro Gln Val Leu Pro Gln
385                 390                 395                 400

Ala Pro Ala Pro Ala Pro Ala Pro Ala Met Val Ser Ala Leu Ala Gln
                405                 410                 415

Ala Pro Ala Pro Val Pro Val Leu Ala Pro Gly Pro Pro Gln Ala Val
            420                 425                 430

Ala Pro Pro Ala Pro Lys Pro Thr Gln Ala Gly Glu Gly Thr Leu Ser
        435                 440                 445

Glu Ala Leu Leu Gln Leu Gln Phe Asp Asp Glu Asp Leu Gly Ala Leu
    450                 455                 460

Leu Gly Asn Ser Thr Asp Pro Ala Val Phe Thr Asp Leu Ala Ser Val
465                 470                 475                 480

Asp Asn Ser Glu Phe Gln Gln Leu Leu Asn Gln Gly Ile Pro Val Ala
                485                 490                 495

Pro His Thr Thr Glu Pro Met Leu Met Glu Tyr Pro Glu Ala Ile Thr
            500                 505                 510

Arg Leu Val Thr Gly Ala Gln Arg Pro Pro Asp Pro Ala Pro Ala Pro
        515                 520                 525

Leu Gly Ala Pro Gly Leu Pro Asn Gly Leu Leu Ser Gly Asp Glu Asp
    530                 535                 540
```

```
Phe Ser Ser Ile Ala Asp Met Asp Phe Ser Ala Leu Leu Gly Ser Gly
545                 550                 555                 560


Ser Gly Ser Arg Asp Ser Arg Glu Gly Met Phe Leu Pro Lys Pro Glu
                565                 570                 575


Ala Gly Ser Ala Ile Ser Asp Val Phe Glu Gly Arg Glu Val Cys Gln
            580                 585                 590


Pro Lys Arg Ile Arg Pro Phe His Pro Pro Gly Ser Pro Trp Ala Asn
        595                 600                 605


Arg Pro Leu Pro Ala Ser Leu Ala Pro Thr Pro Thr Gly Pro Val His
    610                 615                 620


Glu Pro Val Gly Ser Leu Thr Pro Ala Pro Val Pro Gln Pro Leu Asp
625                 630                 635                 640


Pro Ala Pro Ala Val Thr Pro Glu Ala Ser His Leu Leu Glu Asp Pro
                645                 650                 655


Asp Glu Glu Thr Ser Gln Ala Val Lys Ala Leu Arg Glu Met Ala Asp
            660                 665                 670


Thr Val Ile Pro Gln Lys Glu Glu Ala Ala Ile Cys Gly Gln Met Asp
        675                 680                 685


Leu Ser His Pro Pro Pro Arg Gly His Leu Asp Glu Leu Thr Thr Thr
    690                 695                 700


Leu Glu Ser Met Thr Glu Asp Leu Asn Leu Asp Ser Pro Leu Thr Pro
705                 710                 715                 720


Glu Leu Asn Glu Ile Leu Asp Thr Phe Leu Asn Asp Glu Cys Leu Leu
                725                 730                 735


His Ala Met His Ile Ser Thr Gly Leu Ser Ile Phe Asp Thr Ser Leu
            740                 745                 750
```

Phe

<210> 101
<211> 272
<212> PRT
<213> Artificial Sequence

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

<400> 101
Met Ala Pro Lys Lys Lys Arg Lys Val Gly Ile His Gly Val Pro Ala
1 5 10 15

Ala Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys
20 25 30

Ser Phe Ser Arg Ser Asp Asn Leu Val Arg His Gln Arg Thr His Thr
35 40 45

Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser His
50 55 60

Arg Thr Thr Leu Thr Asn His Gln Arg Thr His Thr Gly Glu Lys Pro
65 70 75 80

Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Glu Asp Asn Leu
85 90 95

His Thr His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro
100 105 110

Glu Cys Gly Lys Ser Phe Ser Thr Ser His Ser Leu Thr Glu His Gln
115 120 125

Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys
130 135 140

Ser Phe Ser Gln Ser Ser Ser Leu Val Arg His Gln Arg Thr His Thr
145 150 155 160

```
Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg
                165                 170                 175

Glu Asp Asn Leu His Thr His Gln Arg Thr His Thr Gly Lys Lys Thr
            180                 185                 190

Ser Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys
        195                 200                 205

Lys Gly Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Leu Glu Asp Ala
    210                 215                 220

Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp
225                 230                 235                 240

Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu
                245                 250                 255

Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
            260                 265                 270
```

<210> 102
<211> 272
<212> PRT
<213> Artificial Sequence

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

<400> 102

```
Met Ala Pro Lys Lys Lys Arg Lys Val Gly Ile His Gly Val Pro Ala
1               5                   10                  15

Ala Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys
            20                  25                  30

Ser Phe Ser Arg Ser Asp Asn Leu Val Arg His Gln Arg Thr His Thr
        35                  40                  45

Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg
    50                  55                  60
```

```
Glu Asp Asn Leu His Thr His Gln Arg Thr His Thr Gly Glu Lys Pro
65                  70                  75                  80

Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Ser Asp Glu Leu
                85                  90                  95

Val Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro
            100                 105                 110

Glu Cys Gly Lys Ser Phe Ser Gln Ser Gly Asn Leu Thr Glu His Gln
        115                 120                 125

Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys
    130                 135                 140

Ser Phe Ser Thr Ser Gly His Leu Val Arg His Gln Arg Thr His Thr
145                 150                 155                 160

Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln
                165                 170                 175

Asn Ser Thr Leu Thr Glu His Gln Arg Thr His Thr Gly Lys Lys Thr
            180                 185                 190

Ser Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys
        195                 200                 205

Lys Gly Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Leu Glu Asp Ala
    210                 215                 220

Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp
225                 230                 235                 240

Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu
                245                 250                 255

Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
            260                 265                 270
```

<210> 103
<211> 580

<212> PRT
<213> Artificial Sequence

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

<400> 103
Met Ala Ala Asp His Leu Met Leu Ala Glu Gly Tyr Arg Leu Val Gln
1 5 10 15

Arg Pro Pro Ser Ala Ala Ala Ala His Gly Pro His Ala Leu Arg Thr
20 25 30

Leu Pro Pro Tyr Ala Gly Pro Gly Leu Asp Ser Gly Leu Arg Pro Arg
35 40 45

Gly Ala Pro Leu Gly Pro Pro Pro Pro Arg Gln Pro Gly Ala Leu Ala
50 55 60

Tyr Gly Ala Phe Gly Pro Pro Ser Ser Phe Gln Pro Phe Pro Ala Val
65 70 75 80

Pro Pro Pro Ala Ala Gly Ile Ala His Leu Gln Pro Val Ala Thr Pro
85 90 95

Tyr Pro Gly Arg Ala Ala Ala Pro Pro Asn Ala Pro Gly Gly Pro Pro
100 105 110

Gly Pro Gln Pro Ala Pro Ser Ala Ala Ala Pro Pro Pro Pro Ala His
115 120 125

Ala Leu Gly Gly Met Asp Ala Glu Leu Ile Asp Glu Glu Ala Leu Thr
130 135 140

Ser Leu Glu Leu Glu Leu Gly Leu His Arg Val Arg Glu Leu Pro Glu
145 150 155 160

Leu Phe Leu Gly Gln Ser Glu Phe Asp Cys Phe Ser Asp Leu Gly Ser
165 170 175

Ala Pro Pro Ala Gly Ser Val Ser Cys Gly Gly Ser Gly Gly Gly Ser
180 185 190

```
Gly Gln Ser Gln Leu Ile Lys Pro Ser Arg Met Arg Lys Tyr Pro Asn
        195                 200                 205

Arg Pro Ser Lys Thr Pro Pro His Glu Arg Pro Tyr Ala Cys Pro Val
    210                 215                 220

Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Asn Leu Val Arg His
225                 230                 235                 240

Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met
                245                 250                 255

Arg Asn Phe Ser His Arg Thr Thr Leu Thr Asn His Ile Arg Thr His
            260                 265                 270

Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala
        275                 280                 285

Arg Glu Asp Asn Leu His Thr His Thr Lys Ile His Leu Arg Gln Lys
    290                 295                 300

Asp Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser
305                 310                 315                 320

Thr Ser His Ser Leu Thr Glu His Ile Arg Ile His Thr Gly Gln Lys
                325                 330                 335

Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Gln Ser Ser Ser
            340                 345                 350

Leu Val Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys
        355                 360                 365

Asp Ile Cys Gly Arg Lys Phe Ala Arg Glu Asp Asn Leu His Thr His
    370                 375                 380

Thr Lys Ile His Leu Arg Gln Lys Asp Lys Leu Glu Met Ala Asp His
385                 390                 395                 400
```

```
Leu Met Leu Ala Glu Gly Tyr Arg Leu Val Gln Arg Pro Pro Ser Ala
                405                 410                 415

Ala Ala Ala His Gly Pro His Ala Leu Arg Thr Leu Pro Pro Tyr Ala
            420                 425                 430

Gly Pro Gly Leu Asp Ser Gly Leu Arg Pro Arg Gly Ala Pro Leu Gly
        435                 440                 445

Pro Pro Pro Pro Arg Gln Pro Gly Ala Leu Ala Tyr Gly Ala Phe Gly
    450                 455                 460

Pro Pro Ser Ser Phe Gln Pro Phe Pro Ala Val Pro Pro Pro Ala Ala
465                 470                 475                 480

Gly Ile Ala His Leu Gln Pro Val Ala Thr Pro Tyr Pro Gly Arg Ala
                485                 490                 495

Ala Ala Pro Pro Asn Ala Pro Gly Gly Pro Pro Gly Pro Gln Pro Ala
            500                 505                 510

Pro Ser Ala Ala Ala Pro Pro Pro Pro Ala His Ala Leu Gly Gly Met
        515                 520                 525

Asp Ala Glu Leu Ile Asp Glu Glu Ala Leu Thr Ser Leu Glu Leu Glu
    530                 535                 540

Leu Gly Leu His Arg Val Arg Glu Leu Pro Glu Leu Phe Leu Gly Gln
545                 550                 555                 560

Ser Glu Phe Asp Cys Phe Ser Asp Leu Gly Ser Ala Pro Pro Ala Gly
                565                 570                 575

Ser Val Ser Cys
            580
```

<210> 104
<211> 394
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 104
Met Ala Ala Asp His Leu Met Leu Ala Glu Gly Tyr Arg Leu Val Gln
1 5 10 15

Arg Pro Pro Ser Ala Ala Ala Ala His Gly Pro His Ala Leu Arg Thr
20 25 30

Leu Pro Pro Tyr Ala Gly Pro Gly Leu Asp Ser Gly Leu Arg Pro Arg
35 40 45

Gly Ala Pro Leu Gly Pro Pro Pro Pro Arg Gln Pro Gly Ala Leu Ala
50 55 60

Tyr Gly Ala Phe Gly Pro Pro Ser Ser Phe Gln Pro Phe Pro Ala Val
65 70 75 80

Pro Pro Pro Ala Ala Gly Ile Ala His Leu Gln Pro Val Ala Thr Pro
85 90 95

Tyr Pro Gly Arg Ala Ala Ala Pro Pro Asn Ala Pro Gly Gly Pro Pro
100 105 110

Gly Pro Gln Pro Ala Pro Ser Ala Ala Ala Pro Pro Pro Pro Ala His
115 120 125

Ala Leu Gly Gly Met Asp Ala Glu Leu Ile Asp Glu Glu Ala Leu Thr
130 135 140

Ser Leu Glu Leu Glu Leu Gly Leu His Arg Val Arg Glu Leu Pro Glu
145 150 155 160

Leu Phe Leu Gly Gln Ser Glu Phe Asp Cys Phe Ser Asp Leu Gly Ser
165 170 175

Ala Pro Pro Ala Gly Ser Val Ser Cys Gly Gly Ser Gly Gly Gly Ser
180 185 190

Gly Gln Ser Gln Leu Ile Lys Pro Ser Arg Met Arg Lys Tyr Pro Asn
195 200 205

```
Arg Pro Ser Lys Thr Pro Pro His Glu Arg Pro Tyr Ala Cys Pro Val
    210                 215                 220

Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Asn Leu Val Arg His
225                 230                 235                 240

Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met
                245                 250                 255

Arg Asn Phe Ser His Arg Thr Thr Leu Thr Asn His Ile Arg Thr His
            260                 265                 270

Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala
        275                 280                 285

Arg Glu Asp Asn Leu His Thr His Thr Lys Ile His Leu Arg Gln Lys
    290                 295                 300

Asp Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser
305                 310                 315                 320

Thr Ser His Ser Leu Thr Glu His Ile Arg Ile His Thr Gly Gln Lys
                325                 330                 335

Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Gln Ser Ser Ser
            340                 345                 350

Leu Val Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys
        355                 360                 365

Asp Ile Cys Gly Arg Lys Phe Ala Arg Glu Asp Asn Leu His Thr His
    370                 375                 380

Thr Lys Ile His Leu Arg Gln Lys Asp Lys
385                 390
```

<210> 105
<211> 580
<212> PRT
<213> Artificial Sequence

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

<400> 105
Met Ala Ala Asp His Leu Met Leu Ala Glu Gly Tyr Arg Leu Val Gln
1 5 10 15

Arg Pro Pro Ser Ala Ala Ala Ala His Gly Pro His Ala Leu Arg Thr
20 25 30

Leu Pro Pro Tyr Ala Gly Pro Gly Leu Asp Ser Gly Leu Arg Pro Arg
35 40 45

Gly Ala Pro Leu Gly Pro Pro Pro Arg Gln Pro Gly Ala Leu Ala
50 55 60

Tyr Gly Ala Phe Gly Pro Pro Ser Ser Phe Gln Pro Phe Pro Ala Val
65 70 75 80

Pro Pro Pro Ala Ala Gly Ile Ala His Leu Gln Pro Val Ala Thr Pro
85 90 95

Tyr Pro Gly Arg Ala Ala Ala Pro Pro Asn Ala Pro Gly Gly Pro Pro
100 105 110

Gly Pro Gln Pro Ala Pro Ser Ala Ala Ala Pro Pro Pro Pro Ala His
115 120 125

Ala Leu Gly Gly Met Asp Ala Glu Leu Ile Asp Glu Glu Ala Leu Thr
130 135 140

Ser Leu Glu Leu Glu Leu Gly Leu His Arg Val Arg Glu Leu Pro Glu
145 150 155 160

Leu Phe Leu Gly Gln Ser Glu Phe Asp Cys Phe Ser Asp Leu Gly Ser
165 170 175

Ala Pro Pro Ala Gly Ser Val Ser Cys Gly Gly Ser Gly Gly Gly Ser
180 185 190

```
Gly Gln Ser Gln Leu Ile Lys Pro Ser Arg Met Arg Lys Tyr Pro Asn
        195                 200                 205

Arg Pro Ser Lys Thr Pro Pro His Glu Arg Pro Tyr Ala Cys Pro Val
    210                 215                 220

Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Asn Leu Val Arg His
225                 230                 235                 240

Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met
                245                 250                 255

Arg Asn Phe Ser Arg Glu Asp Asn Leu His Thr His Ile Arg Thr His
            260                 265                 270

Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala
        275                 280                 285

Arg Ser Asp Glu Leu Val Arg His Thr Lys Ile His Leu Arg Gln Lys
    290                 295                 300

Asp Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser
305                 310                 315                 320

Gln Ser Gly Asn Leu Thr Glu His Ile Arg Ile His Thr Gly Gln Lys
                325                 330                 335

Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Thr Ser Gly His
            340                 345                 350

Leu Val Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys
        355                 360                 365

Asp Ile Cys Gly Arg Lys Phe Ala Gln Asn Ser Thr Leu Thr Glu His
    370                 375                 380

Thr Lys Ile His Leu Arg Gln Lys Asp Lys Leu Glu Met Ala Asp His
385                 390                 395                 400

Leu Met Leu Ala Glu Gly Tyr Arg Leu Val Gln Arg Pro Pro Ser Ala
                405                 410                 415
```

```
Ala Ala Ala His Gly Pro His Ala Leu Arg Thr Leu Pro Pro Tyr Ala
            420                 425                 430

Gly Pro Gly Leu Asp Ser Gly Leu Arg Pro Arg Gly Ala Pro Leu Gly
        435                 440                 445

Pro Pro Pro Pro Arg Gln Pro Gly Ala Leu Ala Tyr Gly Ala Phe Gly
    450                 455                 460

Pro Pro Ser Ser Phe Gln Pro Phe Pro Ala Val Pro Pro Pro Ala Ala
465                 470                 475                 480

Gly Ile Ala His Leu Gln Pro Val Ala Thr Pro Tyr Pro Gly Arg Ala
                485                 490                 495

Ala Ala Pro Pro Asn Ala Pro Gly Gly Pro Pro Gly Pro Gln Pro Ala
            500                 505                 510

Pro Ser Ala Ala Ala Pro Pro Pro Pro Ala His Ala Leu Gly Gly Met
        515                 520                 525

Asp Ala Glu Leu Ile Asp Glu Glu Ala Leu Thr Ser Leu Glu Leu Glu
    530                 535                 540

Leu Gly Leu His Arg Val Arg Glu Leu Pro Glu Leu Phe Leu Gly Gln
545                 550                 555                 560

Ser Glu Phe Asp Cys Phe Ser Asp Leu Gly Ser Ala Pro Pro Ala Gly
                565                 570                 575

Ser Val Ser Cys
            580
```

<210> 106
<211> 394
<212> PRT
<213> Artificial Sequence

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

<400> 106
Met Ala Ala Asp His Leu Met Leu Ala Glu Gly Tyr Arg Leu Val Gln
1   5   10   15

Arg Pro Pro Ser Ala Ala Ala Ala His Gly Pro His Ala Leu Arg Thr
            20   25   30

Leu Pro Pro Tyr Ala Gly Pro Gly Leu Asp Ser Gly Leu Arg Pro Arg
        35   40   45

Gly Ala Pro Leu Gly Pro Pro Pro Pro Arg Gln Pro Gly Ala Leu Ala
    50   55   60

Tyr Gly Ala Phe Gly Pro Pro Ser Ser Phe Gln Pro Phe Pro Ala Val
65   70   75   80

Pro Pro Pro Ala Ala Gly Ile Ala His Leu Gln Pro Val Ala Thr Pro
                85   90   95

Tyr Pro Gly Arg Ala Ala Ala Pro Pro Asn Ala Pro Gly Gly Pro Pro
            100   105   110

Gly Pro Gln Pro Ala Pro Ser Ala Ala Ala Pro Pro Pro Pro Ala His
        115   120   125

Ala Leu Gly Gly Met Asp Ala Glu Leu Ile Asp Glu Glu Ala Leu Thr
    130   135   140

Ser Leu Glu Leu Glu Leu Gly Leu His Arg Val Arg Glu Leu Pro Glu
145   150   155   160

Leu Phe Leu Gly Gln Ser Glu Phe Asp Cys Phe Ser Asp Leu Gly Ser
                165   170   175

Ala Pro Pro Ala Gly Ser Val Ser Cys Gly Gly Ser Gly Gly Gly Ser
            180   185   190

Gly Gln Ser Gln Leu Ile Lys Pro Ser Arg Met Arg Lys Tyr Pro Asn
        195   200   205

```
Arg Pro Ser Lys Thr Pro Pro His Glu Arg Pro Tyr Ala Cys Pro Val
    210                 215                 220

Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Asn Leu Val Arg His
225                 230                 235                 240

Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met
                245                 250                 255

Arg Asn Phe Ser Arg Glu Asp Asn Leu His Thr His Ile Arg Thr His
            260                 265                 270

Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala
        275                 280                 285

Arg Ser Asp Glu Leu Val Arg His Thr Lys Ile His Leu Arg Gln Lys
    290                 295                 300

Asp Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser
305                 310                 315                 320

Gln Ser Gly Asn Leu Thr Glu His Ile Arg Ile His Thr Gly Gln Lys
                325                 330                 335

Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Thr Ser Gly His
            340                 345                 350

Leu Val Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys
        355                 360                 365

Asp Ile Cys Gly Arg Lys Phe Ala Gln Asn Ser Thr Leu Thr Glu His
    370                 375                 380

Thr Lys Ile His Leu Arg Gln Lys Asp Lys
385                 390
```

<210> 107
<211> 388
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 107
Met Gln Ser Gln Leu Ile Lys Pro Ser Arg Met Arg Lys Tyr Pro Asn
1 5 10 15

Arg Pro Ser Lys Thr Pro Pro His Glu Arg Pro Tyr Ala Cys Pro Val
20 25 30

Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Asn Leu Val Arg His
35 40 45

Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met
50 55 60

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

Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala
85 90 95

Arg Ser Asp Glu Leu Val Arg His Thr Lys Ile His Leu Arg Gln Lys
100 105 110

Asp Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser
115 120 125

Gln Ser Gly Asn Leu Thr Glu His Ile Arg Ile His Thr Gly Gln Lys
130 135 140

Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Thr Ser Gly His
145 150 155 160

Leu Val Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys
165 170 175

Asp Ile Cys Gly Arg Lys Phe Ala Gln Asn Ser Thr Leu Thr Glu His
180 185 190

Thr Lys Ile His Leu Arg Gln Lys Asp Lys Leu Glu Met Ala Asp His
195 200 205

Leu Met Leu Ala Glu Gly Tyr Arg Leu Val Gln Arg Pro Pro Ser Ala
210 215 220

Ala Ala Ala His Gly Pro His Ala Leu Arg Thr Leu Pro Pro Tyr Ala
225 230 235 240

Gly Pro Gly Leu Asp Ser Gly Leu Arg Pro Arg Gly Ala Pro Leu Gly
245 250 255

Pro Pro Pro Pro Arg Gln Pro Gly Ala Leu Ala Tyr Gly Ala Phe Gly
260 265 270

Pro Pro Ser Ser Phe Gln Pro Phe Pro Ala Val Pro Pro Pro Ala Ala
275 280 285

Gly Ile Ala His Leu Gln Pro Val Ala Thr Pro Tyr Pro Gly Arg Ala
290 295 300

Ala Ala Pro Pro Asn Ala Pro Gly Gly Pro Pro Gly Pro Gln Pro Ala
305 310 315 320

Pro Ser Ala Ala Ala Pro Pro Pro Pro Ala His Ala Leu Gly Gly Met
325 330 335

Asp Ala Glu Leu Ile Asp Glu Glu Ala Leu Thr Ser Leu Glu Leu Glu
340 345 350

Leu Gly Leu His Arg Val Arg Glu Leu Pro Glu Leu Phe Leu Gly Gln
355 360 365

Ser Glu Phe Asp Cys Phe Ser Asp Leu Gly Ser Ala Pro Pro Ala Gly
370 375 380

Ser Val Ser Cys
385

<210> 108
<211> 479
<212> PRT
<213> Artificial Sequence

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

<400> 108
Met Gln Ser Gln Leu Ile Lys Pro Ser Arg Met Arg Lys Tyr Pro Asn
1 5 10 15

Arg Pro Ser Lys Thr Pro Pro His Glu Arg Pro Tyr Ala Cys Pro Val
20 25 30

Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Asn Leu Val Arg His
35 40 45

Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met
50 55 60

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

Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala
85 90 95

Arg Ser Asp Glu Leu Val Arg His Thr Lys Ile His Leu Arg Gln Lys
100 105 110

Asp Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser
115 120 125

Gln Ser Gly Asn Leu Thr Glu His Ile Arg Ile His Thr Gly Gln Lys
130 135 140

Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Thr Ser Gly His
145 150 155 160

Leu Val Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys
165 170 175

Asp Ile Cys Gly Arg Lys Phe Ala Gln Asn Ser Thr Leu Thr Glu His
180 185 190

```
Thr Lys Ile His Leu Arg Gln Lys Asp Lys Leu Glu Met Ser Gly Leu
        195                 200                 205

Glu Met Ala Asp His Met Met Ala Met Asn His Gly Arg Phe Pro Asp
    210                 215                 220

Gly Thr Asn Gly Leu His His His Pro Ala His Arg Met Gly Met Gly
225                 230                 235                 240

Gln Phe Pro Ser Pro His His His Gln Gln Gln Gln Pro Gln His Ala
                245                 250                 255

Phe Asn Ala Leu Met Gly Glu His Ile His Tyr Gly Ala Gly Asn Met
            260                 265                 270

Asn Ala Thr Ser Gly Ile Arg His Ala Met Gly Pro Gly Thr Val Asn
        275                 280                 285

Gly Gly His Pro Pro Ser Ala Leu Ala Pro Ala Ala Arg Phe Asn Asn
    290                 295                 300

Ser Gln Phe Met Gly Pro Pro Val Ala Ser Gln Gly Gly Ser Leu Pro
305                 310                 315                 320

Ala Ser Met Gln Leu Gln Lys Leu Asn Asn Gln Tyr Phe Asn His His
                325                 330                 335

Pro Tyr Pro His Asn His Tyr Met Pro Asp Leu His Pro Ala Ala Gly
            340                 345                 350

His Gln Met Asn Gly Thr Asn Gln His Phe Arg Asp Cys Asn Pro Lys
        355                 360                 365

His Ser Gly Gly Ser Ser Thr Pro Gly Gly Ser Gly Gly Ser Ser Thr
    370                 375                 380

Pro Gly Gly Ser Gly Ser Ser Ser Gly Gly Gly Ala Gly Ser Ser Asn
385                 390                 395                 400

Ser Gly Gly Gly Ser Gly Ser Gly Asn Met Pro Ala Ser Val Ala His
                405                 410                 415
```

Val Pro Ala Ala Met Leu Pro Pro Asn Val Ile Asp Thr Asp Phe Ile
420 425 430

Asp Glu Glu Val Leu Met Ser Leu Val Ile Glu Met Gly Leu Asp Arg
435 440 445

Ile Lys Glu Leu Pro Glu Leu Trp Leu Gly Gln Asn Glu Phe Asp Phe
450 455 460

Met Thr Asp Phe Val Cys Lys Gln Gln Pro Ser Arg Val Ser Cys
465 470 475

<210> 109
<211> 476
<212> PRT
<213> Artificial Sequence

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

<400> 109
Met Ser Gly Leu Glu Met Ala Asp His Met Met Ala Met Asn His Gly
1 5 10 15

Arg Phe Pro Asp Gly Thr Asn Gly Leu His His His Pro Ala His Arg
20 25 30

Met Gly Met Gly Gln Phe Pro Ser Pro His His His Gln Gln Gln Gln
35 40 45

Pro Gln His Ala Phe Asn Ala Leu Met Gly Glu His Ile His Tyr Gly
50 55 60

Ala Gly Asn Met Asn Ala Thr Ser Gly Val Arg His Ala Met Gly Pro
65 70 75 80

Gly Thr Val Asn Gly Gly His Pro Pro Ser Ala Leu Ala Pro Ala Ala
85 90 95

Arg Phe Asn Asn Ser Gln Phe Met Gly Pro Pro Val Ala Ser Gln Gly
100 105 110

```
Gly Ser Leu Pro Ala Ser Met Gln Leu Gln Lys Leu Asn Asn Gln Tyr
        115                 120                 125

Phe Asn His His Pro Tyr Pro His Asn His Tyr Met Pro Asp Leu His
    130                 135                 140

Pro Ala Ala Gly His Gln Met Asn Gly Thr Asn Gln His Phe Arg Asp
145                 150                 155                 160

Cys Asn Pro Lys His Ser Gly Gly Ser Ser Thr Pro Gly Gly Ser Gly
                165                 170                 175

Gly Ser Ser Thr Pro Gly Gly Ser Gly Ser Ser Ser Gly Gly Gly Ala
            180                 185                 190

Gly Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gly Asn Met Pro Ala
        195                 200                 205

Ser Val Ala His Val Pro Ala Ala Met Leu Pro Pro Asn Val Ile Asp
    210                 215                 220

Thr Asp Phe Ile Asp Glu Glu Val Leu Met Ser Leu Val Ile Glu Met
225                 230                 235                 240

Gly Leu Asp Arg Ile Lys Glu Leu Pro Glu Leu Trp Leu Gly Gln Asn
                245                 250                 255

Glu Phe Asp Phe Met Thr Asp Phe Val Cys Lys Gln Gln Pro Ser Arg
            260                 265                 270

Val Ser Cys Gln Ser Gln Leu Ile Lys Pro Ser Arg Met Arg Lys Tyr
        275                 280                 285

Pro Asn Arg Pro Ser Lys Thr Pro Pro His Glu Arg Pro Tyr Ala Cys
    290                 295                 300

Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Asn Leu Val
305                 310                 315                 320
```

```
Arg His Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile
                325                 330                 335

Cys Met Arg Asn Phe Ser Arg Glu Asp Asn Leu His Thr His Ile Arg
            340                 345                 350

Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys
        355                 360                 365

Phe Ala Arg Ser Asp Glu Leu Val Arg His Thr Lys Ile His Leu Arg
    370                 375                 380

Gln Lys Asp Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg
385                 390                 395                 400

Phe Ser Gln Ser Gly Asn Leu Thr Glu His Ile Arg Ile His Thr Gly
                405                 410                 415

Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Thr Ser
            420                 425                 430

Gly His Leu Val Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
        435                 440                 445

Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Gln Asn Ser Thr Leu Thr
    450                 455                 460

Glu His Thr Lys Ile His Leu Arg Gln Lys Asp Lys
465                 470                 475
```

<210> 110
<211> 554
<212> PRT
<213> Artificial Sequence

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

<400> 110

```
Met Ala Ala Asp His Leu Met Leu Ala Glu Gly Tyr Arg Leu Val Gln
1               5                   10                  15
```

```
Arg Pro Pro Ser Ala Ala Ala Ala His Gly Pro His Ala Leu Arg Thr
            20                  25                  30

Leu Pro Pro Tyr Ala Gly Pro Gly Leu Asp Ser Gly Leu Arg Pro Arg
        35                  40                  45

Gly Ala Pro Leu Gly Pro Pro Pro Pro Arg Gln Pro Gly Ala Leu Ala
    50                  55                  60

Tyr Gly Ala Phe Gly Pro Pro Ser Ser Phe Gln Pro Phe Pro Ala Val
65                  70                  75                  80

Pro Pro Pro Ala Ala Gly Ile Ala His Leu Gln Pro Val Ala Thr Pro
                85                  90                  95

Tyr Pro Gly Arg Ala Ala Ala Pro Pro Asn Ala Pro Gly Gly Pro Pro
            100                 105                 110

Gly Pro Gln Pro Ala Pro Ser Ala Ala Ala Pro Pro Pro Pro Ala His
        115                 120                 125

Ala Leu Gly Gly Met Asp Ala Glu Leu Ile Asp Glu Glu Ala Leu Thr
    130                 135                 140

Ser Leu Glu Leu Glu Leu Gly Leu His Arg Val Arg Glu Leu Pro Glu
145                 150                 155                 160

Leu Phe Leu Gly Gln Ser Glu Phe Asp Cys Phe Ser Asp Leu Gly Ser
                165                 170                 175

Ala Pro Pro Ala Gly Ser Val Ser Cys Gly Gly Ser Gly Gly Gly Ser
            180                 185                 190

Gly Arg Pro His Ala Cys Pro Ala Glu Gly Cys Asp Arg Arg Phe Ser
        195                 200                 205

Arg Ser Asp Asn Leu Val Arg His Leu Arg Ile His Thr Gly His Lys
    210                 215                 220

Pro Phe Gln Cys Arg Ile Cys Met Arg Ser Phe Ser Arg Glu Asp Asn
225                 230                 235                 240
```

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

Glu Phe Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Leu Val Arg His
            260                 265                 270

Ala Lys Ile His Leu Lys Gln Lys Glu His Ala Cys Pro Ala Glu Gly
        275                 280                 285

Cys Asp Arg Arg Phe Ser Gln Ser Gly Asn Leu Thr Glu His Leu Arg
    290                 295                 300

Ile His Thr Gly His Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Ser
305                 310                 315                 320

Phe Ser Thr Ser Gly His Leu Val Arg His Ile Arg Thr His Thr Gly
                325                 330                 335

Glu Lys Pro Phe Ala Cys Glu Phe Cys Gly Arg Lys Phe Ala Gln Asn
            340                 345                 350

Ser Thr Leu Thr Glu His Ala Lys Ile His Leu Lys Gln Lys Glu Lys
        355                 360                 365

Leu Glu Met Ala Asp His Leu Met Leu Ala Glu Gly Tyr Arg Leu Val
    370                 375                 380

Gln Arg Pro Pro Ser Ala Ala Ala Ala His Gly Pro His Ala Leu Arg
385                 390                 395                 400

Thr Leu Pro Pro Tyr Ala Gly Pro Gly Leu Asp Ser Gly Leu Arg Pro
                405                 410                 415

Arg Gly Ala Pro Leu Gly Pro Pro Pro Pro Arg Gln Pro Gly Ala Leu
            420                 425                 430

Ala Tyr Gly Ala Phe Gly Pro Pro Ser Ser Phe Gln Pro Phe Pro Ala
        435                 440                 445
```

Val Pro Pro Pro Ala Ala Gly Ile Ala His Leu Gln Pro Val Ala Thr
450 455 460

Pro Tyr Pro Gly Arg Ala Ala Ala Pro Pro Asn Ala Pro Gly Gly Pro
465 470 475 480

Pro Gly Pro Gln Pro Ala Pro Ser Ala Ala Ala Pro Pro Pro Pro Ala
485 490 495

His Ala Leu Gly Gly Met Asp Ala Glu Leu Ile Asp Glu Glu Ala Leu
500 505 510

Thr Ser Leu Glu Leu Glu Leu Gly Leu His Arg Val Arg Glu Leu Pro
515 520 525

Glu Leu Phe Leu Gly Gln Ser Glu Phe Asp Cys Phe Ser Asp Leu Gly
530 535 540

Ser Ala Pro Pro Ala Gly Ser Val Ser Cys
545 550

<210> 111
<211> 362
<212> PRT
<213> Artificial Sequence

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

<400> 111
Met Arg Pro His Ala Cys Pro Ala Glu Gly Cys Asp Arg Arg Phe Ser
1 5 10 15

Arg Ser Asp Asn Leu Val Arg His Leu Arg Ile His Thr Gly His Lys
20 25 30

Pro Phe Gln Cys Arg Ile Cys Met Arg Ser Phe Ser Arg Glu Asp Asn
35 40 45

Leu His Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys
50 55 60

```
Glu Phe Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Leu Val Arg His
65                  70                  75                  80

Ala Lys Ile His Leu Lys Gln Lys Glu His Ala Cys Pro Ala Glu Gly
                85                  90                  95

Cys Asp Arg Arg Phe Ser Gln Ser Gly Asn Leu Thr Glu His Leu Arg
            100                 105                 110

Ile His Thr Gly His Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Ser
        115                 120                 125

Phe Ser Thr Ser Gly His Leu Val Arg His Ile Arg Thr His Thr Gly
    130                 135                 140

Glu Lys Pro Phe Ala Cys Glu Phe Cys Gly Arg Lys Phe Ala Gln Asn
145                 150                 155                 160

Ser Thr Leu Thr Glu His Ala Lys Ile His Leu Lys Gln Lys Glu Lys
                165                 170                 175

Leu Glu Met Ala Asp His Leu Met Leu Ala Glu Gly Tyr Arg Leu Val
            180                 185                 190

Gln Arg Pro Pro Ser Ala Ala Ala Ala His Gly Pro His Ala Leu Arg
        195                 200                 205

Thr Leu Pro Pro Tyr Ala Gly Pro Gly Leu Asp Ser Gly Leu Arg Pro
    210                 215                 220

Arg Gly Ala Pro Leu Gly Pro Pro Pro Pro Arg Gln Pro Gly Ala Leu
225                 230                 235                 240

Ala Tyr Gly Ala Phe Gly Pro Pro Ser Ser Phe Gln Pro Phe Pro Ala
                245                 250                 255

Val Pro Pro Pro Ala Ala Gly Ile Ala His Leu Gln Pro Val Ala Thr
            260                 265                 270

Pro Tyr Pro Gly Arg Ala Ala Ala Pro Pro Asn Ala Pro Gly Gly Pro
        275                 280                 285
```

Pro Gly Pro Gln Pro Ala Pro Ser Ala Ala Ala Pro Pro Pro Pro Ala
290 295 300

His Ala Leu Gly Gly Met Asp Ala Glu Leu Ile Asp Glu Glu Ala Leu
305 310 315 320

Thr Ser Leu Glu Leu Glu Leu Gly Leu His Arg Val Arg Glu Leu Pro
325 330 335

Glu Leu Phe Leu Gly Gln Ser Glu Phe Asp Cys Phe Ser Asp Leu Gly
340 345 350

Ser Ala Pro Pro Ala Gly Ser Val Ser Cys
355 360

<210> 112
<211> 479
<212> PRT
<213> Artificial Sequence

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

<400> 112
Met Arg Pro His Ala Cys Pro Ala Glu Gly Cys Asp Arg Arg Phe Ser
1 5 10 15

Arg Ser Asp Asn Leu Val Arg His Leu Arg Ile His Thr Gly His Lys
20 25 30

Pro Phe Gln Cys Arg Ile Cys Met Arg Ser Phe Ser Arg Glu Asp Asn
35 40 45

Leu His Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys
50 55 60

Glu Phe Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Leu Val Arg His
65 70 75 80

Ala Lys Ile His Leu Lys Gln Lys Glu His Ala Cys Pro Ala Glu Gly
85 90 95

```
Cys Asp Arg Arg Phe Ser Gln Ser Gly Asn Leu Thr Glu His Leu Arg
            100                 105                 110

Ile His Thr Gly His Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Ser
        115                 120                 125

Phe Ser Thr Ser Gly His Leu Val Arg His Ile Arg Thr His Thr Gly
    130                 135                 140

Glu Lys Pro Phe Ala Cys Glu Phe Cys Gly Arg Lys Phe Ala Gln Asn
145                 150                 155                 160

Ser Thr Leu Thr Glu His Ala Lys Ile His Leu Lys Gln Lys Glu Lys
                165                 170                 175

Lys Ala Glu Lys Gly Gly Ala Pro Ser Ala Ser Ser Ala Pro Pro Val
            180                 185                 190

Ser Leu Ala Pro Val Val Thr Thr Cys Ala Leu Glu Met Ser Gly Leu
        195                 200                 205

Glu Met Ala Asp His Met Met Ala Met Asn His Gly Arg Phe Pro Asp
    210                 215                 220

Gly Thr Asn Gly Leu His His His Pro Ala His Arg Met Gly Met Gly
225                 230                 235                 240

Gln Phe Pro Ser Pro His His His Gln Gln Gln Gln Pro Gln His Ala
                245                 250                 255

Phe Asn Ala Leu Met Gly Glu His Ile His Tyr Gly Ala Gly Asn Met
            260                 265                 270

Asn Ala Thr Ser Gly Ile Arg His Ala Met Gly Pro Gly Thr Val Asn
        275                 280                 285

Gly Gly His Pro Pro Ser Ala Leu Ala Pro Ala Ala Arg Phe Asn Asn
    290                 295                 300
```

```
Ser Gln Phe Met Gly Pro Pro Val Ala Ser Gln Gly Gly Ser Leu Pro
305                 310                 315                 320

Ala Ser Met Gln Leu Gln Lys Leu Asn Asn Gln Tyr Phe Asn His His
                325                 330                 335

Pro Tyr Pro His Asn His Tyr Met Pro Asp Leu His Pro Ala Ala Gly
            340                 345                 350

His Gln Met Asn Gly Thr Asn Gln His Phe Arg Asp Cys Asn Pro Lys
        355                 360                 365

His Ser Gly Gly Ser Ser Thr Pro Gly Gly Ser Gly Gly Ser Ser Thr
    370                 375                 380

Pro Gly Gly Ser Gly Ser Ser Ser Gly Gly Gly Ala Gly Ser Ser Asn
385                 390                 395                 400

Ser Gly Gly Gly Ser Gly Ser Gly Asn Met Pro Ala Ser Val Ala His
                405                 410                 415

Val Pro Ala Ala Met Leu Pro Pro Asn Val Ile Asp Thr Asp Phe Ile
            420                 425                 430

Asp Glu Glu Val Leu Met Ser Leu Val Ile Glu Met Gly Leu Asp Arg
        435                 440                 445

Ile Lys Glu Leu Pro Glu Leu Trp Leu Gly Gln Asn Glu Phe Asp Phe
    450                 455                 460

Met Thr Asp Phe Val Cys Lys Gln Gln Pro Ser Arg Val Ser Cys
465                 470                 475
```

<210> 113
<211> 476
<212> PRT
<213> Artificial Sequence

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

<400> 113

```
Met Ser Gly Leu Glu Met Ala Asp His Met Met Ala Met Asn His Gly
1               5                  10                  15

Arg Phe Pro Asp Gly Thr Asn Gly Leu His His His Pro Ala His Arg
            20                  25                  30

Met Gly Met Gly Gln Phe Pro Ser Pro His His His Gln Gln Gln Gln
        35                  40                  45

Pro Gln His Ala Phe Asn Ala Leu Met Gly Glu His Ile His Tyr Gly
    50                  55                  60

Ala Gly Asn Met Asn Ala Thr Ser Gly Val Arg His Ala Met Gly Pro
65                  70                  75                  80

Gly Thr Val Asn Gly Gly His Pro Pro Ser Ala Leu Ala Pro Ala Ala
                85                  90                  95

Arg Phe Asn Asn Ser Gln Phe Met Gly Pro Pro Val Ala Ser Gln Gly
            100                 105                 110

Gly Ser Leu Pro Ala Ser Met Gln Leu Gln Lys Leu Asn Asn Gln Tyr
        115                 120                 125

Phe Asn His His Pro Tyr Pro His Asn His Tyr Met Pro Asp Leu His
    130                 135                 140

Pro Ala Ala Gly His Gln Met Asn Gly Thr Asn Gln His Phe Arg Asp
145                 150                 155                 160

Cys Asn Pro Lys His Ser Gly Gly Ser Ser Thr Pro Gly Gly Ser Gly
                165                 170                 175

Gly Ser Ser Thr Pro Gly Gly Ser Gly Ser Ser Ser Gly Gly Gly Ala
            180                 185                 190

Gly Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gly Asn Met Pro Ala
        195                 200                 205

Ser Val Ala His Val Pro Ala Ala Met Leu Pro Pro Asn Val Ile Asp
    210                 215                 220
```

```
Thr Asp Phe Ile Asp Glu Glu Val Leu Met Ser Leu Val Ile Glu Met
225                 230                 235                 240


Gly Leu Asp Arg Ile Lys Glu Leu Pro Glu Leu Trp Leu Gly Gln Asn
                245                 250                 255


Glu Phe Asp Phe Met Thr Asp Phe Val Cys Lys Gln Gln Pro Ser Arg
            260                 265                 270


Val Ser Cys Arg Pro His Ala Cys Pro Ala Glu Gly Cys Asp Arg Arg
        275                 280                 285


Phe Ser Arg Ser Asp Asn Leu Val Arg His Leu Arg Ile His Thr Gly
    290                 295                 300


His Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Ser Phe Ser Arg Glu
305                 310                 315                 320


Asp Asn Leu His Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
                325                 330                 335


Ala Cys Glu Phe Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Leu Val
            340                 345                 350


Arg His Ala Lys Ile His Leu Lys Gln Lys Glu His Ala Cys Pro Ala
        355                 360                 365


Glu Gly Cys Asp Arg Arg Phe Ser Gln Ser Gly Asn Leu Thr Glu His
    370                 375                 380


Leu Arg Ile His Thr Gly His Lys Pro Phe Gln Cys Arg Ile Cys Met
385                 390                 395                 400


Arg Ser Phe Ser Thr Ser Gly His Leu Val Arg His Ile Arg Thr His
                405                 410                 415


Thr Gly Glu Lys Pro Phe Ala Cys Glu Phe Cys Gly Arg Lys Phe Ala
            420                 425                 430
```

```
Gln Asn Ser Thr Leu Thr Glu His Ala Lys Ile His Leu Lys Gln Lys
        435                 440                 445


Glu Lys Lys Ala Glu Lys Gly Gly Ala Pro Ser Ala Ser Ser Ala Pro
    450                 455                 460


Pro Val Ser Leu Ala Pro Val Val Thr Thr Cys Ala
465                 470                 475


<210> 114
<211> 559
<212> PRT
<213> Artificial Sequence

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

<400> 114
Met Thr Gly Lys Leu Ala Glu Lys Leu Pro Val Thr Met Ser Ser Leu
1               5                   10                  15


Leu Asn Gln Leu Pro Asp Asn Leu Tyr Pro Glu Glu Ile Pro Ser Ala
            20                  25                  30


Leu Asn Leu Phe Ser Gly Ser Ser Asp Ser Val Val His Tyr Asn Gln
        35                  40                  45


Met Ala Thr Glu Asn Val Met Asp Ile Gly Leu Thr Asn Glu Lys Pro
    50                  55                  60


Asn Pro Glu Leu Ser Tyr Ser Gly Ser Phe Gln Pro Ala Pro Gly Asn
65                  70                  75                  80


Lys Thr Val Thr Tyr Leu Gly Lys Phe Ala Phe Asp Ser Pro Ser Asn
                85                  90                  95


Trp Cys Gln Asp Asn Ile Ile Ser Leu Met Ser Ala Gly Ile Leu Gly
            100                 105                 110


Val Pro Pro Ala Ser Gly Ala Leu Ser Thr Gln Thr Ser Thr Ala Ser
        115                 120                 125
```

```
Met Val Gln Pro Pro Gln Gly Asp Val Glu Ala Met Tyr Pro Ala Leu
    130                 135                 140

Pro Pro Tyr Ser Asn Cys Gly Asp Leu Tyr Ser Glu Pro Val Ser Phe
145                 150                 155                 160

His Asp Pro Gln Gly Asn Pro Gly Leu Ala Tyr Ser Pro Gln Asp Tyr
                165                 170                 175

Gln Ser Ala Lys Pro Ala Leu Asp Ser Asn Leu Phe Pro Met Ile Pro
            180                 185                 190

Asp Tyr Asn Leu Tyr His His Pro Asn Asp Met Gly Ser Ile Pro Glu
        195                 200                 205

His Lys Pro Phe Gln Gly Met Asp Pro Ile Arg Val Asn Pro Pro Pro
    210                 215                 220

Ile Thr Pro Leu Glu Thr Ile Lys Ala Phe Lys Asp Lys Gln Ile His
225                 230                 235                 240

Pro Gly Phe Gly Ser Leu Pro Gln Pro Pro Leu Thr Leu Lys Pro Ile
                245                 250                 255

Arg Pro Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Leu His Glu
            260                 265                 270

Arg Pro His Ala Cys Pro Ala Glu Gly Cys Asp Arg Arg Phe Ser Arg
        275                 280                 285

Arg Asp Glu Leu Asn Val His Leu Arg Ile His Thr Gly His Lys Pro
    290                 295                 300

Phe Gln Cys Arg Ile Cys Met Arg Ser Phe Ser Arg Ser Asp His Leu
305                 310                 315                 320

Thr Asn His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Glu
                325                 330                 335

Phe Cys Gly Arg Lys Phe Ala Arg Ser Asp Asp Leu Val Arg His Ala
            340                 345                 350
```

```
Lys Ile His Leu Lys Gln Lys Glu His Ala Cys Pro Ala Glu Gly Cys
        355                 360                 365

Asp Arg Arg Phe Ser Arg Ser Asp Asn Leu Val Arg His Leu Arg Ile
    370                 375                 380

His Thr Gly His Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Ser Phe
385                 390                 395                 400

Ser His Arg Thr Thr Leu Thr Asn His Ile Arg Thr His Thr Gly Glu
                405                 410                 415

Lys Pro Phe Ala Cys Glu Phe Cys Gly Arg Lys Phe Ala Arg Glu Asp
            420                 425                 430

Asn Leu His Thr His Ala Lys Ile His Leu Lys Gln Lys Glu His Ala
        435                 440                 445

Cys Pro Ala Glu Gly Cys Asp Arg Arg Phe Ser Thr Ser His Ser Leu
    450                 455                 460

Thr Glu His Leu Arg Ile His Thr Gly His Lys Pro Phe Gln Cys Arg
465                 470                 475                 480

Ile Cys Met Arg Ser Phe Ser Gln Ser Ser Ser Leu Val Arg His Ile
                485                 490                 495

Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Glu Phe Cys Gly Arg
            500                 505                 510

Lys Phe Ala Arg Glu Asp Asn Leu His Thr His Ala Lys Ile His Leu
        515                 520                 525

Lys Gln Lys Glu Lys Lys Ala Glu Lys Gly Gly Ala Pro Ser Ala Ser
    530                 535                 540

Ser Ala Pro Pro Val Ser Leu Ala Pro Val Val Thr Thr Cys Ala
545                 550                 555
```

<210> 115
<211> 631
<212> PRT
<213> Artificial Sequence

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

<400> 115
Met Ala Ala Ala Lys Ala Glu Met Gln Leu Met Ser Pro Leu Gln Ile
1 5 10 15

Ser Asp Pro Phe Gly Ser Phe Pro His Ser Pro Thr Met Asp Asn Tyr
20 25 30

Pro Lys Leu Glu Glu Met Met Leu Leu Ser Asn Gly Ala Pro Gln Phe
35 40 45

Leu Gly Ala Ala Gly Ala Pro Glu Gly Ser Gly Ser Asn Ser Ser Ser
50 55 60

Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Ser Asn Ser Ser
65 70 75 80

Ser Ser Ser Ser Thr Phe Asn Pro Gln Ala Asp Thr Gly Glu Gln Pro
85 90 95

Tyr Glu His Leu Thr Ala Glu Ser Phe Pro Asp Ile Ser Leu Asn Asn
100 105 110

Glu Lys Val Leu Val Glu Thr Ser Tyr Pro Ser Gln Thr Thr Arg Leu
115 120 125

Pro Pro Ile Thr Tyr Thr Gly Arg Phe Ser Leu Glu Pro Ala Pro Asn
130 135 140

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

Leu Val Ser Met Thr Asn Pro Pro Ala Ser Ser Ser Ser Ala Pro Ser
165 170 175

```
Pro Ala Ala Ser Ser Ala Ser Ala Ser Gln Ser Pro Pro Leu Ser Cys
            180                 185                 190

Ala Val Pro Ser Asn Asp Ser Ser Pro Ile Tyr Ser Ala Ala Pro Thr
        195                 200                 205

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

Phe Pro Gly Ser Ala Gly Thr Ala Leu Gln Tyr Pro Pro Pro Ala Tyr
225                 230                 235                 240

Pro Ala Ala Lys Gly Gly Phe Gln Val Pro Met Ile Pro Asp Tyr Leu
                245                 250                 255

Phe Pro Gln Gln Gln Gly Asp Leu Gly Leu Gly Thr Pro Asp Gln Lys
            260                 265                 270

Pro Phe Gln Gly Leu Glu Ser Arg Thr Gln Gln Pro Ser Leu Thr Pro
        275                 280                 285

Leu Ser Thr Ile Lys Ala Phe Ala Thr Gln Ser Gly Ser Gln Asp Leu
    290                 295                 300

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

Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Pro His Glu Arg
                325                 330                 335

Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser
            340                 345                 350

Asp Asn Leu Val Arg His Ile Arg Ile His Thr Gly Gln Lys Pro Phe
        355                 360                 365

Gln Cys Arg Ile Cys Met Arg Asn Phe Ser His Arg Thr Thr Leu Thr
    370                 375                 380

Asn His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile
385                 390                 395                 400
```

```
Cys Gly Arg Lys Phe Ala Arg Glu Asp Asn Leu His Thr His Thr Lys
                405                 410                 415

Ile His Leu Arg Gln Lys Asp Arg Pro Tyr Ala Cys Pro Val Glu Ser
            420                 425                 430

Cys Asp Arg Arg Phe Ser Thr Ser His Ser Leu Thr Glu His Ile Arg
        435                 440                 445

Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn
    450                 455                 460

Phe Ser Gln Ser Ser Ser Leu Val Arg His Ile Arg Thr His Thr Gly
465                 470                 475                 480

Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Glu
                485                 490                 495

Asp Asn Leu His Thr His Thr Lys Ile His Leu Arg Gln Lys Asp Lys
            500                 505                 510

Lys Ala Asp Lys Ser Val Val Ala Ser Ser Ala Thr Ser Ser Leu Ser
        515                 520                 525

Ser Tyr Pro Ser Pro Val Ala Thr Ser Tyr Pro Ser Pro Val Thr Thr
    530                 535                 540

Ser Tyr Pro Ser Pro Ala Thr Thr Ser Tyr Pro Ser Pro Val Pro Thr
545                 550                 555                 560

Ser Phe Ser Ser Pro Gly Ser Ser Thr Tyr Pro Ser Pro Val His Ser
                565                 570                 575

Gly Phe Pro Ser Pro Ser Val Ala Thr Thr Tyr Ser Ser Val Pro Pro
            580                 585                 590

Ala Phe Pro Ala Gln Val Ser Ser Phe Pro Ser Ser Ala Val Thr Asn
        595                 600                 605
```

Ser Phe Ser Ala Ser Thr Gly Leu Ser Asp Met Thr Ala Thr Phe Ser
610 615 620

Pro Arg Thr Ile Glu Ile Cys
625 630

<210> 116
<211> 719
<212> PRT
<213> Artificial Sequence

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

<400> 116
Met Ala Ala Ala Lys Ala Glu Met Gln Leu Met Ser Pro Leu Gln Ile
1 5 10 15

Ser Asp Pro Phe Gly Ser Phe Pro His Ser Pro Thr Met Asp Asn Tyr
20 25 30

Pro Lys Leu Glu Glu Met Met Leu Leu Ser Asn Gly Ala Pro Gln Phe
35 40 45

Leu Gly Ala Ala Gly Ala Pro Glu Gly Ser Gly Ser Asn Ser Ser Ser
50 55 60

Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Ser Asn Ser Ser
65 70 75 80

Ser Ser Ser Ser Thr Phe Asn Pro Gln Ala Asp Thr Gly Glu Gln Pro
85 90 95

Tyr Glu His Leu Thr Ala Glu Ser Phe Pro Asp Ile Ser Leu Asn Asn
100 105 110

Glu Lys Val Leu Val Glu Thr Ser Tyr Pro Ser Gln Thr Thr Arg Leu
115 120 125

Pro Pro Ile Thr Tyr Thr Gly Arg Phe Ser Leu Glu Pro Ala Pro Asn
130 135 140

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

Leu Val Ser Met Thr Asn Pro Pro Ala Ser Ser Ser Ser Ala Pro Ser
                165                 170                 175

Pro Ala Ala Ser Ser Ala Ser Ala Ser Gln Ser Pro Pro Leu Ser Cys
            180                 185                 190

Ala Val Pro Ser Asn Asp Ser Ser Pro Ile Tyr Ser Ala Ala Pro Thr
        195                 200                 205

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

Phe Pro Gly Ser Ala Gly Thr Ala Leu Gln Tyr Pro Pro Pro Ala Tyr
225                 230                 235                 240

Pro Ala Ala Lys Gly Gly Phe Gln Val Pro Met Ile Pro Asp Tyr Leu
                245                 250                 255

Phe Pro Gln Gln Gln Gly Asp Leu Gly Leu Gly Thr Pro Asp Gln Lys
            260                 265                 270

Pro Phe Gln Gly Leu Glu Ser Arg Thr Gln Gln Pro Ser Leu Thr Pro
        275                 280                 285

Leu Ser Thr Ile Lys Ala Phe Ala Thr Gln Ser Gly Ser Gln Asp Leu
    290                 295                 300

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

Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Pro His Glu Arg
                325                 330                 335

Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Arg
            340                 345                 350

Asp Glu Leu Asn Val His Ile Arg Ile His Thr Gly Gln Lys Pro Phe
        355                 360                 365
```

```
Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu Thr
    370                 375                 380

Asn His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile
385                 390                 395                 400

Cys Gly Arg Lys Phe Ala Arg Ser Asp Asp Leu Val Arg His Thr Lys
                405                 410                 415

Ile His Leu Arg Gln Lys Asp Arg Pro Tyr Ala Cys Pro Val Glu Ser
            420                 425                 430

Cys Asp Arg Arg Phe Ser Arg Ser Asp Asn Leu Val Arg His Ile Arg
        435                 440                 445

Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn
    450                 455                 460

Phe Ser His Arg Thr Thr Leu Thr Asn His Ile Arg Thr His Thr Gly
465                 470                 475                 480

Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Glu
                485                 490                 495

Asp Asn Leu His Thr His Thr Lys Ile His Leu Arg Gln Lys Asp Arg
            500                 505                 510

Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Thr Ser
        515                 520                 525

His Ser Leu Thr Glu His Ile Arg Ile His Thr Gly Gln Lys Pro Phe
    530                 535                 540

Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Gln Ser Ser Ser Leu Val
545                 550                 555                 560

Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile
                565                 570                 575
```

```
Cys Gly Arg Lys Phe Ala Arg Glu Asp Asn Leu His Thr His Thr Lys
            580                 585                 590

Ile His Leu Arg Gln Lys Asp Lys Lys Ala Asp Lys Ser Val Val Ala
        595                 600                 605

Ser Ser Ala Thr Ser Ser Leu Ser Ser Tyr Pro Ser Pro Val Ala Thr
    610                 615                 620

Ser Tyr Pro Ser Pro Val Thr Thr Ser Tyr Pro Ser Pro Ala Thr Thr
625                 630                 635                 640

Ser Tyr Pro Ser Pro Val Pro Thr Ser Phe Ser Ser Pro Gly Ser Ser
                645                 650                 655

Thr Tyr Pro Ser Pro Val His Ser Gly Phe Pro Ser Pro Ser Val Ala
            660                 665                 670

Thr Thr Tyr Ser Ser Val Pro Pro Ala Phe Pro Ala Gln Val Ser Ser
        675                 680                 685

Phe Pro Ser Ser Ala Val Thr Asn Ser Phe Ser Ala Ser Thr Gly Leu
    690                 695                 700

Ser Asp Met Thr Ala Thr Phe Ser Pro Arg Thr Ile Glu Ile Cys
705                 710                 715


<210> 117
<211> 627
<212> PRT
<213> Artificial Sequence

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

<400> 117
Met Ala Ala Ala Lys Ala Glu Met Gln Leu Met Ser Pro Leu Gln Ile
1               5                   10                  15

Ser Asp Pro Phe Gly Ser Phe Pro His Ser Pro Thr Met Asp Asn Tyr
            20                  25                  30
```

```
Pro Lys Leu Glu Glu Met Met Leu Leu Ser Asn Gly Ala Pro Gln Phe
        35                  40                  45

Leu Gly Ala Ala Gly Ala Pro Glu Gly Ser Gly Ser Asn Ser Ser Ser
    50                  55                  60

Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Ser Asn Ser Ser
65                  70                  75                  80

Ser Ser Ser Ser Thr Phe Asn Pro Gln Ala Asp Thr Gly Glu Gln Pro
                85                  90                  95

Tyr Glu His Leu Thr Ala Glu Ser Phe Pro Asp Ile Ser Leu Asn Asn
            100                 105                 110

Glu Lys Val Leu Val Glu Thr Ser Tyr Pro Ser Gln Thr Thr Arg Leu
        115                 120                 125

Pro Pro Ile Thr Tyr Thr Gly Arg Phe Ser Leu Glu Pro Ala Pro Asn
    130                 135                 140

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

Leu Val Ser Met Thr Asn Pro Pro Ala Ser Ser Ser Ser Ala Pro Ser
                165                 170                 175

Pro Ala Ala Ser Ser Ala Ser Ala Ser Gln Ser Pro Pro Leu Ser Cys
            180                 185                 190

Ala Val Pro Ser Asn Asp Ser Ser Pro Ile Tyr Ser Ala Ala Pro Thr
        195                 200                 205

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

Phe Pro Gly Ser Ala Gly Thr Ala Leu Gln Tyr Pro Pro Pro Ala Tyr
225                 230                 235                 240

Pro Ala Ala Lys Gly Gly Phe Gln Val Pro Met Ile Pro Asp Tyr Leu
                245                 250                 255
```

```
Phe Pro Gln Gln Gln Gly Asp Leu Gly Leu Gly Thr Pro Asp Gln Lys
            260                 265                 270

Pro Phe Gln Gly Leu Glu Ser Arg Thr Gln Gln Pro Ser Leu Thr Pro
        275                 280                 285

Leu Ser Thr Ile Lys Ala Phe Ala Thr Gln Ser Gly Ser Gln Asp Leu
    290                 295                 300

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

Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Pro His Glu Arg
                325                 330                 335

Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser
            340                 345                 350

Asp Asn Leu Val Arg His Ile Arg Ile His Thr Gly Gln Lys Pro Phe
        355                 360                 365

Gln Cys Arg Ile Cys Met Arg Asn Phe Ser His Arg Thr Thr Leu Thr
    370                 375                 380

Asn His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile
385                 390                 395                 400

Cys Gly Arg Lys Phe Ala Arg Glu Asp Asn Leu His Thr His Ile Arg
                405                 410                 415

Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys
            420                 425                 430

Phe Ser Thr Ser His Ser Leu Thr Glu His Ile Arg Ile His Thr Gly
        435                 440                 445

Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Gln Ser
    450                 455                 460
```

```
Ser Ser Leu Val Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
465                 470                 475                 480


Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Glu Asp Asn Leu His
                485                 490                 495


Thr His Thr Lys Ile His Leu Arg Gln Lys Asp Lys Lys Ala Asp Lys
            500                 505                 510


Ser Val Val Ala Ser Ser Ala Thr Ser Ser Leu Ser Ser Tyr Pro Ser
        515                 520                 525


Pro Val Ala Thr Ser Tyr Pro Ser Pro Val Thr Thr Ser Tyr Pro Ser
    530                 535                 540


Pro Ala Thr Thr Ser Tyr Pro Ser Pro Val Pro Thr Ser Phe Ser Ser
545                 550                 555                 560


Pro Gly Ser Ser Thr Tyr Pro Ser Pro Val His Ser Gly Phe Pro Ser
                565                 570                 575


Pro Ser Val Ala Thr Thr Tyr Ser Ser Val Pro Pro Ala Phe Pro Ala
            580                 585                 590


Gln Val Ser Ser Phe Pro Ser Ser Ala Val Thr Asn Ser Phe Ser Ala
        595                 600                 605


Ser Thr Gly Leu Ser Asp Met Thr Ala Thr Phe Ser Pro Arg Thr Ile
    610                 615                 620


Glu Ile Cys
625


<210> 118
<211> 631
<212> PRT
<213> Artificial Sequence

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

<400> 118
```

```
Met Ala Ala Ala Lys Ala Glu Met Gln Leu Met Ser Pro Leu Gln Ile
1               5                   10                  15

Ser Asp Pro Phe Gly Ser Phe Pro His Ser Pro Thr Met Asp Asn Tyr
            20                  25                  30

Pro Lys Leu Glu Glu Met Met Leu Leu Ser Asn Gly Ala Pro Gln Phe
        35                  40                  45

Leu Gly Ala Ala Gly Ala Pro Glu Gly Ser Gly Ser Asn Ser Ser Ser
    50                  55                  60

Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Ser Asn Ser Ser
65                  70                  75                  80

Ser Ser Ser Ser Thr Phe Asn Pro Gln Ala Asp Thr Gly Glu Gln Pro
                85                  90                  95

Tyr Glu His Leu Thr Ala Glu Ser Phe Pro Asp Ile Ser Leu Asn Asn
            100                 105                 110

Glu Lys Val Leu Val Glu Thr Ser Tyr Pro Ser Gln Thr Thr Arg Leu
        115                 120                 125

Pro Pro Ile Thr Tyr Thr Gly Arg Phe Ser Leu Glu Pro Ala Pro Asn
    130                 135                 140

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

Leu Val Ser Met Thr Asn Pro Pro Ala Ser Ser Ser Ser Ala Pro Ser
                165                 170                 175

Pro Ala Ala Ser Ser Ala Ser Ala Ser Gln Ser Pro Pro Leu Ser Cys
            180                 185                 190

Ala Val Pro Ser Asn Asp Ser Ser Pro Ile Tyr Ser Ala Ala Pro Thr
        195                 200                 205

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

```
Phe Pro Gly Ser Ala Gly Thr Ala Leu Gln Tyr Pro Pro Pro Ala Tyr
225                 230                 235                 240

Pro Ala Ala Lys Gly Gly Phe Gln Val Pro Met Ile Pro Asp Tyr Leu
                245                 250                 255

Phe Pro Gln Gln Gln Gly Asp Leu Gly Leu Gly Thr Pro Asp Gln Lys
            260                 265                 270

Pro Phe Gln Gly Leu Glu Ser Arg Thr Gln Gln Pro Ser Leu Thr Pro
        275                 280                 285

Leu Ser Thr Ile Lys Ala Phe Ala Thr Gln Ser Gly Ser Gln Asp Leu
    290                 295                 300

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

Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Pro His Glu Arg
                325                 330                 335

Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser
            340                 345                 350

Asp Asn Leu Val Arg His Ile Arg Ile His Thr Gly Gln Lys Pro Phe
        355                 360                 365

Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Glu Asp Asn Leu His
    370                 375                 380

Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile
385                 390                 395                 400

Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Leu Val Arg His Thr Lys
                405                 410                 415

Ile His Leu Arg Gln Lys Asp Arg Pro Tyr Ala Cys Pro Val Glu Ser
            420                 425                 430
```

```
Cys Asp Arg Arg Phe Ser Gln Ser Gly Asn Leu Thr Glu His Ile Arg
        435                 440                 445

Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn
    450                 455                 460

Phe Ser Thr Ser Gly His Leu Val Arg His Ile Arg Thr His Thr Gly
465                 470                 475                 480

Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Gln Asn
                485                 490                 495

Ser Thr Leu Thr Glu His Thr Lys Ile His Leu Arg Gln Lys Asp Lys
            500                 505                 510

Lys Ala Asp Lys Ser Val Val Ala Ser Ser Ala Thr Ser Ser Leu Ser
        515                 520                 525

Ser Tyr Pro Ser Pro Val Ala Thr Ser Tyr Pro Ser Pro Val Thr Thr
    530                 535                 540

Ser Tyr Pro Ser Pro Ala Thr Thr Ser Tyr Pro Ser Pro Val Pro Thr
545                 550                 555                 560

Ser Phe Ser Ser Pro Gly Ser Ser Thr Tyr Pro Ser Pro Val His Ser
                565                 570                 575

Gly Phe Pro Ser Pro Ser Val Ala Thr Thr Tyr Ser Ser Val Pro Pro
            580                 585                 590

Ala Phe Pro Ala Gln Val Ser Ser Phe Pro Ser Ser Ala Val Thr Asn
        595                 600                 605

Ser Phe Ser Ala Ser Thr Gly Leu Ser Asp Met Thr Ala Thr Phe Ser
    610                 615                 620

Pro Arg Thr Ile Glu Ile Cys
625                 630
```

<210> 119
<211> 473

<212> PRT
<213> Artificial Sequence

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

<400> 119
Met Thr Gly Lys Leu Ala Glu Lys Leu Pro Val Thr Met Ser Ser Leu
1 5 10 15

Leu Asn Gln Leu Pro Asp Asn Leu Tyr Pro Glu Glu Ile Pro Ser Ala
20 25 30

Leu Asn Leu Phe Ser Gly Ser Ser Asp Ser Val Val His Tyr Asn Gln
35 40 45

Met Ala Thr Glu Asn Val Met Asp Ile Gly Leu Thr Asn Glu Lys Pro
50 55 60

Asn Pro Glu Leu Ser Tyr Ser Gly Ser Phe Gln Pro Ala Pro Gly Asn
65 70 75 80

Lys Thr Val Thr Tyr Leu Gly Lys Phe Ala Phe Asp Ser Pro Ser Asn
85 90 95

Trp Cys Gln Asp Asn Ile Ile Ser Leu Met Ser Ala Gly Ile Leu Gly
100 105 110

Val Pro Pro Ala Ser Gly Ala Leu Ser Thr Gln Thr Ser Thr Ala Ser
115 120 125

Met Val Gln Pro Pro Gln Gly Asp Val Glu Ala Met Tyr Pro Ala Leu
130 135 140

Pro Pro Tyr Ser Asn Cys Gly Asp Leu Tyr Ser Glu Pro Val Ser Phe
145 150 155 160

His Asp Pro Gln Gly Asn Pro Gly Leu Ala Tyr Ser Pro Gln Asp Tyr
165 170 175

Gln Ser Ala Lys Pro Ala Leu Asp Ser Asn Leu Phe Pro Met Ile Pro
180 185 190

```
Asp Tyr Asn Leu Tyr His His Pro Asn Asp Met Gly Ser Ile Pro Glu
        195                 200                 205

His Lys Pro Phe Gln Gly Met Asp Pro Ile Arg Val Asn Pro Pro Pro
    210                 215                 220

Ile Thr Pro Leu Glu Thr Ile Lys Ala Phe Lys Asp Lys Gln Ile His
225                 230                 235                 240

Pro Gly Phe Gly Ser Leu Pro Gln Pro Pro Leu Thr Leu Lys Pro Ile
                245                 250                 255

Arg Pro Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Leu His Glu
            260                 265                 270

Arg Pro His Ala Cys Pro Ala Glu Gly Cys Asp Arg Arg Phe Ser Arg
        275                 280                 285

Ser Asp Asn Leu Val Arg His Leu Arg Ile His Thr Gly His Lys Pro
    290                 295                 300

Phe Gln Cys Arg Ile Cys Met Arg Ser Phe Ser His Arg Thr Thr Leu
305                 310                 315                 320

Thr Asn His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Glu
                325                 330                 335

Phe Cys Gly Arg Lys Phe Ala Arg Glu Asp Asn Leu His Thr His Ala
            340                 345                 350

Lys Ile His Leu Lys Gln Lys Glu His Ala Cys Pro Ala Glu Gly Cys
        355                 360                 365

Asp Arg Arg Phe Ser Thr Ser His Ser Leu Thr Glu His Leu Arg Ile
    370                 375                 380

His Thr Gly His Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Ser Phe
385                 390                 395                 400
```

Ser Gln Ser Ser Ser Leu Val Arg His Ile Arg Thr His Thr Gly Glu
405 410 415

Lys Pro Phe Ala Cys Glu Phe Cys Gly Arg Lys Phe Ala Arg Glu Asp
420 425 430

Asn Leu His Thr His Ala Lys Ile His Leu Lys Gln Lys Glu Lys Lys
435 440 445

Ala Glu Lys Gly Gly Ala Pro Ser Ala Ser Ser Ala Pro Pro Val Ser
450 455 460

Leu Ala Pro Val Val Thr Thr Cys Ala
465 470

<210> 120
<211> 719
<212> PRT
<213> Artificial Sequence

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

<400> 120
Met Ala Ala Ala Lys Ala Glu Met Gln Leu Met Ser Pro Leu Gln Ile
1 5 10 15

Ser Asp Pro Phe Gly Ser Phe Pro His Ser Pro Thr Met Asp Asn Tyr
20 25 30

Pro Lys Leu Glu Glu Met Met Leu Leu Ser Asn Gly Ala Pro Gln Phe
35 40 45

Leu Gly Ala Ala Gly Ala Pro Glu Gly Ser Gly Ser Asn Ser Ser Ser
50 55 60

Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Ser Asn Ser Ser
65 70 75 80

Ser Ser Ser Ser Thr Phe Asn Pro Gln Ala Asp Thr Gly Glu Gln Pro
85 90 95

```
Tyr Glu His Leu Thr Ala Glu Ser Phe Pro Asp Ile Ser Leu Asn Asn
            100                 105                 110

Glu Lys Val Leu Val Glu Thr Ser Tyr Pro Ser Gln Thr Thr Arg Leu
        115                 120                 125

Pro Pro Ile Thr Tyr Thr Gly Arg Phe Ser Leu Glu Pro Ala Pro Asn
    130                 135                 140

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

Leu Val Ser Met Thr Asn Pro Pro Ala Ser Ser Ser Ser Ala Pro Ser
                165                 170                 175

Pro Ala Ala Ser Ser Ala Ser Ala Ser Gln Ser Pro Pro Leu Ser Cys
            180                 185                 190

Ala Val Pro Ser Asn Asp Ser Ser Pro Ile Tyr Ser Ala Ala Pro Thr
        195                 200                 205

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

Phe Pro Gly Ser Ala Gly Thr Ala Leu Gln Tyr Pro Pro Pro Ala Tyr
225                 230                 235                 240

Pro Ala Ala Lys Gly Gly Phe Gln Val Pro Met Ile Pro Asp Tyr Leu
                245                 250                 255

Phe Pro Gln Gln Gln Gly Asp Leu Gly Leu Gly Thr Pro Asp Gln Lys
            260                 265                 270

Pro Phe Gln Gly Leu Glu Ser Arg Thr Gln Gln Pro Ser Leu Thr Pro
        275                 280                 285

Leu Ser Thr Ile Lys Ala Phe Ala Thr Gln Ser Gly Ser Gln Asp Leu
    290                 295                 300

Lys Ala Leu Asn Thr Ser Tyr Gln Ser Gln Leu Ile Lys Pro Ser Arg
305                 310                 315                 320
```

```
Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Pro His Glu Arg
                325                 330                 335

Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Asp Pro
            340                 345                 350

Gly Ala Leu Val Arg His Ile Arg Ile His Thr Gly Gln Lys Pro Phe
        355                 360                 365

Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Asn Leu Val
    370                 375                 380

Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile
385                 390                 395                 400

Cys Gly Arg Lys Phe Ala Gln Ser Gly Asp Leu Arg Arg His Thr Lys
                405                 410                 415

Ile His Leu Arg Gln Lys Asp Arg Pro Tyr Ala Cys Pro Val Glu Ser
            420                 425                 430

Cys Asp Arg Arg Phe Ser Thr His Leu Asp Leu Ile Arg His Ile Arg
        435                 440                 445

Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn
    450                 455                 460

Phe Ser Thr Ser Gly Asn Leu Val Arg His Ile Arg Thr His Thr Gly
465                 470                 475                 480

Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser
                485                 490                 495

Asp Asn Leu Val Arg His Thr Lys Ile His Leu Arg Gln Lys Asp Arg
            500                 505                 510

Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Gln Ser
        515                 520                 525
```

Gly His Leu Thr Glu His Ile Arg Ile His Thr Gly Gln Lys Pro Phe
530 535 540

Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Glu Arg Ser His Leu Arg
545 550 555 560

Glu His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile
565 570 575

Cys Gly Arg Lys Phe Ala Gln Ala Gly His Leu Ala Ser His Thr Lys
580 585 590

Ile His Leu Arg Gln Lys Asp Lys Lys Ala Asp Lys Ser Val Val Ala
595 600 605

Ser Ser Ala Thr Ser Ser Leu Ser Ser Tyr Pro Ser Pro Val Ala Thr
610 615 620

Ser Tyr Pro Ser Pro Val Thr Thr Ser Tyr Pro Ser Pro Ala Thr Thr
625 630 635 640

Ser Tyr Pro Ser Pro Val Pro Thr Ser Phe Ser Ser Pro Gly Ser Ser
645 650 655

Thr Tyr Pro Ser Pro Val His Ser Gly Phe Pro Ser Pro Ser Val Ala
660 665 670

Thr Thr Tyr Ser Ser Val Pro Pro Ala Phe Pro Ala Gln Val Ser Ser
675 680 685

Phe Pro Ser Ser Ala Val Thr Asn Ser Phe Ser Ala Ser Thr Gly Leu
690 695 700

Ser Asp Met Thr Ala Thr Phe Ser Pro Arg Thr Ile Glu Ile Cys
705 710 715

<210> 121
<211> 627
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 121
Met Ala Ala Ala Lys Ala Glu Met Gln Leu Met Ser Pro Leu Gln Ile
1 5 10 15

Ser Asp Pro Phe Gly Ser Phe Pro His Ser Pro Thr Met Asp Asn Tyr
20 25 30

Pro Lys Leu Glu Glu Met Met Leu Leu Ser Asn Gly Ala Pro Gln Phe
35 40 45

Leu Gly Ala Ala Gly Ala Pro Glu Gly Ser Gly Ser Asn Ser Ser Ser
50 55 60

Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Ser Asn Ser Ser
65 70 75 80

Ser Ser Ser Ser Thr Phe Asn Pro Gln Ala Asp Thr Gly Glu Gln Pro
85 90 95

Tyr Glu His Leu Thr Ala Glu Ser Phe Pro Asp Ile Ser Leu Asn Asn
100 105 110

Glu Lys Val Leu Val Glu Thr Ser Tyr Pro Ser Gln Thr Thr Arg Leu
115 120 125

Pro Pro Ile Thr Tyr Thr Gly Arg Phe Ser Leu Glu Pro Ala Pro Asn
130 135 140

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

Leu Val Ser Met Thr Asn Pro Pro Ala Ser Ser Ser Ser Ala Pro Ser
165 170 175

Pro Ala Ala Ser Ser Ala Ser Ala Ser Gln Ser Pro Pro Leu Ser Cys
180 185 190

Ala Val Pro Ser Asn Asp Ser Ser Pro Ile Tyr Ser Ala Ala Pro Thr
195 200 205

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

Phe Pro Gly Ser Ala Gly Thr Ala Leu Gln Tyr Pro Pro Pro Ala Tyr
225                 230                 235                 240

Pro Ala Ala Lys Gly Gly Phe Gln Val Pro Met Ile Pro Asp Tyr Leu
                245                 250                 255

Phe Pro Gln Gln Gln Gly Asp Leu Gly Leu Gly Thr Pro Asp Gln Lys
            260                 265                 270

Pro Phe Gln Gly Leu Glu Ser Arg Thr Gln Gln Pro Ser Leu Thr Pro
        275                 280                 285

Leu Ser Thr Ile Lys Ala Phe Ala Thr Gln Ser Gly Ser Gln Asp Leu
    290                 295                 300

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

Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Pro His Glu Arg
                325                 330                 335

Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser
            340                 345                 350

Asp Asn Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys Pro Phe
        355                 360                 365

Gln Cys Arg Ile Cys Met Arg Asn Phe Ser His Ser Thr Thr Leu Thr
    370                 375                 380

Asn His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile
385                 390                 395                 400

Cys Gly Arg Lys Phe Ala Arg Ser Asp Asn Arg Lys Thr His Ile Arg
                405                 410                 415
```

```
Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys
            420                 425                 430

Phe Ser Thr Ser His Ser Leu Thr Glu His Ile Arg Ile His Thr Gly
        435                 440                 445

Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Gln Ser
    450                 455                 460

Ser Ser Leu Thr Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
465                 470                 475                 480

Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Asn Arg Lys
                485                 490                 495

Thr His Thr Lys Ile His Leu Arg Gln Lys Asp Lys Lys Ala Asp Lys
            500                 505                 510

Ser Val Val Ala Ser Ser Ala Thr Ser Ser Leu Ser Ser Tyr Pro Ser
        515                 520                 525

Pro Val Ala Thr Ser Tyr Pro Ser Pro Val Thr Thr Ser Tyr Pro Ser
    530                 535                 540

Pro Ala Thr Thr Ser Tyr Pro Ser Pro Val Pro Thr Ser Phe Ser Ser
545                 550                 555                 560

Pro Gly Ser Ser Thr Tyr Pro Ser Pro Val His Ser Gly Phe Pro Ser
                565                 570                 575

Pro Ser Val Ala Thr Thr Tyr Ser Ser Val Pro Pro Ala Phe Pro Ala
            580                 585                 590

Gln Val Ser Ser Phe Pro Ser Ser Ala Val Thr Asn Ser Phe Ser Ala
        595                 600                 605

Ser Thr Gly Leu Ser Asp Met Thr Ala Thr Phe Ser Pro Arg Thr Ile
    610                 615                 620

Glu Ile Cys
625
```

<210> 122
<211> 473
<212> PRT
<213> Artificial Sequence

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

<400> 122
Met Thr Gly Lys Leu Ala Glu Lys Leu Pro Val Thr Met Ser Ser Leu
1 5 10 15

Leu Asn Gln Leu Pro Asp Asn Leu Tyr Pro Glu Glu Ile Pro Ser Ala
20 25 30

Leu Asn Leu Phe Ser Gly Ser Ser Asp Ser Val Val His Tyr Asn Gln
35 40 45

Met Ala Thr Glu Asn Val Met Asp Ile Gly Leu Thr Asn Glu Lys Pro
50 55 60

Asn Pro Glu Leu Ser Tyr Ser Gly Ser Phe Gln Pro Ala Pro Gly Asn
65 70 75 80

Lys Thr Val Thr Tyr Leu Gly Lys Phe Ala Phe Asp Ser Pro Ser Asn
85 90 95

Trp Cys Gln Asp Asn Ile Ile Ser Leu Met Ser Ala Gly Ile Leu Gly
100 105 110

Val Pro Pro Ala Ser Gly Ala Leu Ser Thr Gln Thr Ser Thr Ala Ser
115 120 125

Met Val Gln Pro Pro Gln Gly Asp Val Glu Ala Met Tyr Pro Ala Leu
130 135 140

Pro Pro Tyr Ser Asn Cys Gly Asp Leu Tyr Ser Glu Pro Val Ser Phe
145 150 155 160

His Asp Pro Gln Gly Asn Pro Gly Leu Ala Tyr Ser Pro Gln Asp Tyr
165 170 175

```
Gln Ser Ala Lys Pro Ala Leu Asp Ser Asn Leu Phe Pro Met Ile Pro
            180                 185                 190

Asp Tyr Asn Leu Tyr His His Pro Asn Asp Met Gly Ser Ile Pro Glu
        195                 200                 205

His Lys Pro Phe Gln Gly Met Asp Pro Ile Arg Val Asn Pro Pro Pro
    210                 215                 220

Ile Thr Pro Leu Glu Thr Ile Lys Ala Phe Lys Asp Lys Gln Ile His
225                 230                 235                 240

Pro Gly Phe Gly Ser Leu Pro Gln Pro Pro Leu Thr Leu Lys Pro Ile
                245                 250                 255

Arg Pro Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Leu His Glu
            260                 265                 270

Arg Pro His Ala Cys Pro Ala Glu Gly Cys Asp Arg Arg Phe Ser Arg
        275                 280                 285

Ser Asp Asn Leu Val Arg His Leu Arg Ile His Thr Gly His Lys Pro
    290                 295                 300

Phe Gln Cys Arg Ile Cys Met Arg Ser Phe Ser Arg Glu Asp Asn Leu
305                 310                 315                 320

His Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Glu
                325                 330                 335

Phe Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Leu Val Arg His Ala
            340                 345                 350

Lys Ile His Leu Lys Gln Lys Glu His Ala Cys Pro Ala Glu Gly Cys
        355                 360                 365

Asp Arg Arg Phe Ser Gln Ser Gly Asn Leu Thr Glu His Leu Arg Ile
    370                 375                 380
```

```
His Thr Gly His Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Ser Phe
385                 390                 395                 400


Ser Thr Ser Gly His Leu Val Arg His Ile Arg Thr His Thr Gly Glu
                405                 410                 415


Lys Pro Phe Ala Cys Glu Phe Cys Gly Arg Lys Phe Ala Gln Asn Ser
            420                 425                 430


Thr Leu Thr Glu His Ala Lys Ile His Leu Lys Gln Lys Glu Lys Lys
        435                 440                 445


Ala Glu Lys Gly Gly Ala Pro Ser Ala Ser Ser Ala Pro Pro Val Ser
    450                 455                 460


Leu Ala Pro Val Val Thr Thr Cys Ala
465                 470


<210> 123
<211> 627
<212> PRT
<213> Artificial Sequence

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

<400> 123
Met Ala Ala Ala Lys Ala Glu Met Gln Leu Met Ser Pro Leu Gln Ile
1               5                   10                  15


Ser Asp Pro Phe Gly Ser Phe Pro His Ser Pro Thr Met Asp Asn Tyr
            20                  25                  30


Pro Lys Leu Glu Glu Met Met Leu Leu Ser Asn Gly Ala Pro Gln Phe
        35                  40                  45


Leu Gly Ala Ala Gly Ala Pro Glu Gly Ser Gly Ser Asn Ser Ser Ser
    50                  55                  60


Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Ser Asn Ser Ser
65                  70                  75                  80
```

```
Ser Ser Ser Ser Thr Phe Asn Pro Gln Ala Asp Thr Gly Glu Gln Pro
                85                  90                  95

Tyr Glu His Leu Thr Ala Glu Ser Phe Pro Asp Ile Ser Leu Asn Asn
            100                 105                 110

Glu Lys Val Leu Val Glu Thr Ser Tyr Pro Ser Gln Thr Thr Arg Leu
        115                 120                 125

Pro Pro Ile Thr Tyr Thr Gly Arg Phe Ser Leu Glu Pro Ala Pro Asn
    130                 135                 140

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

Leu Val Ser Met Thr Asn Pro Pro Ala Ser Ser Ser Ser Ala Pro Ser
                165                 170                 175

Pro Ala Ala Ser Ser Ala Ser Ala Ser Gln Ser Pro Pro Leu Ser Cys
            180                 185                 190

Ala Val Pro Ser Asn Asp Ser Ser Pro Ile Tyr Ser Ala Ala Pro Thr
        195                 200                 205

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

Phe Pro Gly Ser Ala Gly Thr Ala Leu Gln Tyr Pro Pro Pro Ala Tyr
225                 230                 235                 240

Pro Ala Ala Lys Gly Gly Phe Gln Val Pro Met Ile Pro Asp Tyr Leu
                245                 250                 255

Phe Pro Gln Gln Gln Gly Asp Leu Gly Leu Gly Thr Pro Asp Gln Lys
            260                 265                 270

Pro Phe Gln Gly Leu Glu Ser Arg Thr Gln Gln Pro Ser Leu Thr Pro
        275                 280                 285

Leu Ser Thr Ile Lys Ala Phe Ala Thr Gln Ser Gly Ser Gln Asp Leu
    290                 295                 300
```

```
Lys Ala Leu Asn Thr Ser Tyr Gln Ser Gln Leu Ile Lys Pro Ser Arg
305                 310                 315                 320

Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Pro His Glu Arg
                325                 330                 335

Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser
            340                 345                 350

Asp Asn Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys Pro Phe
        355                 360                 365

Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Asn Leu Thr
    370                 375                 380

Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile
385                 390                 395                 400

Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His Ile Arg
                405                 410                 415

Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys
            420                 425                 430

Phe Ser Gln Ser Gly Asn Leu Thr Glu His Ile Arg Ile His Thr Gly
        435                 440                 445

Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Thr Ser
    450                 455                 460

Gly His Leu Thr Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
465                 470                 475                 480

Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Gln Ser Ser Thr Arg Lys
                485                 490                 495

Glu His Thr Lys Ile His Leu Arg Gln Lys Asp Lys Lys Ala Asp Lys
            500                 505                 510
```

Ser Val Val Ala Ser Ser Ala Thr Ser Ser Leu Ser Ser Tyr Pro Ser
        515   520   525

Pro Val Ala Thr Ser Tyr Pro Ser Pro Val Thr Thr Ser Tyr Pro Ser
    530   535   540

Pro Ala Thr Thr Ser Tyr Pro Ser Pro Val Pro Thr Ser Phe Ser Ser
545   550   555   560

Pro Gly Ser Ser Thr Tyr Pro Ser Pro Val His Ser Gly Phe Pro Ser
                565   570   575

Pro Ser Val Ala Thr Thr Tyr Ser Ser Val Pro Pro Ala Phe Pro Ala
            580   585   590

Gln Val Ser Ser Phe Pro Ser Ser Ala Val Thr Asn Ser Phe Ser Ala
        595   600   605

Ser Thr Gly Leu Ser Asp Met Thr Ala Thr Phe Ser Pro Arg Thr Ile
    610   615   620

Glu Ile Cys
625

<210> 124
<211> 627
<212> PRT
<213> Artificial Sequence

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

<400> 124
Met Ala Ala Ala Lys Ala Glu Met Gln Leu Met Ser Pro Leu Gln Ile
1   5   10   15

Ser Asp Pro Phe Gly Ser Phe Pro His Ser Pro Thr Met Asp Asn Tyr
            20   25   30

Pro Lys Leu Glu Glu Met Met Leu Leu Ser Asn Gly Ala Pro Gln Phe
        35   40   45

```
Leu Gly Ala Ala Gly Ala Pro Glu Gly Ser Gly Ser Asn Ser Ser Ser
    50                  55                  60

Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Ser Asn Ser Ser
65                  70                  75                  80

Ser Ser Ser Ser Thr Phe Asn Pro Gln Ala Asp Thr Gly Glu Gln Pro
                85                  90                  95

Tyr Glu His Leu Thr Ala Glu Ser Phe Pro Asp Ile Ser Leu Asn Asn
            100                 105                 110

Glu Lys Val Leu Val Glu Thr Ser Tyr Pro Ser Gln Thr Thr Arg Leu
        115                 120                 125

Pro Pro Ile Thr Tyr Thr Gly Arg Phe Ser Leu Glu Pro Ala Pro Asn
    130                 135                 140

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

Leu Val Ser Met Thr Asn Pro Pro Ala Ser Ser Ser Ser Ala Pro Ser
                165                 170                 175

Pro Ala Ala Ser Ser Ala Ser Ala Ser Gln Ser Pro Pro Leu Ser Cys
            180                 185                 190

Ala Val Pro Ser Asn Asp Ser Ser Pro Ile Tyr Ser Ala Ala Pro Thr
        195                 200                 205

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

Phe Pro Gly Ser Ala Gly Thr Ala Leu Gln Tyr Pro Pro Pro Ala Tyr
225                 230                 235                 240

Pro Ala Ala Lys Gly Gly Phe Gln Val Pro Met Ile Pro Asp Tyr Leu
                245                 250                 255

Phe Pro Gln Gln Gln Gly Asp Leu Gly Leu Gly Thr Pro Asp Gln Lys
            260                 265                 270
```

```
Pro Phe Gln Gly Leu Glu Ser Arg Thr Gln Gln Pro Ser Leu Thr Pro
        275                 280                 285

Leu Ser Thr Ile Lys Ala Phe Ala Thr Gln Ser Gly Ser Gln Asp Leu
    290                 295                 300

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

Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Pro His Glu Arg
                325                 330                 335

Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser
            340                 345                 350

Asp Asn Leu Val Arg His Ile Arg Ile His Thr Gly Gln Lys Pro Phe
        355                 360                 365

Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Glu Asp Asn Leu His
    370                 375                 380

Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile
385                 390                 395                 400

Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Leu Val Arg His Ile Arg
                405                 410                 415

Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys
            420                 425                 430

Phe Ser Gln Ser Gly Asn Leu Thr Glu His Ile Arg Ile His Thr Gly
        435                 440                 445

Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Thr Ser
    450                 455                 460

Gly His Leu Val Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
465                 470                 475                 480
```

```
Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Gln Asn Ser Thr Leu Thr
                485                 490                 495

Glu His Thr Lys Ile His Leu Arg Gln Lys Asp Lys Lys Ala Asp Lys
            500                 505                 510

Ser Val Val Ala Ser Ser Ala Thr Ser Ser Leu Ser Ser Tyr Pro Ser
        515                 520                 525

Pro Val Ala Thr Ser Tyr Pro Ser Pro Val Thr Thr Ser Tyr Pro Ser
    530                 535                 540

Pro Ala Thr Thr Ser Tyr Pro Ser Pro Val Pro Thr Ser Phe Ser Ser
545                 550                 555                 560

Pro Gly Ser Ser Thr Tyr Pro Ser Pro Val His Ser Gly Phe Pro Ser
                565                 570                 575

Pro Ser Val Ala Thr Thr Tyr Ser Ser Val Pro Pro Ala Phe Pro Ala
            580                 585                 590

Gln Val Ser Ser Phe Pro Ser Ser Ala Val Thr Asn Ser Phe Ser Ala
        595                 600                 605

Ser Thr Gly Leu Ser Asp Met Thr Ala Thr Phe Ser Pro Arg Thr Ile
    610                 615                 620

Glu Ile Cys
625


<210> 125
<211> 272
<212> PRT
<213> Artificial Sequence

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

<400> 125
Met Ala Pro Lys Lys Lys Arg Lys Val Gly Ile His Gly Val Pro Ala
1               5                   10                  15
```

```
Ala Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys
            20                  25                  30

Ser Phe Ser Ser Pro Ala Asp Leu Thr Arg His Gln Arg Thr His Thr
        35                  40                  45

Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg
    50                  55                  60

Ser Asp Asn Leu Val Arg His Gln Arg Thr His Thr Gly Glu Lys Pro
65                  70                  75                  80

Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Glu Asp Asn Leu
                85                  90                  95

His Thr His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro
            100                 105                 110

Glu Cys Gly Lys Ser Phe Ser Arg Ser Asp Glu Leu Val Arg His Gln
        115                 120                 125

Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys
    130                 135                 140

Ser Phe Ser Gln Ser Gly Asn Leu Thr Glu His Gln Arg Thr His Thr
145                 150                 155                 160

Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Thr
                165                 170                 175

Ser Gly His Leu Val Arg His Gln Arg Thr His Thr Gly Lys Lys Thr
            180                 185                 190

Ser Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys
        195                 200                 205

Lys Gly Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Leu Glu Asp Ala
    210                 215                 220

Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp
225                 230                 235                 240
```

```
Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu
                245                 250                 255


Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
            260                 265                 270


<210> 126
<211> 272
<212> PRT
<213> Artificial Sequence

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

<400> 126
Met Ala Pro Lys Lys Lys Arg Lys Val Gly Ile His Gly Val Pro Ala
1               5                   10                  15


Ala Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys
            20                  25                  30


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


Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg
    50                  55                  60


Ser Asp Asn Leu Val Arg His Gln Arg Thr His Thr Gly Glu Lys Pro
65                  70                  75                  80


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


Arg Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro
            100                 105                 110


Glu Cys Gly Lys Ser Phe Ser Thr His Leu Asp Leu Ile Arg His Gln
        115                 120                 125


Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys
    130                 135                 140
```

```
Ser Phe Ser Thr Ser Gly Asn Leu Val Arg His Gln Arg Thr His Thr
145                 150                 155                 160


Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg
                165                 170                 175


Ser Asp Asn Leu Val Arg His Gln Arg Thr His Thr Gly Lys Lys Thr
            180                 185                 190


Ser Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys
        195                 200                 205


Lys Gly Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Leu Glu Asp Ala
    210                 215                 220


Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp
225                 230                 235                 240


Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu
                245                 250                 255


Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
            260                 265                 270


<210> 127
<211> 261
<212> PRT
<213> Artificial Sequence

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

<400> 127
Met Ala Pro Lys Lys Lys Arg Lys Val Gly Ile His Gly Val Pro Ala
1               5                   10                  15


Ala Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys
            20                  25                  30


Ser Phe Ser Arg Ser Asp Asn Leu Val Arg His Gln Arg Thr His Thr
        35                  40                  45
```

```
Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg
    50                  55                  60

Glu Asp Asn Leu His Thr His Gln Arg Thr His Thr Gly Glu Lys Pro
65                  70                  75                  80

Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Ser Asp Glu Leu
                85                  90                  95

Val Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro
            100                 105                 110

Glu Cys Gly Lys Ser Phe Ser Gln Ser Gly Asn Leu Thr Glu His Gln
        115                 120                 125

Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys
    130                 135                 140

Ser Phe Ser Thr Ser Gly His Leu Val Arg His Gln Arg Thr His Thr
145                 150                 155                 160

Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln
                165                 170                 175

Asn Ser Thr Leu Thr Glu His Gln Arg Thr His Thr Gly Lys Lys Thr
            180                 185                 190

Ser Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys
        195                 200                 205

Lys Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser
    210                 215                 220

Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu
225                 230                 235                 240

Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe
                245                 250                 255
```

Asp Leu Asp Met Leu
260

<210> 128
<211> 386
<212> PRT
<213> Artificial Sequence

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

<400> 128
Met Ala Ala Asp His Leu Met Leu Ala Glu Gly Tyr Arg Leu Val Gln
1 5 10 15

Arg Pro Pro Ser Ala Ala Ala Ala His Gly Pro His Ala Leu Arg Thr
20 25 30

Leu Pro Pro Tyr Ala Gly Pro Gly Leu Asp Ser Gly Leu Arg Pro Arg
35 40 45

Gly Ala Pro Leu Gly Pro Pro Pro Pro Arg Gln Pro Gly Ala Leu Ala
50 55 60

Tyr Gly Ala Phe Gly Pro Pro Ser Ser Phe Gln Pro Phe Pro Ala Val
65 70 75 80

Pro Pro Pro Ala Ala Gly Ile Ala His Leu Gln Pro Val Ala Thr Pro
85 90 95

Tyr Pro Gly Arg Ala Ala Ala Pro Pro Asn Ala Pro Gly Gly Pro Pro
100 105 110

Gly Pro Gln Pro Ala Pro Ser Ala Ala Ala Pro Pro Pro Pro Ala His
115 120 125

Ala Leu Gly Gly Met Asp Ala Glu Leu Ile Asp Glu Glu Ala Leu Thr
130 135 140

Ser Leu Glu Leu Glu Leu Gly Leu His Arg Val Arg Glu Leu Pro Glu
145 150 155 160

```
Leu Phe Leu Gly Gln Ser Glu Phe Asp Cys Phe Ser Asp Leu Gly Ser
                165                 170                 175

Ala Pro Pro Ala Gly Ser Val Ser Cys Gln Ser Gln Leu Ile Lys Pro
            180                 185                 190

Ser Arg Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Pro His
        195                 200                 205

Glu Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser
    210                 215                 220

Arg Ser Asp Asn Leu Val Arg His Ile Arg Ile His Thr Gly Gln Lys
225                 230                 235                 240

Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Glu Asp Asn
                245                 250                 255

Leu His Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys
            260                 265                 270

Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Leu Val Arg His
        275                 280                 285

Thr Lys Ile His Leu Arg Gln Lys Asp Arg Pro Tyr Ala Cys Pro Val
    290                 295                 300

Glu Ser Cys Asp Arg Arg Phe Ser Gln Ser Gly Asn Leu Thr Glu His
305                 310                 315                 320

Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met
                325                 330                 335

Arg Asn Phe Ser Thr Ser Gly His Leu Val Arg His Ile Arg Thr His
            340                 345                 350

Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala
        355                 360                 365

Gln Asn Ser Thr Leu Thr Glu His Thr Lys Ile His Leu Arg Gln Lys
    370                 375                 380
```

Asp Lys
385

<210> 129
<211> 402
<212> PRT
<213> Artificial Sequence

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

<400> 129
Met Ala Ala Asp His Leu Met Leu Ala Glu Gly Tyr Arg Leu Val Gln
1 5 10 15

Arg Pro Pro Ser Ala Ala Ala Ala His Gly Pro His Ala Leu Arg Thr
20 25 30

Leu Pro Pro Tyr Ala Gly Pro Gly Leu Asp Ser Gly Leu Arg Pro Arg
35 40 45

Gly Ala Pro Leu Gly Pro Pro Pro Pro Arg Gln Pro Gly Ala Leu Ala
50 55 60

Tyr Gly Ala Phe Gly Pro Pro Ser Ser Phe Gln Pro Phe Pro Ala Val
65 70 75 80

Pro Pro Pro Ala Ala Gly Ile Ala His Leu Gln Pro Val Ala Thr Pro
85 90 95

Tyr Pro Gly Arg Ala Ala Ala Pro Pro Asn Ala Pro Gly Gly Pro Pro
100 105 110

Gly Pro Gln Pro Ala Pro Ser Ala Ala Ala Pro Pro Pro Pro Ala His
115 120 125

Ala Leu Gly Gly Met Asp Ala Glu Leu Ile Asp Glu Glu Ala Leu Thr
130 135 140

Ser Leu Glu Leu Glu Leu Gly Leu His Arg Val Arg Glu Leu Pro Glu
145 150 155 160

```
Leu Phe Leu Gly Gln Ser Glu Phe Asp Cys Phe Ser Asp Leu Gly Ser
                165                 170                 175

Ala Pro Pro Ala Gly Ser Val Ser Cys Gly Gly Ser Gly Gly Gly Ser
            180                 185                 190

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gln Ser Gln Leu Ile Lys Pro
        195                 200                 205

Ser Arg Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Pro His
    210                 215                 220

Glu Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser
225                 230                 235                 240

Arg Ser Asp Asn Leu Val Arg His Ile Arg Ile His Thr Gly Gln Lys
                245                 250                 255

Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Glu Asp Asn
            260                 265                 270

Leu His Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys
        275                 280                 285

Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Leu Val Arg His
    290                 295                 300

Thr Lys Ile His Leu Arg Gln Lys Asp Arg Pro Tyr Ala Cys Pro Val
305                 310                 315                 320

Glu Ser Cys Asp Arg Arg Phe Ser Gln Ser Gly Asn Leu Thr Glu His
                325                 330                 335

Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met
            340                 345                 350

Arg Asn Phe Ser Thr Ser Gly His Leu Val Arg His Ile Arg Thr His
        355                 360                 365
```

```
Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala
    370                 375                 380


Gln Asn Ser Thr Leu Thr Glu His Thr Lys Ile His Leu Arg Gln Lys
385                 390                 395                 400


Asp Lys
```

<210> 130
<211> 569
<212> PRT
<213> Artificial Sequence

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

<400> 130

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Met Ala Ala Asp His Leu Met Leu Ala Glu Gly Tyr Arg Leu Val Gln
1               5                   10                  15


Arg Pro Pro Ser Ala Ala Ala Ala His Gly Pro His Ala Leu Arg Thr
            20                  25                  30


Leu Pro Pro Tyr Ala Gly Pro Gly Leu Asp Ser Gly Leu Arg Pro Arg
        35                  40                  45


Gly Ala Pro Leu Gly Pro Pro Pro Pro Arg Gln Pro Gly Ala Leu Ala
    50                  55                  60


Tyr Gly Ala Phe Gly Pro Pro Ser Ser Phe Gln Pro Phe Pro Ala Val
65                  70                  75                  80


Pro Pro Pro Ala Ala Gly Ile Ala His Leu Gln Pro Val Ala Thr Pro
                85                  90                  95


Tyr Pro Gly Arg Ala Ala Ala Pro Pro Asn Ala Pro Gly Gly Pro Pro
            100                 105                 110


Gly Pro Gln Pro Ala Pro Ser Ala Ala Ala Pro Pro Pro Pro Ala His
        115                 120                 125
```

```
Ala Leu Gly Gly Met Asp Ala Glu Leu Ile Asp Glu Glu Ala Leu Thr
    130                 135                 140

Ser Leu Glu Leu Glu Leu Gly Leu His Arg Val Arg Glu Leu Pro Glu
145                 150                 155                 160

Leu Phe Leu Gly Gln Ser Glu Phe Asp Cys Phe Ser Asp Leu Gly Ser
                165                 170                 175

Ala Pro Pro Ala Gly Ser Val Ser Cys Ala Asp His Leu Met Leu Ala
            180                 185                 190

Glu Gly Tyr Arg Leu Val Gln Arg Pro Pro Ser Ala Ala Ala Ala His
        195                 200                 205

Gly Pro His Ala Leu Arg Thr Leu Pro Pro Tyr Ala Gly Pro Gly Leu
    210                 215                 220

Asp Ser Gly Leu Arg Pro Arg Gly Ala Pro Leu Gly Pro Pro Pro Pro
225                 230                 235                 240

Arg Gln Pro Gly Ala Leu Ala Tyr Gly Ala Phe Gly Pro Pro Ser Ser
                245                 250                 255

Phe Gln Pro Phe Pro Ala Val Pro Pro Pro Ala Ala Gly Ile Ala His
            260                 265                 270

Leu Gln Pro Val Ala Thr Pro Tyr Pro Gly Arg Ala Ala Ala Pro Pro
        275                 280                 285

Asn Ala Pro Gly Gly Pro Pro Gly Pro Gln Pro Ala Pro Ser Ala Ala
    290                 295                 300

Ala Pro Pro Pro Pro Ala His Ala Leu Gly Gly Met Asp Ala Glu Leu
305                 310                 315                 320

Ile Asp Glu Glu Ala Leu Thr Ser Leu Glu Leu Glu Leu Gly Leu His
                325                 330                 335

Arg Val Arg Glu Leu Pro Glu Leu Phe Leu Gly Gln Ser Glu Phe Asp
            340                 345                 350
```

```
Cys Phe Ser Asp Leu Gly Ser Ala Pro Pro Ala Gly Ser Val Ser Cys
        355                 360                 365

Gln Ser Gln Leu Ile Lys Pro Ser Arg Met Arg Lys Tyr Pro Asn Arg
    370                 375                 380

Pro Ser Lys Thr Pro Pro His Glu Arg Pro Tyr Ala Cys Pro Val Glu
385                 390                 395                 400

Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Asn Leu Val Arg His Ile
                405                 410                 415

Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg
            420                 425                 430

Asn Phe Ser Arg Glu Asp Asn Leu His Thr His Ile Arg Thr His Thr
        435                 440                 445

Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg
    450                 455                 460

Ser Asp Glu Leu Val Arg His Thr Lys Ile His Leu Arg Gln Lys Asp
465                 470                 475                 480

Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Gln
                485                 490                 495

Ser Gly Asn Leu Thr Glu His Ile Arg Ile His Thr Gly Gln Lys Pro
            500                 505                 510

Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Thr Ser Gly His Leu
        515                 520                 525

Val Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp
    530                 535                 540

Ile Cys Gly Arg Lys Phe Ala Gln Asn Ser Thr Leu Thr Glu His Thr
545                 550                 555                 560
```

Lys Ile His Leu Arg Gln Lys Asp Lys
565

<210> 131
<211> 585
<212> PRT
<213> Artificial Sequence

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

<400> 131
Met Ala Ala Asp His Leu Met Leu Ala Glu Gly Tyr Arg Leu Val Gln
1 5 10 15

Arg Pro Pro Ser Ala Ala Ala Ala His Gly Pro His Ala Leu Arg Thr
20 25 30

Leu Pro Pro Tyr Ala Gly Pro Gly Leu Asp Ser Gly Leu Arg Pro Arg
35 40 45

Gly Ala Pro Leu Gly Pro Pro Pro Pro Arg Gln Pro Gly Ala Leu Ala
50 55 60

Tyr Gly Ala Phe Gly Pro Pro Ser Ser Phe Gln Pro Phe Pro Ala Val
65 70 75 80

Pro Pro Pro Ala Ala Gly Ile Ala His Leu Gln Pro Val Ala Thr Pro
85 90 95

Tyr Pro Gly Arg Ala Ala Ala Pro Pro Asn Ala Pro Gly Gly Pro Pro
100 105 110

Gly Pro Gln Pro Ala Pro Ser Ala Ala Ala Pro Pro Pro Pro Ala His
115 120 125

Ala Leu Gly Gly Met Asp Ala Glu Leu Ile Asp Glu Glu Ala Leu Thr
130 135 140

Ser Leu Glu Leu Glu Leu Gly Leu His Arg Val Arg Glu Leu Pro Glu
145 150 155 160

```
Leu Phe Leu Gly Gln Ser Glu Phe Asp Cys Phe Ser Asp Leu Gly Ser
                165                 170                 175

Ala Pro Pro Ala Gly Ser Val Ser Cys Gly Gly Ser Gly Gly Gly Ser
            180                 185                 190

Gly Ala Asp His Leu Met Leu Ala Glu Gly Tyr Arg Leu Val Gln Arg
        195                 200                 205

Pro Pro Ser Ala Ala Ala Ala His Gly Pro His Ala Leu Arg Thr Leu
    210                 215                 220

Pro Pro Tyr Ala Gly Pro Gly Leu Asp Ser Gly Leu Arg Pro Arg Gly
225                 230                 235                 240

Ala Pro Leu Gly Pro Pro Pro Pro Arg Gln Pro Gly Ala Leu Ala Tyr
                245                 250                 255

Gly Ala Phe Gly Pro Pro Ser Ser Phe Gln Pro Phe Pro Ala Val Pro
            260                 265                 270

Pro Pro Ala Ala Gly Ile Ala His Leu Gln Pro Val Ala Thr Pro Tyr
        275                 280                 285

Pro Gly Arg Ala Ala Ala Pro Pro Asn Ala Pro Gly Gly Pro Pro Gly
    290                 295                 300

Pro Gln Pro Ala Pro Ser Ala Ala Ala Pro Pro Pro Pro Ala His Ala
305                 310                 315                 320

Leu Gly Gly Met Asp Ala Glu Leu Ile Asp Glu Glu Ala Leu Thr Ser
                325                 330                 335

Leu Glu Leu Glu Leu Gly Leu His Arg Val Arg Glu Leu Pro Glu Leu
            340                 345                 350

Phe Leu Gly Gln Ser Glu Phe Asp Cys Phe Ser Asp Leu Gly Ser Ala
        355                 360                 365

Pro Pro Ala Gly Ser Val Ser Cys Gly Gly Ser Gly Gly Gly Ser Gly
    370                 375                 380
```

```
Gln Ser Gln Leu Ile Lys Pro Ser Arg Met Arg Lys Tyr Pro Asn Arg
385                 390                 395                 400

Pro Ser Lys Thr Pro Pro His Glu Arg Pro Tyr Ala Cys Pro Val Glu
                405                 410                 415

Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Asn Leu Val Arg His Ile
            420                 425                 430

Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg
        435                 440                 445

Asn Phe Ser Arg Glu Asp Asn Leu His Thr His Ile Arg Thr His Thr
    450                 455                 460

Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg
465                 470                 475                 480

Ser Asp Glu Leu Val Arg His Thr Lys Ile His Leu Arg Gln Lys Asp
                485                 490                 495

Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Gln
            500                 505                 510

Ser Gly Asn Leu Thr Glu His Ile Arg Ile His Thr Gly Gln Lys Pro
        515                 520                 525

Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Thr Ser Gly His Leu
    530                 535                 540

Val Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp
545                 550                 555                 560

Ile Cys Gly Arg Lys Phe Ala Gln Asn Ser Thr Leu Thr Glu His Thr
                565                 570                 575

Lys Ile His Leu Arg Gln Lys Asp Lys
            580                 585
```

<210> 132
<211> 523
<212> PRT
<213> Artificial Sequence

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

<400> 132
Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu
1 5 10 15

Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe
20 25 30

Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp
35 40 45

Met Leu Ile Asn Ser Arg Ser Ser Gly Ser Pro Lys Lys Lys Arg Lys
50 55 60

Val Gly Ser Gln Tyr Leu Pro Asp Thr Asp Asp Arg His Arg Ile Glu
65 70 75 80

Glu Lys Arg Lys Arg Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys Lys
85 90 95

Ser Pro Phe Ser Gly Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg Ile
100 105 110

Ala Val Pro Ser Arg Ser Ser Ala Ser Val Pro Lys Pro Ala Pro Gln
115 120 125

Pro Tyr Pro Phe Thr Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu Phe
130 135 140

Pro Thr Met Val Phe Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala Leu
145 150 155 160

Ala Pro Ala Pro Pro Gln Val Leu Pro Gln Ala Pro Ala Pro Ala Pro
165 170 175

```
Ala Pro Ala Met Val Ser Ala Leu Ala Gln Ala Pro Ala Pro Val Pro
            180                 185                 190

Val Leu Ala Pro Gly Pro Pro Gln Ala Val Ala Pro Pro Ala Pro Lys
        195                 200                 205

Pro Thr Gln Ala Gly Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln Leu
    210                 215                 220

Gln Phe Asp Asp Glu Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr Asp
225                 230                 235                 240

Pro Ala Val Phe Thr Asp Leu Ala Ser Val Asp Asn Ser Glu Phe Gln
                245                 250                 255

Gln Leu Leu Asn Gln Gly Ile Pro Val Ala Pro His Thr Thr Glu Pro
            260                 265                 270

Met Leu Met Glu Tyr Pro Glu Ala Ile Thr Arg Leu Val Thr Gly Ala
        275                 280                 285

Gln Arg Pro Pro Asp Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly Leu
    290                 295                 300

Pro Asn Gly Leu Leu Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala Asp
305                 310                 315                 320

Met Asp Phe Ser Ala Leu Leu Gly Ser Gly Ser Gly Ser Arg Asp Ser
                325                 330                 335

Arg Glu Gly Met Phe Leu Pro Lys Pro Glu Ala Gly Ser Ala Ile Ser
            340                 345                 350

Asp Val Phe Glu Gly Arg Glu Val Cys Gln Pro Lys Arg Ile Arg Pro
        355                 360                 365

Phe His Pro Pro Gly Ser Pro Trp Ala Asn Arg Pro Leu Pro Ala Ser
    370                 375                 380

Leu Ala Pro Thr Pro Thr Gly Pro Val His Glu Pro Val Gly Ser Leu
385                 390                 395                 400
```

Thr Pro Ala Pro Val Pro Gln Pro Leu Asp Pro Ala Pro Ala Val Thr
405 410 415

Pro Glu Ala Ser His Leu Leu Glu Asp Pro Asp Glu Glu Thr Ser Gln
420 425 430

Ala Val Lys Ala Leu Arg Glu Met Ala Asp Thr Val Ile Pro Gln Lys
435 440 445

Glu Glu Ala Ala Ile Cys Gly Gln Met Asp Leu Ser His Pro Pro Pro
450 455 460

Arg Gly His Leu Asp Glu Leu Thr Thr Thr Leu Glu Ser Met Thr Glu
465 470 475 480

Asp Leu Asn Leu Asp Ser Pro Leu Thr Pro Glu Leu Asn Glu Ile Leu
485 490 495

Asp Thr Phe Leu Asn Asp Glu Cys Leu Leu His Ala Met His Ile Ser
500 505 510

Thr Gly Leu Ser Ile Phe Asp Thr Ser Leu Phe
515 520

<210> 133
<211> 50
<212> PRT
<213> Artificial Sequence

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

<400> 133
Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu
1 5 10 15

Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe
20 25 30

Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp
35 40 45

Met Leu
50

<210> 134
<211> 275
<212> PRT
<213> Artificial Sequence

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

<400> 134
Met Ser Gly Leu Glu Met Ala Asp His Met Met Ala Met Asn His Gly
1 5 10 15

Arg Phe Pro Asp Gly Thr Asn Gly Leu His His His Pro Ala His Arg
20 25 30

Met Gly Met Gly Gln Phe Pro Ser Pro His His His Gln Gln Gln Gln
35 40 45

Pro Gln His Ala Phe Asn Ala Leu Met Gly Glu His Ile His Tyr Gly
50 55 60

Ala Gly Asn Met Asn Ala Thr Ser Gly Ile Arg His Ala Met Gly Pro
65 70 75 80

Gly Thr Val Asn Gly Gly His Pro Pro Ser Ala Leu Ala Pro Ala Ala
85 90 95

Arg Phe Asn Asn Ser Gln Phe Met Gly Pro Pro Val Ala Ser Gln Gly
100 105 110

Gly Ser Leu Pro Ala Ser Met Gln Leu Gln Lys Leu Asn Asn Gln Tyr
115 120 125

Phe Asn His His Pro Tyr Pro His Asn His Tyr Met Pro Asp Leu His
130 135 140

Pro Ala Ala Gly His Gln Met Asn Gly Thr Asn Gln His Phe Arg Asp
145 150 155 160

```
Cys Asn Pro Lys His Ser Gly Gly Ser Ser Thr Pro Gly Gly Ser Gly
                165                 170                 175

Gly Ser Ser Thr Pro Gly Gly Ser Gly Ser Ser Ser Gly Gly Gly Ala
            180                 185                 190

Gly Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gly Asn Met Pro Ala
        195                 200                 205

Ser Val Ala His Val Pro Ala Ala Met Leu Pro Pro Asn Val Ile Asp
    210                 215                 220

Thr Asp Phe Ile Asp Glu Glu Val Leu Met Ser Leu Val Ile Glu Met
225                 230                 235                 240

Gly Leu Asp Arg Ile Lys Glu Leu Pro Glu Leu Trp Leu Gly Gln Asn
                245                 250                 255

Glu Phe Asp Phe Met Thr Asp Phe Val Cys Lys Gln Gln Pro Ser Arg
            260                 265                 270

Val Ser Cys
        275
```

<210> 135
<211> 183
<212> PRT
<213> Artificial Sequence

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

<400> 135

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Ala Asp His Leu Met Leu Ala Glu Gly Tyr Arg Leu Val Gln Arg Pro
1               5                   10                  15

Pro Ser Ala Ala Ala Ala His Gly Pro His Ala Leu Arg Thr Leu Pro
            20                  25                  30

Pro Tyr Ala Gly Pro Gly Leu Asp Ser Gly Leu Arg Pro Arg Gly Ala
        35                  40                  45
```

Pro Leu Gly Pro Pro Pro Pro Arg Gln Pro Gly Ala Leu Ala Tyr Gly
    50   55   60

Ala Phe Gly Pro Pro Ser Ser Phe Gln Pro Phe Pro Ala Val Pro Pro
65   70   75   80

Pro Ala Ala Gly Ile Ala His Leu Gln Pro Val Ala Thr Pro Tyr Pro
                85   90   95

Gly Arg Ala Ala Ala Pro Pro Asn Ala Pro Gly Gly Pro Pro Gly Pro
            100   105   110

Gln Pro Ala Pro Ser Ala Ala Ala Pro Pro Pro Pro Ala His Ala Leu
        115   120   125

Gly Gly Met Asp Ala Glu Leu Ile Asp Glu Glu Ala Leu Thr Ser Leu
    130   135   140

Glu Leu Glu Leu Gly Leu His Arg Val Arg Glu Leu Pro Glu Leu Phe
145   150   155   160

Leu Gly Gln Ser Glu Phe Asp Cys Phe Ser Asp Leu Gly Ser Ala Pro
                165   170   175

Pro Ala Gly Ser Val Ser Cys
            180

<210> 136
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Any amino acid

<220>

<221> MOD_RES
<222> (4)..(4)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Any amino acid

<400> 136
Cys Xaa Cys Xaa His Xaa His
1   5

<210> 137
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (8)..(10)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (12)..(12)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (16)..(16)
<223> Any amino acid

<400> 137
Cys Xaa Cys Xaa Cys Xaa His Xaa Xaa Xaa Cys Xaa Cys Xaa Cys Xaa
1   5   10   15

Cys

<210> 138
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (8)..(10)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (12)..(12)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (16)..(16)
<223> Any amino acid

<400> 138
Cys Xaa Cys Xaa Cys Xaa Cys Xaa Xaa Xaa His Xaa Cys Xaa Cys Xaa
1   5   10   15

Cys

<210> 139
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (12)..(12)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (15)..(15)
<223> Cys, His, or Asp

<400> 139
Cys Xaa Cys Xaa His Xaa Cys Xaa Cys Xaa Cys Xaa Cys Xaa Xaa
1   5   10   15

<210> 140
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (8)..(10)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (12)..(12)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (14)..(14)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (16)..(16)
<223> Any amino acid

<400> 140
Cys Xaa Cys Xaa Cys Xaa Cys Xaa Xaa Xaa Cys Xaa Cys Xaa Cys Xaa
1   5   10   15

Cys

<210> 141
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
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<220>
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<223> Any amino acid

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<400> 141
Cys Xaa Cys Xaa Cys Xaa His
1   5

<210> 142
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      peptide

<220>
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<220>
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<223> Any amino acid

<400> 142
Cys Xaa Cys Xaa His Xaa Cys
1   5

<210> 143
<211> 17
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<220>
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<223> Any amino acid

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<223> Any amino acid

<220>
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1   5   10   15

Cys

<210> 144
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<220>
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peptide

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<223> Any amino acid

<400> 144
Cys Xaa Cys Xaa Cys Xaa Cys Xaa Xaa Xaa Cys Xaa Cys Xaa His Xaa
1   5   10   15

Cys

<210> 145
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<223> Any amino acid

<220>
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<223> Any amino acid

<400> 145
Cys Xaa Cys Xaa Cys Xaa Cys
1   5

<210> 146
<211> 17
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peptide

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<223> Any amino acid

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<222> (16)..(16)
<223> Any amino acid

<400> 146
Cys Xaa Cys Xaa Cys Xaa Cys Xaa Xaa Xaa Cys Xaa His Xaa His Xaa
1 5 10 15

Cys

<210> 147
<211> 344
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<213> Artificial Sequence

<220>
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polypeptide

<220>
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<222> (8)..(322)
<223> This region may encompass 1-15 "Tyr Lys Cys Pro Glu Cys
Gly Lys Ser Phe Ser His Gln Arg Thr His Thr Gly Glu Lys
Pro" repeating units

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<222> (39)..(40)

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<222> (60)..(61)

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<222> (81)..(82)

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<222> (123)..(124)

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<222> (144)..(145)

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<220>
<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 147
Leu Glu Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser
1 5 10 15

Phe Ser His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro
20 25 30

Glu Cys Gly Lys Ser Phe Ser His Gln Arg Thr His Thr Gly Glu Lys
35 40 45

Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser His Gln Arg Thr
50 55 60

His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe
65 70 75 80

Ser His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu
85 90 95

Cys Gly Lys Ser Phe Ser His Gln Arg Thr His Thr Gly Glu Lys Pro

```
            100                 105                 110

Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser His Gln Arg Thr His
        115                 120                 125

Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser
    130                 135                 140

His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys
145                 150                 155                 160

Gly Lys Ser Phe Ser His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr
                165                 170                 175

Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser His Gln Arg Thr His Thr
            180                 185                 190

Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser His
        195                 200                 205

Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly
    210                 215                 220

Lys Ser Phe Ser His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys
225                 230                 235                 240

Cys Pro Glu Cys Gly Lys Ser Phe Ser His Gln Arg Thr His Thr Gly
                245                 250                 255

Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser His Gln
            260                 265                 270

Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys
        275                 280                 285

Ser Phe Ser His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys
    290                 295                 300

Pro Glu Cys Gly Lys Ser Phe Ser His Gln Arg Thr His Thr Gly Glu
305                 310                 315                 320
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Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser His Gln Arg
325 330 335

Thr His Thr Gly Lys Lys Thr Ser
340

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<211> 292
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
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<222> (8)..(57)
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<220>
<221> MISC_FEATURE
<222> (8)..(57)
<223> This region may encompass 1-50 residues

<220>
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<222> (65)..(114)
<223> Any amino acid

<220>
<221> MISC_FEATURE
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<223> This region may encompass 1-50 residues

<220>
<221> MOD_RES
<222> (122)..(171)
<223> Any amino acid

<220>
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<223> This region may encompass 1-50 residues

<220>
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<223> This region may encompass 1-50 residues

<220>
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<223> Any amino acid

<220>
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<222> (236)..(285)
<223> This region may encompass 1-50 residues

<400> 148
Arg Ser Asp Asn Leu Val Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1   5   10   15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20   25   30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        35   40   45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Glu Asp Asn Leu His Thr
    50   55   60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65   70   75   80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                85   90   95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            100   105   110

Xaa Xaa Arg Ser Asp Glu Leu Val Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        115   120   125

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    130   135   140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
145   150   155   160

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Ser Gly Asn Leu
165 170 175

Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
210 215 220

Xaa Xaa Xaa Xaa Thr Ser Gly His Leu Val Arg Xaa Xaa Xaa Xaa Xaa
225 230 235 240

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
245 250 255

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
260 265 270

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Asn Ser
275 280 285

Thr Leu Thr Glu
290

<210> 149
<211> 292
<212> PRT
<213> Artificial Sequence

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

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<223> Any amino acid

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<221> MISC_FEATURE
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<223> Any amino acid

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<223> This region may encompass 1-50 residues

<220>
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<222> (179)..(228)
<223> Any amino acid

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<223> This region may encompass 1-50 residues

<220>
<221> MOD_RES
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<223> Any amino acid

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<221> MISC_FEATURE
<222> (236)..(285)
<223> This region may encompass 1-50 residues

<400> 149
Arg Ser Asp Asn Leu Val Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1   5   10   15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20   25   30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Arg Thr Thr Leu Thr Asn
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Xaa Xaa Arg Glu Asp Asn Leu His Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa
115 120 125

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
145 150 155 160

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser His Ser Leu
165 170 175

Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
210 215 220

Xaa Xaa Xaa Xaa Gln Ser Ser Ser Leu Val Arg Xaa Xaa Xaa Xaa Xaa
225 230 235 240

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
245 250 255

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            260   265   270

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Glu Asp
        275   280   285

Asn Leu His Thr
    290

<210> 150
<211> 292
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<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<220>
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<222> (236)..(285)
<223> This region may encompass 1-50 residues

<400> 150
Asp Pro Gly Ala Leu Val Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1   5   10   15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20   25   30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        35   40   45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Ser Asp Asn Leu Val Arg
    50   55   60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65   70   75   80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                85   90   95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            100   105   110

Xaa Xaa Gln Ser Gly Asp Leu Arg Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        115   120   125

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    130   135   140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
145 150 155 160

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr His Leu Asp Leu
165 170 175

Ile Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
210 215 220

Xaa Xaa Xaa Xaa Thr Ser Gly Asn Leu Val Arg Xaa Xaa Xaa Xaa Xaa
225 230 235 240

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
245 250 255

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
260 265 270

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Ser Asp
275 280 285

Asn Leu Val Arg
290

<210> 151
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<220>
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<220>
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<222> (65)..(114)
<223> This region may encompass 1-50 residues

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<222> (122)..(171)
<223> Any amino acid

<220>
<221> MISC_FEATURE
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<223> Any amino acid

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<221> MISC_FEATURE
<222> (179)..(228)
<223> This region may encompass 1-50 residues

<220>
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<222> (236)..(285)
<223> Any amino acid

<220>
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<222> (236)..(285)
<223> This region may encompass 1-50 residues

<220>
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<220>

<221> MISC_FEATURE
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<223> This region may encompass 1-50 residues

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<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (350)..(399)
<223> This region may encompass 1-50 residues

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<222> (407)..(456)
<223> Any amino acid

<220>
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<222> (407)..(456)
<223> This region may encompass 1-50 residues

<400> 151
Arg Arg Asp Glu Leu Asn Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1   5   10   15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20   25   30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        35   40   45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Ser Asp His Leu Thr Asn
    50   55   60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65   70   75   80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                85   90   95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            100   105   110

Xaa Xaa Arg Ser Asp Asp Leu Val Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

```
        115                 120                 125

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    130                 135                 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
145                 150                 155                 160

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Ser Asp Asn Leu
                165                 170                 175

Val Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            180                 185                 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        195                 200                 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    210                 215                 220

Xaa Xaa Xaa Xaa His Arg Thr Thr Leu Thr Asn Xaa Xaa Xaa Xaa Xaa
225                 230                 235                 240

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                245                 250                 255

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            260                 265                 270

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Glu Asp
        275                 280                 285

Asn Leu His Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    290                 295                 300

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
305                 310                 315                 320

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                325                 330                 335
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Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser His Ser Leu Thr Glu Xaa Xaa Xaa
340 345 350

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
355 360 365

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
370 375 380

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln
385 390 395 400

Ser Ser Ser Leu Val Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
405 410 415

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
420 425 430

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
435 440 445

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Glu Asp Asn Leu His Thr
450 455 460

<210> 152
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 152
Arg Ser Asp Asn Leu Val Arg
1 5

<210> 153
<211> 7
<212> PRT
<213> Artificial Sequence

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

peptide

<400> 153
Arg Glu Asp Asn Leu His Thr
1 5

<210> 154
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 154
Arg Ser Asp Glu Leu Val Arg
1 5

<210> 155
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<400> 155
Gln Ser Gly Asn Leu Thr Glu
1 5

<210> 156
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 156
Thr Ser Gly His Leu Val Arg
1 5

<210> 157
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 157
Gln Asn Ser Thr Leu Thr Glu
1 5

<210> 158
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 158
Asp Pro Gly Ala Leu Val Arg
1 5

<210> 159
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 159
His Arg Thr Thr Leu Thr Asn
1 5

<210> 160
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 160
Gln Ser Gly Asp Leu Arg Arg
1 5

<210> 161
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 161
Thr Ser His Ser Leu Thr Glu
1 5

<210> 162
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 162
Thr His Leu Asp Leu Ile Arg
1 5

<210> 163
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 163
Gln Ser Ser Ser Leu Val Arg
1 5

<210> 164
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 164
Thr Ser Gly Asn Leu Val Arg
1 5

<210> 165

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

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 165
Arg Arg Asp Glu Leu Asn Val
1 5

<210> 166
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 166
Arg Ser Asp Asp Leu Val Arg
1 5

<210> 167
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 167
Arg Ser Asp His Leu Thr Asn
1 5

<210> 168
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 168
Leu Ile Lys Pro Ser Arg Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys
1 5 10 15

<210> 169
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 169
Pro Lys Lys Lys Arg Lys Val
1 5

<210> 170
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 170
Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys Lys
1 5 10 15

<210> 171
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 171
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

<210> 172
<211> 2009
<212> PRT
<213> Homo sapiens

<400> 172
Met Glu Gln Thr Val Leu Val Pro Pro Gly Pro Asp Ser Phe Asn Phe
1 5 10 15

Phe Thr Arg Glu Ser Leu Ala Ala Ile Glu Arg Arg Ile Ala Glu Glu

```
            20                  25                  30

Lys Ala Lys Asn Pro Lys Pro Asp Lys Lys Asp Asp Asp Glu Asn Gly
        35                  40                  45

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

Tyr Gly Asp Ile Pro Pro Glu Met Val Ser Glu Pro Leu Glu Asp Leu
65                  70                  75                  80

Asp Pro Tyr Tyr Ile Asn Lys Lys Thr Phe Ile Val Leu Asn Lys Gly
                85                  90                  95

Lys Ala Ile Phe Arg Phe Ser Ala Thr Ser Ala Leu Tyr Ile Leu Thr
            100                 105                 110

Pro Phe Asn Pro Leu Arg Lys Ile Ala Ile Lys Ile Leu Val His Ser
        115                 120                 125

Leu Phe Ser Met Leu Ile Met Cys Thr Ile Leu Thr Asn Cys Val Phe
    130                 135                 140

Met Thr Met Ser Asn Pro Pro Asp Trp Thr Lys Asn Val Glu Tyr Thr
145                 150                 155                 160

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

Gly Phe Cys Leu Glu Asp Phe Thr Phe Leu Arg Asp Pro Trp Asn Trp
            180                 185                 190

Leu Asp Phe Thr Val Ile Thr Phe Ala Tyr Val Thr Glu Phe Val Asp
        195                 200                 205

Leu Gly Asn Val Ser Ala Leu Arg Thr Phe Arg Val Leu Arg Ala Leu
    210                 215                 220

Lys Thr Ile Ser Val Ile Pro Gly Leu Lys Thr Ile Val Gly Ala Leu
225                 230                 235                 240
```

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

Cys Leu Ser Val Phe Ala Leu Ile Gly Leu Gln Leu Phe Met Gly Asn
            260                 265                 270

Leu Arg Asn Lys Cys Ile Gln Trp Pro Pro Thr Asn Ala Ser Leu Glu
        275                 280                 285

Glu His Ser Ile Glu Lys Asn Ile Thr Val Asn Tyr Asn Gly Thr Leu
    290                 295                 300

Ile Asn Glu Thr Val Phe Glu Phe Asp Trp Lys Ser Tyr Ile Gln Asp
305                 310                 315                 320

Ser Arg Tyr His Tyr Phe Leu Glu Gly Phe Leu Asp Ala Leu Leu Cys
                325                 330                 335

Gly Asn Ser Ser Asp Ala Gly Gln Cys Pro Glu Gly Tyr Met Cys Val
            340                 345                 350

Lys Ala Gly Arg Asn Pro Asn Tyr Gly Tyr Thr Ser Phe Asp Thr Phe
        355                 360                 365

Ser Trp Ala Phe Leu Ser Leu Phe Arg Leu Met Thr Gln Asp Phe Trp
    370                 375                 380

Glu Asn Leu Tyr Gln Leu Thr Leu Arg Ala Ala Gly Lys Thr Tyr Met
385                 390                 395                 400

Ile Phe Phe Val Leu Val Ile Phe Leu Gly Ser Phe Tyr Leu Ile Asn
                405                 410                 415

Leu Ile Leu Ala Val Val Ala Met Ala Tyr Glu Glu Gln Asn Gln Ala
            420                 425                 430

Thr Leu Glu Glu Ala Glu Gln Lys Glu Ala Glu Phe Gln Gln Met Ile
        435                 440                 445

Glu Gln Leu Lys Lys Gln Gln Glu Ala Ala Gln Gln Ala Ala Thr Ala
```

```
    450                 455                 460

Thr Ala Ser Glu His Ser Arg Glu Pro Ser Ala Ala Gly Arg Leu Ser
465                 470                 475                 480

Asp Ser Ser Ser Glu Ala Ser Lys Leu Ser Ser Lys Ser Ala Lys Glu
                485                 490                 495

Arg Arg Asn Arg Arg Lys Lys Arg Lys Gln Lys Glu Gln Ser Gly Gly
            500                 505                 510

Glu Glu Lys Asp Glu Asp Glu Phe Gln Lys Ser Glu Ser Glu Asp Ser
        515                 520                 525

Ile Arg Arg Lys Gly Phe Arg Phe Ser Ile Glu Gly Asn Arg Leu Thr
    530                 535                 540

Tyr Glu Lys Arg Tyr Ser Ser Pro His Gln Ser Leu Leu Ser Ile Arg
545                 550                 555                 560

Gly Ser Leu Phe Ser Pro Arg Arg Asn Ser Arg Thr Ser Leu Phe Ser
                565                 570                 575

Phe Arg Gly Arg Ala Lys Asp Val Gly Ser Glu Asn Asp Phe Ala Asp
            580                 585                 590

Asp Glu His Ser Thr Phe Glu Asp Asn Glu Ser Arg Arg Asp Ser Leu
        595                 600                 605

Phe Val Pro Arg Arg His Gly Glu Arg Arg Asn Ser Asn Leu Ser Gln
    610                 615                 620

Thr Ser Arg Ser Ser Arg Met Leu Ala Val Phe Pro Ala Asn Gly Lys
625                 630                 635                 640

Met His Ser Thr Val Asp Cys Asn Gly Val Val Ser Leu Val Gly Gly
                645                 650                 655

Pro Ser Val Pro Thr Ser Pro Val Gly Gln Leu Leu Pro Glu Val Ile
            660                 665                 670
```

```
Ile Asp Lys Pro Ala Thr Asp Asp Asn Gly Thr Thr Thr Glu Thr Glu
        675                 680                 685

Met Arg Lys Arg Arg Ser Ser Ser Phe His Val Ser Met Asp Phe Leu
    690                 695                 700

Glu Asp Pro Ser Gln Arg Gln Arg Ala Met Ser Ile Ala Ser Ile Leu
705                 710                 715                 720

Thr Asn Thr Val Glu Glu Leu Glu Glu Ser Arg Gln Lys Cys Pro Pro
                725                 730                 735

Cys Trp Tyr Lys Phe Ser Asn Ile Phe Leu Ile Trp Asp Cys Ser Pro
            740                 745                 750

Tyr Trp Leu Lys Val Lys His Val Val Asn Leu Val Val Met Asp Pro
        755                 760                 765

Phe Val Asp Leu Ala Ile Thr Ile Cys Ile Val Leu Asn Thr Leu Phe
    770                 775                 780

Met Ala Met Glu His Tyr Pro Met Thr Asp His Phe Asn Asn Val Leu
785                 790                 795                 800

Thr Val Gly Asn Leu Val Phe Thr Gly Ile Phe Thr Ala Glu Met Phe
                805                 810                 815

Leu Lys Ile Ile Ala Met Asp Pro Tyr Tyr Tyr Phe Gln Glu Gly Trp
            820                 825                 830

Asn Ile Phe Asp Gly Phe Ile Val Thr Leu Ser Leu Val Glu Leu Gly
        835                 840                 845

Leu Ala Asn Val Glu Gly Leu Ser Val Leu Arg Ser Phe Arg Leu Leu
    850                 855                 860

Arg Val Phe Lys Leu Ala Lys Ser Trp Pro Thr Leu Asn Met Leu Ile
865                 870                 875                 880

Lys Ile Ile Gly Asn Ser Val Gly Ala Leu Gly Asn Leu Thr Leu Val
```

```
               885                 890                 895

Leu Ala Ile Ile Val Phe Ile Phe Ala Val Val Gly Met Gln Leu Phe
            900                 905                 910

Gly Lys Ser Tyr Lys Asp Cys Val Cys Lys Ile Ala Ser Asp Cys Gln
        915                 920                 925

Leu Pro Arg Trp His Met Asn Asp Phe Phe His Ser Phe Leu Ile Val
    930                 935                 940

Phe Arg Val Leu Cys Gly Glu Trp Ile Glu Thr Met Trp Asp Cys Met
945                 950                 955                 960

Glu Val Ala Gly Gln Ala Met Cys Leu Thr Val Phe Met Met Val Met
                965                 970                 975

Val Ile Gly Asn Leu Val Val Leu Asn Leu Phe Leu Ala Leu Leu Leu
            980                 985                 990

Ser Ser Phe Ser Ala Asp Asn Leu  Ala Ala Thr Asp Asp  Asp Asn Glu
        995                 1000                1005

Met Asn  Asn Leu Gln Ile Ala  Val Asp Arg Met His  Lys Gly Val
    1010                1015                1020

Ala Tyr  Val Lys Arg Lys Ile  Tyr Glu Phe Ile Gln  Gln Ser Phe
    1025                1030                1035

Ile Arg  Lys Gln Lys Ile Leu  Asp Glu Ile Lys Pro  Leu Asp Asp
    1040                1045                1050

Leu Asn  Asn Lys Lys Asp Ser  Cys Met Ser Asn His  Thr Ala Glu
    1055                1060                1065

Ile Gly  Lys Asp Leu Asp Tyr  Leu Lys Asp Val Asn  Gly Thr Thr
    1070                1075                1080

Ser Gly  Ile Gly Thr Gly Ser  Ser Val Glu Lys Tyr  Ile Ile Asp
    1085                1090                1095
```

```
Glu Ser  Asp Tyr Met Ser Phe  Ile Asn Asn Pro Ser  Leu Thr Val
    1100                1105                1110

Thr Val  Pro Ile Ala Val Gly  Glu Ser Asp Phe Glu  Asn Leu Asn
    1115                1120                1125

Thr Glu  Asp Phe Ser Ser Glu  Ser Asp Leu Glu Glu  Ser Lys Glu
    1130                1135                1140

Lys Leu  Asn Glu Ser Ser Ser  Ser Ser Glu Gly Ser  Thr Val Asp
    1145                1150                1155

Ile Gly  Ala Pro Val Glu Glu  Gln Pro Val Val Glu  Pro Glu Glu
    1160                1165                1170

Thr Leu  Glu Pro Glu Ala Cys  Phe Thr Glu Gly Cys  Val Gln Arg
    1175                1180                1185

Phe Lys  Cys Cys Gln Ile Asn  Val Glu Glu Gly Arg  Gly Lys Gln
    1190                1195                1200

Trp Trp  Asn Leu Arg Arg Thr  Cys Phe Arg Ile Val  Glu His Asn
    1205                1210                1215

Trp Phe  Glu Thr Phe Ile Val  Phe Met Ile Leu Leu  Ser Ser Gly
    1220                1225                1230

Ala Leu  Ala Phe Glu Asp Ile  Tyr Ile Asp Gln Arg  Lys Thr Ile
    1235                1240                1245

Lys Thr  Met Leu Glu Tyr Ala  Asp Lys Val Phe Thr  Tyr Ile Phe
    1250                1255                1260

Ile Leu  Glu Met Leu Leu Lys  Trp Val Ala Tyr Gly  Tyr Gln Thr
    1265                1270                1275

Tyr Phe  Thr Asn Ala Trp Cys  Trp Leu Asp Phe Leu  Ile Val Asp
    1280                1285                1290

Val Ser  Leu Val Ser Leu Thr  Ala Asn Ala Leu Gly  Tyr Ser Glu
```

```
    1295                1300                1305

Leu Gly  Ala Ile Lys Ser Leu  Arg Thr Leu Arg Ala  Leu Arg Pro
    1310                1315                1320

Leu Arg  Ala Leu Ser Arg Phe  Glu Gly Met Arg Val  Val Val Asn
    1325                1330                1335

Ala Leu  Leu Gly Ala Ile Pro  Ser Ile Met Asn Val  Leu Leu Val
    1340                1345                1350

Cys Leu  Ile Phe Trp Leu Ile  Phe Ser Ile Met Gly  Val Asn Leu
    1355                1360                1365

Phe Ala  Gly Lys Phe Tyr His  Cys Ile Asn Thr Thr  Thr Gly Asp
    1370                1375                1380

Arg Phe  Asp Ile Glu Asp Val  Asn Asn His Thr Asp  Cys Leu Lys
    1385                1390                1395

Leu Ile  Glu Arg Asn Glu Thr  Ala Arg Trp Lys Asn  Val Lys Val
    1400                1405                1410

Asn Phe  Asp Asn Val Gly Phe  Gly Tyr Leu Ser Leu  Leu Gln Val
    1415                1420                1425

Ala Thr  Phe Lys Gly Trp Met  Asp Ile Met Tyr Ala  Ala Val Asp
    1430                1435                1440

Ser Arg  Asn Val Glu Leu Gln  Pro Lys Tyr Glu Glu  Ser Leu Tyr
    1445                1450                1455

Met Tyr  Leu Tyr Phe Val Ile  Phe Ile Ile Phe Gly  Ser Phe Phe
    1460                1465                1470

Thr Leu  Asn Leu Phe Ile Gly  Val Ile Ile Asp Asn  Phe Asn Gln
    1475                1480                1485

Gln Lys  Lys Lys Phe Gly Gly  Gln Asp Ile Phe Met  Thr Glu Glu
    1490                1495                1500
```

```
Gln Lys  Lys Tyr Tyr Asn Ala  Met Lys Lys Leu Gly  Ser Lys Lys
    1505                1510                1515

Pro Gln  Lys Pro Ile Pro Arg  Pro Gly Asn Lys Phe  Gln Gly Met
    1520                1525                1530

Val Phe  Asp Phe Val Thr Arg  Gln Val Phe Asp Ile  Ser Ile Met
    1535                1540                1545

Ile Leu  Ile Cys Leu Asn Met  Val Thr Met Met Val  Glu Thr Asp
    1550                1555                1560

Asp Gln  Ser Glu Tyr Val Thr  Thr Ile Leu Ser Arg  Ile Asn Leu
    1565                1570                1575

Val Phe  Ile Val Leu Phe Thr  Gly Glu Cys Val Leu  Lys Leu Ile
    1580                1585                1590

Ser Leu  Arg His Tyr Tyr Phe  Thr Ile Gly Trp Asn  Ile Phe Asp
    1595                1600                1605

Phe Val  Val Val Ile Leu Ser  Ile Val Gly Met Phe  Leu Ala Glu
    1610                1615                1620

Leu Ile  Glu Lys Tyr Phe Val  Ser Pro Thr Leu Phe  Arg Val Ile
    1625                1630                1635

Arg Leu  Ala Arg Ile Gly Arg  Ile Leu Arg Leu Ile  Lys Gly Ala
    1640                1645                1650

Lys Gly  Ile Arg Thr Leu Leu  Phe Ala Leu Met Met  Ser Leu Pro
    1655                1660                1665

Ala Leu  Phe Asn Ile Gly Leu  Leu Leu Phe Leu Val  Met Phe Ile
    1670                1675                1680

Tyr Ala  Ile Phe Gly Met Ser  Asn Phe Ala Tyr Val  Lys Arg Glu
    1685                1690                1695

Val Gly  Ile Asp Asp Met Phe  Asn Phe Glu Thr Phe  Gly Asn Ser
```

```
    1700                1705                1710

Met Ile  Cys Leu Phe Gln Ile  Thr Thr Ser Ala Gly  Trp Asp Gly
    1715                1720                1725

Leu Leu  Ala Pro Ile Leu Asn  Ser Lys Pro Pro Asp  Cys Asp Pro
    1730                1735                1740

Asn Lys  Val Asn Pro Gly Ser  Ser Val Lys Gly Asp  Cys Gly Asn
    1745                1750                1755

Pro Ser  Val Gly Ile Phe Phe  Phe Val Ser Tyr Ile  Ile Ile Ser
    1760                1765                1770

Phe Leu  Val Val Val Asn Met  Tyr Ile Ala Val Ile  Leu Glu Asn
    1775                1780                1785

Phe Ser  Val Ala Thr Glu Glu  Ser Ala Glu Pro Leu  Ser Glu Asp
    1790                1795                1800

Asp Phe  Glu Met Phe Tyr Glu  Val Trp Glu Lys Phe  Asp Pro Asp
    1805                1810                1815

Ala Thr  Gln Phe Met Glu Phe  Glu Lys Leu Ser Gln  Phe Ala Ala
    1820                1825                1830

Ala Leu  Glu Pro Pro Leu Asn  Leu Pro Gln Pro Asn  Lys Leu Gln
    1835                1840                1845

Leu Ile  Ala Met Asp Leu Pro  Met Val Ser Gly Asp  Arg Ile His
    1850                1855                1860

Cys Leu  Asp Ile Leu Phe Ala  Phe Thr Lys Arg Val  Leu Gly Glu
    1865                1870                1875

Ser Gly  Glu Met Asp Ala Leu  Arg Ile Gln Met Glu  Glu Arg Phe
    1880                1885                1890

Met Ala  Ser Asn Pro Ser Lys  Val Ser Tyr Gln Pro  Ile Thr Thr
    1895                1900                1905
```

```
Thr Leu  Lys Arg Lys Gln Glu  Glu Val Ser Ala Val  Ile Ile Gln
    1910                1915                1920


Arg Ala  Tyr Arg Arg His Leu  Leu Lys Arg Thr Val  Lys Gln Ala
    1925                1930                1935


Ser Phe  Thr Tyr Asn Lys Asn  Lys Ile Lys Gly Gly  Ala Asn Leu
    1940                1945                1950


Leu Ile  Lys Glu Asp Met Ile  Ile Asp Arg Ile Asn  Glu Asn Ser
    1955                1960                1965


Ile Thr  Glu Lys Thr Asp Leu  Thr Met Ser Thr Ala  Ala Cys Pro
    1970                1975                1980


Pro Ser  Tyr Asp Arg Val Thr  Lys Pro Ile Val Glu  Lys His Glu
    1985                1990                1995


Gln Glu  Gly Lys Asp Glu Lys  Ala Lys Gly Lys
    2000                2005


<210> 173
<211> 1052
<212> PRT
<213> Homo sapiens

<400> 173
Lys Arg Asn Tyr Ile Leu Gly Leu Ala Ile Gly Ile Thr Ser Val Gly
1               5                   10                  15


Tyr Gly Ile Ile Asp Tyr Glu Thr Arg Asp Val Ile Asp Ala Gly Val
            20                  25                  30


Arg Leu Phe Lys Glu Ala Asn Val Glu Asn Asn Glu Gly Arg Arg Ser
        35                  40                  45


Lys Arg Gly Ala Arg Arg Leu Lys Arg Arg Arg Arg His Arg Ile Gln
    50                  55                  60


Arg Val Lys Lys Leu Leu Phe Asp Tyr Asn Leu Leu Thr Asp His Ser
65                  70                  75                  80
```

```
Glu Leu Ser Gly Ile Asn Pro Tyr Glu Ala Arg Val Lys Gly Leu Ser
                85                  90                  95

Gln Lys Leu Ser Glu Glu Glu Phe Ser Ala Ala Leu Leu His Leu Ala
            100                 105                 110

Lys Arg Arg Gly Val His Asn Val Asn Glu Val Glu Glu Asp Thr Gly
        115                 120                 125

Asn Glu Leu Ser Thr Lys Glu Gln Ile Ser Arg Asn Ser Lys Ala Leu
    130                 135                 140

Glu Glu Lys Tyr Val Ala Glu Leu Gln Leu Glu Arg Leu Lys Lys Asp
145                 150                 155                 160

Gly Glu Val Arg Gly Ser Ile Asn Arg Phe Lys Thr Ser Asp Tyr Val
                165                 170                 175

Lys Glu Ala Lys Gln Leu Leu Lys Val Gln Lys Ala Tyr His Gln Leu
            180                 185                 190

Asp Gln Ser Phe Ile Asp Thr Tyr Ile Asp Leu Leu Glu Thr Arg Arg
        195                 200                 205

Thr Tyr Tyr Glu Gly Pro Gly Glu Gly Ser Pro Phe Gly Trp Lys Asp
    210                 215                 220

Ile Lys Glu Trp Tyr Glu Met Leu Met Gly His Cys Thr Tyr Phe Pro
225                 230                 235                 240

Glu Glu Leu Arg Ser Val Lys Tyr Ala Tyr Asn Ala Asp Leu Tyr Asn
                245                 250                 255

Ala Leu Asn Asp Leu Asn Asn Leu Val Ile Thr Arg Asp Glu Asn Glu
            260                 265                 270

Lys Leu Glu Tyr Tyr Glu Lys Phe Gln Ile Ile Glu Asn Val Phe Lys
        275                 280                 285

Gln Lys Lys Lys Pro Thr Leu Lys Gln Ile Ala Lys Glu Ile Leu Val
```

```
    290                 295                 300

Asn Glu Glu Asp Ile Lys Gly Tyr Arg Val Thr Ser Thr Gly Lys Pro
305                 310                 315                 320

Glu Phe Thr Asn Leu Lys Val Tyr His Asp Ile Lys Asp Ile Thr Ala
                325                 330                 335

Arg Lys Glu Ile Ile Glu Asn Ala Glu Leu Leu Asp Gln Ile Ala Lys
            340                 345                 350

Ile Leu Thr Ile Tyr Gln Ser Ser Glu Asp Ile Gln Glu Glu Leu Thr
        355                 360                 365

Asn Leu Asn Ser Glu Leu Thr Gln Glu Glu Ile Glu Gln Ile Ser Asn
    370                 375                 380

Leu Lys Gly Tyr Thr Gly Thr His Asn Leu Ser Leu Lys Ala Ile Asn
385                 390                 395                 400

Leu Ile Leu Asp Glu Leu Trp His Thr Asn Asp Asn Gln Ile Ala Ile
                405                 410                 415

Phe Asn Arg Leu Lys Leu Val Pro Lys Lys Val Asp Leu Ser Gln Gln
            420                 425                 430

Lys Glu Ile Pro Thr Thr Leu Val Asp Asp Phe Ile Leu Ser Pro Val
        435                 440                 445

Val Lys Arg Ser Phe Ile Gln Ser Ile Lys Val Ile Asn Ala Ile Ile
    450                 455                 460

Lys Lys Tyr Gly Leu Pro Asn Asp Ile Ile Ile Glu Leu Ala Arg Glu
465                 470                 475                 480

Lys Asn Ser Lys Asp Ala Gln Lys Met Ile Asn Glu Met Gln Lys Arg
                485                 490                 495

Asn Arg Gln Thr Asn Glu Arg Ile Glu Glu Ile Ile Arg Thr Thr Gly
            500                 505                 510
```

```
Lys Glu Asn Ala Lys Tyr Leu Ile Glu Lys Ile Lys Leu His Asp Met
        515                 520                 525

Gln Glu Gly Lys Cys Leu Tyr Ser Leu Glu Ala Ile Pro Leu Glu Asp
    530                 535                 540

Leu Leu Asn Asn Pro Phe Asn Tyr Glu Val Asp His Ile Ile Pro Arg
545                 550                 555                 560

Ser Val Ser Phe Asp Asn Ser Phe Asn Asn Lys Val Leu Val Lys Gln
                565                 570                 575

Glu Glu Ala Ser Lys Lys Gly Asn Arg Thr Pro Phe Gln Tyr Leu Ser
            580                 585                 590

Ser Ser Asp Ser Lys Ile Ser Tyr Glu Thr Phe Lys Lys His Ile Leu
        595                 600                 605

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

Leu Leu Glu Glu Arg Asp Ile Asn Arg Phe Ser Val Gln Lys Asp Phe
625                 630                 635                 640

Ile Asn Arg Asn Leu Val Asp Thr Arg Tyr Ala Thr Arg Gly Leu Met
                645                 650                 655

Asn Leu Leu Arg Ser Tyr Phe Arg Val Asn Asn Leu Asp Val Lys Val
            660                 665                 670

Lys Ser Ile Asn Gly Gly Phe Thr Ser Phe Leu Arg Arg Lys Trp Lys
        675                 680                 685

Phe Lys Lys Glu Arg Asn Lys Gly Tyr Lys His His Ala Glu Asp Ala
    690                 695                 700

Leu Ile Ile Ala Asn Ala Asp Phe Ile Phe Lys Glu Trp Lys Lys Leu
705                 710                 715                 720

Asp Lys Ala Lys Lys Val Met Glu Asn Gln Met Phe Glu Glu Lys Gln
```

```
                725                 730                 735

Ala Glu Ser Met Pro Glu Ile Glu Thr Glu Gln Glu Tyr Lys Glu Ile
            740                 745                 750

Phe Ile Thr Pro His Gln Ile Lys His Ile Lys Asp Phe Lys Asp Tyr
        755                 760                 765

Lys Tyr Ser His Arg Val Asp Lys Lys Pro Asn Arg Glu Leu Ile Asn
    770                 775                 780

Asp Thr Leu Tyr Ser Thr Arg Lys Asp Asp Lys Gly Asn Thr Leu Ile
785                 790                 795                 800

Val Asn Asn Leu Asn Gly Leu Tyr Asp Lys Asp Asn Asp Lys Leu Lys
                805                 810                 815

Lys Leu Ile Asn Lys Ser Pro Glu Lys Leu Leu Met Tyr His His Asp
            820                 825                 830

Pro Gln Thr Tyr Gln Lys Leu Lys Leu Ile Met Glu Gln Tyr Gly Asp
        835                 840                 845

Glu Lys Asn Pro Leu Tyr Lys Tyr Tyr Glu Glu Thr Gly Asn Tyr Leu
    850                 855                 860

Thr Lys Tyr Ser Lys Lys Asp Asn Gly Pro Val Ile Lys Lys Ile Lys
865                 870                 875                 880

Tyr Tyr Gly Asn Lys Leu Asn Ala His Leu Asp Ile Thr Asp Asp Tyr
                885                 890                 895

Pro Asn Ser Arg Asn Lys Val Val Lys Leu Ser Leu Lys Pro Tyr Arg
            900                 905                 910

Phe Asp Val Tyr Leu Asp Asn Gly Val Tyr Lys Phe Val Thr Val Lys
        915                 920                 925

Asn Leu Asp Val Ile Lys Lys Glu Asn Tyr Tyr Glu Val Asn Ser Lys
    930                 935                 940
```

```
Cys Tyr Glu Glu Ala Lys Lys Leu Lys Lys Ile Ser Asn Gln Ala Glu
945                 950                 955                 960


Phe Ile Ala Ser Phe Tyr Asn Asn Asp Leu Ile Lys Ile Asn Gly Glu
                965                 970                 975


Leu Tyr Arg Val Ile Gly Val Asn Asn Asp Leu Leu Asn Arg Ile Glu
            980                 985                 990


Val Asn Met Ile Asp Ile Thr Tyr  Arg Glu Tyr Leu Glu  Asn Met Asn
        995                 1000                1005


Asp Lys  Arg Pro Pro Arg Ile  Ile Lys Thr Ile Ala  Ser Lys Thr
    1010                1015                1020


Gln Ser  Ile Lys Lys Tyr Ser  Thr Asp Ile Leu Gly  Asn Leu Tyr
    1025                1030                1035


Glu Val  Lys Ser Lys Lys His  Pro Gln Ile Ile Lys  Lys Gly
    1040                1045                1050


<210> 174
<211> 1148
<212> PRT
<213> Artificial Sequence

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

<400> 174
Met Ala Pro Lys Lys Lys Arg Lys Val Gly Ile His Gly Val Pro Ala
1               5                   10                  15


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


Gly Tyr Gly Ile Ile Asp Tyr Glu Thr Arg Asp Val Ile Asp Ala Gly
        35                  40                  45


Val Arg Leu Phe Lys Glu Ala Asn Val Glu Asn Asn Glu Gly Arg Arg
    50                  55                  60
```

```
Ser Lys Arg Gly Ala Arg Arg Leu Lys Arg Arg Arg Arg His Arg Ile
65                  70                  75                  80

Gln Arg Val Lys Lys Leu Leu Phe Asp Tyr Asn Leu Leu Thr Asp His
                85                  90                  95

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

Ser Gln Lys Leu Ser Glu Glu Glu Phe Ser Ala Ala Leu Leu His Leu
        115                 120                 125

Ala Lys Arg Arg Gly Val His Asn Val Asn Glu Val Glu Glu Asp Thr
    130                 135                 140

Gly Asn Glu Leu Ser Thr Lys Glu Gln Ile Ser Arg Asn Ser Lys Ala
145                 150                 155                 160

Leu Glu Glu Lys Tyr Val Ala Glu Leu Gln Leu Glu Arg Leu Lys Lys
                165                 170                 175

Asp Gly Glu Val Arg Gly Ser Ile Asn Arg Phe Lys Thr Ser Asp Tyr
            180                 185                 190

Val Lys Glu Ala Lys Gln Leu Leu Lys Val Gln Lys Ala Tyr His Gln
        195                 200                 205

Leu Asp Gln Ser Phe Ile Asp Thr Tyr Ile Asp Leu Leu Glu Thr Arg
    210                 215                 220

Arg Thr Tyr Tyr Glu Gly Pro Gly Glu Gly Ser Pro Phe Gly Trp Lys
225                 230                 235                 240

Asp Ile Lys Glu Trp Tyr Glu Met Leu Met Gly His Cys Thr Tyr Phe
                245                 250                 255

Pro Glu Glu Leu Arg Ser Val Lys Tyr Ala Tyr Asn Ala Asp Leu Tyr
            260                 265                 270

Asn Ala Leu Asn Asp Leu Asn Asn Leu Val Ile Thr Arg Asp Glu Asn
```

```
        275                 280                 285

Glu Lys Leu Glu Tyr Tyr Glu Lys Phe Gln Ile Ile Glu Asn Val Phe
    290                 295                 300

Lys Gln Lys Lys Lys Pro Thr Leu Lys Gln Ile Ala Lys Glu Ile Leu
305                 310                 315                 320

Val Asn Glu Glu Asp Ile Lys Gly Tyr Arg Val Thr Ser Thr Gly Lys
                325                 330                 335

Pro Glu Phe Thr Asn Leu Lys Val Tyr His Asp Ile Lys Asp Ile Thr
            340                 345                 350

Ala Arg Lys Glu Ile Ile Glu Asn Ala Glu Leu Leu Asp Gln Ile Ala
        355                 360                 365

Lys Ile Leu Thr Ile Tyr Gln Ser Ser Glu Asp Ile Gln Glu Glu Leu
    370                 375                 380

Thr Asn Leu Asn Ser Glu Leu Thr Gln Glu Glu Ile Glu Gln Ile Ser
385                 390                 395                 400

Asn Leu Lys Gly Tyr Thr Gly Thr His Asn Leu Ser Leu Lys Ala Ile
                405                 410                 415

Asn Leu Ile Leu Asp Glu Leu Trp His Thr Asn Asp Asn Gln Ile Ala
            420                 425                 430

Ile Phe Asn Arg Leu Lys Leu Val Pro Lys Lys Val Asp Leu Ser Gln
        435                 440                 445

Gln Lys Glu Ile Pro Thr Thr Leu Val Asp Asp Phe Ile Leu Ser Pro
    450                 455                 460

Val Val Lys Arg Ser Phe Ile Gln Ser Ile Lys Val Ile Asn Ala Ile
465                 470                 475                 480

Ile Lys Lys Tyr Gly Leu Pro Asn Asp Ile Ile Ile Glu Leu Ala Arg
                485                 490                 495
```

```
Glu Lys Asn Ser Lys Asp Ala Gln Lys Met Ile Asn Glu Met Gln Lys
            500                 505                 510

Arg Asn Arg Gln Thr Asn Glu Arg Ile Glu Glu Ile Ile Arg Thr Thr
        515                 520                 525

Gly Lys Glu Asn Ala Lys Tyr Leu Ile Glu Lys Ile Lys Leu His Asp
    530                 535                 540

Met Gln Glu Gly Lys Cys Leu Tyr Ser Leu Glu Ala Ile Pro Leu Glu
545                 550                 555                 560

Asp Leu Leu Asn Asn Pro Phe Asn Tyr Glu Val Asp His Ile Ile Pro
                565                 570                 575

Arg Ser Val Ser Phe Asp Asn Ser Phe Asn Asn Lys Val Leu Val Lys
            580                 585                 590

Gln Glu Glu Ala Ser Lys Lys Gly Asn Arg Thr Pro Phe Gln Tyr Leu
        595                 600                 605

Ser Ser Ser Asp Ser Lys Ile Ser Tyr Glu Thr Phe Lys Lys His Ile
    610                 615                 620

Leu Asn Leu Ala Lys Gly Lys Gly Arg Ile Ser Lys Thr Lys Lys Glu
625                 630                 635                 640

Tyr Leu Leu Glu Glu Arg Asp Ile Asn Arg Phe Ser Val Gln Lys Asp
                645                 650                 655

Phe Ile Asn Arg Asn Leu Val Asp Thr Arg Tyr Ala Thr Arg Gly Leu
            660                 665                 670

Met Asn Leu Leu Arg Ser Tyr Phe Arg Val Asn Asn Leu Asp Val Lys
        675                 680                 685

Val Lys Ser Ile Asn Gly Gly Phe Thr Ser Phe Leu Arg Arg Lys Trp
    690                 695                 700

Lys Phe Lys Lys Glu Arg Asn Lys Gly Tyr Lys His His Ala Glu Asp
```

```
705                 710                 715                 720

Ala Leu Ile Ile Ala Asn Ala Asp Phe Ile Phe Lys Glu Trp Lys Lys
                725                 730                 735

Leu Asp Lys Ala Lys Lys Val Met Glu Asn Gln Met Phe Glu Glu Lys
            740                 745                 750

Gln Ala Glu Ser Met Pro Glu Ile Glu Thr Glu Gln Glu Tyr Lys Glu
        755                 760                 765

Ile Phe Ile Thr Pro His Gln Ile Lys His Ile Lys Asp Phe Lys Asp
    770                 775                 780

Tyr Lys Tyr Ser His Arg Val Asp Lys Lys Pro Asn Arg Glu Leu Ile
785                 790                 795                 800

Asn Asp Thr Leu Tyr Ser Thr Arg Lys Asp Asp Lys Gly Asn Thr Leu
                805                 810                 815

Ile Val Asn Asn Leu Asn Gly Leu Tyr Asp Lys Asp Asn Asp Lys Leu
            820                 825                 830

Lys Lys Leu Ile Asn Lys Ser Pro Glu Lys Leu Leu Met Tyr His His
        835                 840                 845

Asp Pro Gln Thr Tyr Gln Lys Leu Lys Leu Ile Met Glu Gln Tyr Gly
    850                 855                 860

Asp Glu Lys Asn Pro Leu Tyr Lys Tyr Tyr Glu Glu Thr Gly Asn Tyr
865                 870                 875                 880

Leu Thr Lys Tyr Ser Lys Lys Asp Asn Gly Pro Val Ile Lys Lys Ile
                885                 890                 895

Lys Tyr Tyr Gly Asn Lys Leu Asn Ala His Leu Asp Ile Thr Asp Asp
            900                 905                 910

Tyr Pro Asn Ser Arg Asn Lys Val Val Lys Leu Ser Leu Lys Pro Tyr
        915                 920                 925
```

```
Arg Phe Asp Val Tyr Leu Asp Asn Gly Val Tyr Lys Phe Val Thr Val
    930                 935                 940

Lys Asn Leu Asp Val Ile Lys Lys Glu Asn Tyr Tyr Glu Val Asn Ser
945                 950                 955                 960

Lys Cys Tyr Glu Glu Ala Lys Lys Leu Lys Lys Ile Ser Asn Gln Ala
                965                 970                 975

Glu Phe Ile Ala Ser Phe Tyr Asn Asn Asp Leu Ile Lys Ile Asn Gly
            980                 985                 990

Glu Leu Tyr Arg Val Ile Gly Val  Asn Asn Asp Leu Leu  Asn Arg Ile
        995                 1000                1005

Glu Val  Asn Met Ile Asp Ile  Thr Tyr Arg Glu Tyr  Leu Glu Asn
    1010                1015                1020

Met Asn  Asp Lys Arg Pro Pro  Arg Ile Ile Lys Thr  Ile Ala Ser
    1025                1030                1035

Lys Thr  Gln Ser Ile Lys Lys  Tyr Ser Thr Asp Ile  Leu Gly Asn
    1040                1045                1050

Leu Tyr  Glu Val Lys Ser Lys  Lys His Pro Gln Ile  Ile Lys Lys
    1055                1060                1065

Gly Lys  Arg Pro Ala Ala Thr  Lys Lys Ala Gly Gln  Ala Lys Lys
    1070                1075                1080

Lys Lys  Gly Ser Tyr Pro Tyr  Asp Val Pro Asp Tyr  Ala Leu Glu
    1085                1090                1095

Asp Ala  Leu Asp Asp Phe Asp  Leu Asp Met Leu Gly  Ser Asp Ala
    1100                1105                1110

Leu Asp  Asp Phe Asp Leu Asp  Met Leu Gly Ser Asp  Ala Leu Asp
    1115                1120                1125

Asp Phe  Asp Leu Asp Met Leu  Gly Ser Asp Ala Leu  Asp Asp Phe
```

1130 1135 1140

Asp Leu Asp Met Leu
1145

<210> 175
<211> 387
<212> PRT
<213> Homo sapiens

<400> 175
Met Thr Gly Lys Leu Ala Glu Lys Leu Pro Val Thr Met Ser Ser Leu
1 5 10 15

Leu Asn Gln Leu Pro Asp Asn Leu Tyr Pro Glu Glu Ile Pro Ser Ala
20 25 30

Leu Asn Leu Phe Ser Gly Ser Ser Asp Ser Val Val His Tyr Asn Gln
35 40 45

Met Ala Thr Glu Asn Val Met Asp Ile Gly Leu Thr Asn Glu Lys Pro
50 55 60

Asn Pro Glu Leu Ser Tyr Ser Gly Ser Phe Gln Pro Ala Pro Gly Asn
65 70 75 80

Lys Thr Val Thr Tyr Leu Gly Lys Phe Ala Phe Asp Ser Pro Ser Asn
85 90 95

Trp Cys Gln Asp Asn Ile Ile Ser Leu Met Ser Ala Gly Ile Leu Gly
100 105 110

Val Pro Pro Ala Ser Gly Ala Leu Ser Thr Gln Thr Ser Thr Ala Ser
115 120 125

Met Val Gln Pro Pro Gln Gly Asp Val Glu Ala Met Tyr Pro Ala Leu
130 135 140

Pro Pro Tyr Ser Asn Cys Gly Asp Leu Tyr Ser Glu Pro Val Ser Phe
145 150 155 160

His Asp Pro Gln Gly Asn Pro Gly Leu Ala Tyr Ser Pro Gln Asp Tyr

```
                165                 170                 175

Gln Ser Ala Lys Pro Ala Leu Asp Ser Asn Leu Phe Pro Met Ile Pro
            180                 185                 190

Asp Tyr Asn Leu Tyr His His Pro Asn Asp Met Gly Ser Ile Pro Glu
        195                 200                 205

His Lys Pro Phe Gln Gly Met Asp Pro Ile Arg Val Asn Pro Pro Pro
    210                 215                 220

Ile Thr Pro Leu Glu Thr Ile Lys Ala Phe Lys Asp Lys Gln Ile His
225                 230                 235                 240

Pro Gly Phe Gly Ser Leu Pro Gln Pro Pro Leu Thr Leu Lys Pro Ile
                245                 250                 255

Arg Pro Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Leu His Glu
            260                 265                 270

Arg Pro His Ala Cys Pro Ala Glu Gly Cys Asp Arg Arg Phe Ser Arg
        275                 280                 285

Ser Asp Glu Leu Thr Arg His Leu Arg Ile His Thr Gly His Lys Pro
    290                 295                 300

Phe Gln Cys Arg Ile Cys Met Arg Ser Phe Ser Arg Ser Asp His Leu
305                 310                 315                 320

Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Glu
                325                 330                 335

Phe Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His Ala
            340                 345                 350

Lys Ile His Leu Lys Gln Lys Glu Lys Lys Ala Glu Lys Gly Gly Ala
        355                 360                 365

Pro Ser Ala Ser Ser Ala Pro Pro Val Ser Leu Ala Pro Val Val Thr
    370                 375                 380
```

Thr Cys Ala
385

<210> 176
<211> 543
<212> PRT
<213> Homo sapiens

<400> 176
Met Ala Ala Ala Lys Ala Glu Met Gln Leu Met Ser Pro Leu Gln Ile
1 5 10 15

Ser Asp Pro Phe Gly Ser Phe Pro His Ser Pro Thr Met Asp Asn Tyr
20 25 30

Pro Lys Leu Glu Glu Met Met Leu Leu Ser Asn Gly Ala Pro Gln Phe
35 40 45

Leu Gly Ala Ala Gly Ala Pro Glu Gly Ser Gly Ser Asn Ser Ser Ser
50 55 60

Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Ser Asn Ser Ser
65 70 75 80

Ser Ser Ser Ser Thr Phe Asn Pro Gln Ala Asp Thr Gly Glu Gln Pro
85 90 95

Tyr Glu His Leu Thr Ala Glu Ser Phe Pro Asp Ile Ser Leu Asn Asn
100 105 110

Glu Lys Val Leu Val Glu Thr Ser Tyr Pro Ser Gln Thr Thr Arg Leu
115 120 125

Pro Pro Ile Thr Tyr Thr Gly Arg Phe Ser Leu Glu Pro Ala Pro Asn
130 135 140

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

Leu Val Ser Met Thr Asn Pro Pro Ala Ser Ser Ser Ser Ala Pro Ser
165 170 175

```
Pro Ala Ala Ser Ser Ala Ser Ala Ser Gln Ser Pro Pro Leu Ser Cys
            180                 185                 190

Ala Val Pro Ser Asn Asp Ser Ser Pro Ile Tyr Ser Ala Ala Pro Thr
        195                 200                 205

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

Phe Pro Gly Ser Ala Gly Thr Ala Leu Gln Tyr Pro Pro Pro Ala Tyr
225                 230                 235                 240

Pro Ala Ala Lys Gly Gly Phe Gln Val Pro Met Ile Pro Asp Tyr Leu
                245                 250                 255

Phe Pro Gln Gln Gln Gly Asp Leu Gly Leu Gly Thr Pro Asp Gln Lys
            260                 265                 270

Pro Phe Gln Gly Leu Glu Ser Arg Thr Gln Gln Pro Ser Leu Thr Pro
        275                 280                 285

Leu Ser Thr Ile Lys Ala Phe Ala Thr Gln Ser Gly Ser Gln Asp Leu
    290                 295                 300

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

Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Pro His Glu Arg
                325                 330                 335

Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser
            340                 345                 350

Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys Pro Phe
        355                 360                 365

Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu Thr
    370                 375                 380

Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile
```

385 390 395 400

Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His Thr Lys
405 410 415

Ile His Leu Arg Gln Lys Asp Lys Lys Ala Asp Lys Ser Val Val Ala
420 425 430

Ser Ser Ala Thr Ser Ser Leu Ser Ser Tyr Pro Ser Pro Val Ala Thr
435 440 445

Ser Tyr Pro Ser Pro Val Thr Thr Ser Tyr Pro Ser Pro Ala Thr Thr
450 455 460

Ser Tyr Pro Ser Pro Val Pro Thr Ser Phe Ser Ser Pro Gly Ser Ser
465 470 475 480

Thr Tyr Pro Ser Pro Val His Ser Gly Phe Pro Ser Pro Ser Val Ala
485 490 495

Thr Thr Tyr Ser Ser Val Pro Pro Ala Phe Pro Ala Gln Val Ser Ser
500 505 510

Phe Pro Ser Ser Ala Val Thr Asn Ser Phe Ser Ala Ser Thr Gly Leu
515 520 525

Ser Asp Met Thr Ala Thr Phe Ser Pro Arg Thr Ile Glu Ile Cys
530 535 540

<210> 177
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 177
Gly Gly Ser Gly Gly Gly Ser Gly
1 5

<210> 178

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

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 178
Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
1 5 10 15

<210> 179
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 179
Gly Gly Gly Ser
1

<210> 180
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 180
Gly Gly Gly Gly Ser
1 5

<210> 181
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 181
Gly Gly Ser Gly
1

<210> 182
<211> 9
<212> DNA
<213> Homo sapiens

<400> 182
gcgkgggcg 9

<210> 183
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 183
gttttagtac tctggaaaca gaatctacta aaacaaggca aaatgccgtg tttatctcgt 60

caacttgttg gcgaga 76

<210> 184
<211> 3871
<212> DNA
<213> Artificial Sequence

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

<400> 184
ggaggaagcc atcaactaaa ctacaatgac tgtaagatac aaaattggga atggtaacat 60

attttgaagt tctgttgaca taaagaatca tgatattaat gcccatggaa atgaaagggc 120

gatcaacact atggtttgaa aaggggaaa ttgtagagca cagatgtgtt cgtgtggcag 180

tgtgctgtct ctagcaatac tcagagaaga gagagaacaa tgaaattctg attggcccca 240

gtgtgagccc agatgaggtt cagctgccaa ctttctcttt cacatcttat gaaagtcatt 300

taagcacaac taacttttt ttttttttt ttttttgag acagagtctt gctctgttgc 360

ccaggacaga gtgcagtagt gactcaatct cggctcactg cagcctccac ctcctaggct 420

caaacggtcc tcctgcatca gcctcccaag tagctggaat tacaggagtg gcccaccatg 480

cccagctaat ttttgtattt ttaatagata cgggggtttc accatatcac ccaggctggt 540

ctcgaactcc tggcctcaag tgatccacct gcctcggcct cccaaagtgc tgggattata 600

ggcgtcagcc actatgccca acccgaccaa cctttttaa aataaatatt taaaaaattg 660

gtatttcaca tatatactag tatttacatt tatccacaca aaacggacgg gcctccgctg 720

aaccagtgag gccccagacg tgcgcataaa taacccctgc gtgctgcacc acctggggag 780

agggggagga ccacggtaaa tggagcgagc gcatagcaaa agggacgcgg ggtccttttc 840

tctgccggtg gcactgggta gctgtggcca ggtgtggtac tttgatgggg cccagggctg 900

gagctcaagg aagcgtcgca gggtcacaga tctgggggaa ccccggggaa aagcactgag 960

gcaaaaccgc cgctcgtctc ctacaatata tgggaggggg aggttgagta cgttctggat 1020

tactcataag acctttttt tttccttccg ggcgcaaaac cgtgagctgg atttataatc 1080

gccctataaa gctccagagg cggtcaggca cctgcagagg agccccgccg ctccgccgac 1140

tagctgcccc cgcgagcaac ggcctcgtga tttccccgcc gatccggtcc ccgcctcccc 1200

actctgcccc cgcctacccc ggagccgtgc agccgcctct ccgaatctct ctcttctcct 1260

ggcgctcgcg tgcgagaggg aactagcgag aacgaggaag cagctggagg tgacgccggg 1320

cagattacgc ctgtcagggc cgagccgagc ggatcgctgg gcgctgtgca gaggaaaggc 1380

gggagtgccc ggctcgctgt cgcagagccg aggtgggtaa gctagcgacc acctggactt 1440

cccagcgccc aaccgtggct tttcagccag gtcctctcct cccgcggctt ctcaaccaac 1500

cccatcccag cgccggccac ccaacctccc gaaatgagtg cttcctgccc cagcagccga 1560

aggcgctact aggaacggta acctgttact tttccagggg ccgtagtcga cccgctgccc 1620

gagttgctgt gcgactgcgc gcgcggggct agagtgcaag gtgactgtgg ttcttctctg 1680

gccaagtccg agggagaacg taaagatatg ggccttttc cccctctcac cttgtctcac 1740

caaagtccct agtccccgga gcagttagcc tctttctttc cagggaatta gccagacaca 1800

acaacgggaa ccagacaccg aaccagacat gcccgccccg tgcgccctcc ccgctcgctg 1860

cctttcctcc ctcttgtctc tccagagccg gatcttcaag gggagcctcc gtgcccccgg 1920

ctgctcagtc cctccggtgt gcaggacccc ggaagtcctc cccgcacagc tctcgcttct 1980

ctttgcagcc tgtttctgcg ccggaccagt cgaggactct ggacagtaga ggccccggga 2040

cgaccgagct ggaattcgcc accatggccg ccgaccacct gatgctcgcc gagggctacc 2100

gcctggtgca gaggccgccg tccgccgccg ccgcccatgg ccctcatgcg ctccggactc 2160

tgccgccgta cgcgggcccg ggcctggaca gtgggctgag gccgcggggg gctccgctgg 2220

ggccgccgcc gccccgccaa cccggggccc tggcgtacgg ggccttcggg ccgccgtcct 2280

ccttccagcc ctttccggcc gtgcctccgc cggccgcggg catcgcgcac ctgcagcctg 2340

tggcgacgcc gtaccccggc cgcgcggccg cgcccccaa cgctccggga ggcccccgg 2400

gcccgcagcc ggccccaagc gccgcagccc cgccgccgcc cgcgcacgcc ctgggcggca 2460

tggacgccga actcatcgac gaggaggcgc tgacgtcgct ggagctggag ctggggctgc 2520

accgcgtgcg cgagctgccc gagctgttcc tgggccagag cgagttcgac tgcttctcgg 2580

acttggggtc cgcgccgccc gccggctccg tgagctgcgg tggttctggt ggtggttctg 2640

gtcagtccca gctcatcaaa cccagccgca tgcgcaagta ccccaaccgg cccagcaaga 2700

cgccccccca cgaacgccct tacgcttgcc cagtggagtc ctgtgatcgc cgcttctccc 2760

gcagcgacaa cctggtgaga cacatccgca tccacacagg ccagaagccc ttccagtgcc 2820

gcatctgcat gagaaacttc agccgagagg ataacttgca cactcacatc cgcacccaca 2880

caggcgaaaa gcccttcgcc tgcgacatct gtggaagaaa gtttgcccgg agcgatgaac 2940

ttgtccgaca taccaagatc cacttgcggc agaaggaccg cccttacgct tgcccagtgg 3000

agtcctgtga tcgccgcttc tcccaatcag ggaatctgac tgagcacatc cgcatccaca 3060

caggccagaa gcccttccag tgccgcatct gcatgagaaa cttcagcaca agtggacatc 3120

tggtacgcca catccgcacc cacacaggcg aaaagccctt cgcctgcgac atctgtggaa 3180

gaaagtttgc ccagaatagt accctgaccg aacataccaa gatccacttg cggcagaagg 3240

acaagtaact cgaggaaacc cagcagacaa tgtagctaga cccagtagcc agatgtagct 3300

aaagagaccg gttcactgtg agaaacccag cagacaatgt agctagaccc agtagccaga 3360

tgtagctaaa gagaccggtt cactgtgaaa gcttgggtgg catccctgtg acccctcccc 3420

agtgcctctc ctggccctgg aagttgccac tccagtgccc accagccttg tcctaataaa 3480

attaagttgc atcattttgt ctgactaggt gtccttctat aatattatgg ggtggagggg 3540

ggtggtatgg agcaaggggc aagttgggaa gacaacctgt agggcctgcg gggtctattg 3600

ggaaccaagc tggagtgcag tggcacaatc ttggctcact gcaatctccg cctcctgggt 3660

tcaagcgatt ctcctgcctc agcctcccga gttgttggga ttccaggcat gcatgaccag 3720

gctcagctaa tttttgtttt tttggtagag acggggtttc accatattgg ccaggctggt 3780

ctccaactcc taatctcagg tgatctaccc accttggcct cccaaattgc tgggattaca 3840

ggcgtgaacc actgctccct tccctgtcct t 3871

<210> 185
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 185
tgtctcggca ttgagaacat tc 22

<210> 186
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 186
attggtggga ggccattgta t 21

<210> 187
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 187
accacagtcc atgccatcac 20

<210> 188
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 188
tccaccaccc tgttgctgta 20

<210> 189
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 189
caaaaaagcc acaaaagcct 20

<210> 190
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 190
ttagctccgc aagaaacatc 20

<210> 191
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 191
ccatggaact ggctcgattt cac 23

<210> 192

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

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 192
attggtggga ggccactgta t 21

<210> 193
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
probe

<400> 193
aggcctgaaa accattgtgg gagccct 27

<210> 194
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 194
gaatgtggga aatcattcag tcgc 24

<210> 195
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 195
gcaagttatc ctctcgtgag aagg 24

<210> 196
<211> 29
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
probe

<400> 196
gcgacaacct ggtgagacat caacgcacc 29

<210> 197
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 197
gctgttatct cttgtgggct gt 22

<210> 198
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 198
aaactcatgg gagctgccgg tt 22

<210> 199
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
probe

<400> 199
ccacacaaat ctctccctgg cattg 25

<210> 200
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 200
gaatgtggga aatcattcag tcgc 24

<210> 201
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 201
gcaagttatc ctctcgtgag aagg 24

<210> 202
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
probe

<400> 202
gcgacaacct ggtgagacat caacgcacc 29

<210> 203
<211> 1182
<212> DNA
<213> Artificial Sequence

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

<400> 203
atggccgccg accacctgat gctcgccgag ggctaccgcc tggtgcagag gccgccgtcc 60

gccgccgccg cccatggccc tcatgcgctc cggactctgc cgccgtacgc gggcccgggc 120

ctggacagtg ggctgaggcc gcgggggct ccgctggggc cgccgccgcc ccgccaaccc 180

ggggccctgg cgtacggggc cttcgggccg ccgtcctcct tccagccctt tccggccgtg 240

cctccgccgg ccgcgggcat cgcgcacctg cagcctgtgg cgacgccgta ccccggccgc 300

gcggccgcgc cccccaacgc tccgggaggc cccccgggcc cgcagccggc cccaagcgcc 360

gcagccccgc cgccgcccgc gcacgccctg ggcggcatgg acgccgaact catcgacgag 420

gaggcgctga cgtcgctgga gctggagctg gggctgcacc gcgtgcgcga gctgcccgag 480

ctgttcctgg gccagagcga gttcgactgc ttctcggact tggggtccgc gccgcccgcc 540

ggctccgtga gctgcggtgg ttctggtggt ggttctggtc agtcccagct catcaaaccc 600

agccgcatgc gcaagtaccc caaccggccc agcaagacgc ccccccacga acgcccttac 660

gcttgcccag tggagtcctg tgatcgccgc ttctcccgca gcgacaacct ggtgagacac 720

atccgcatcc acacaggcca gaagcccttc cagtgccgca tctgcatgag aaacttcagc 780

cgagaggata acttgcacac tcacatccgc acccacacag gcgaaaagcc cttcgcctgc 840

gacatctgtg gaagaaagtt tgcccggagc gatgaacttg tccgacatac caagatccac 900

ttgcggcaga aggaccgccc ttacgcttgc ccagtggagt cctgtgatcg ccgcttctcc 960

caatcaggga atctgactga gcacatccgc atccacacag gccagaagcc cttccagtgc 1020

cgcatctgca tgagaaactt cagcacaagt ggacatctgg tacgccacat ccgcacccac 1080

acaggcgaaa agcccttcgc ctgcgacatc tgtggaagaa agtttgccca gaatagtacc 1140

ctgaccgaac ataccaagat ccacttgcgg cagaaggaca ag 1182

<210> 204
<211> 1206
<212> DNA
<213> Artificial Sequence

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

<400> 204
atggccgccg accacctgat gctcgccgag ggctaccgcc tggtgcagag gccgccgtcc 60

gccgccgccg cccatggccc tcatgcgctc cggactctgc cgccgtacgc gggcccgggc 120

ctggacagtg ggctgaggcc gcgggggct ccgctggggc cgccgccgcc ccgccaaccc 180

ggggccctgg cgtacggggc cttcgggccg ccgtcctcct tccagccctt tccggccgtg 240

cctccgccgg ccgcgggcat cgcgcacctg cagcctgtgg cgacgccgta ccccggccgc 300

gcggccgcgc cccccaacgc tccgggaggc cccccgggcc cgcagccggc cccaagcgcc 360

gcagccccgc cgccgcccgc gcacgccctg ggcggcatgg acgccgaact catcgacgag 420

gaggcgctga cgtcgctgga gctggagctg gggctgcacc gcgtgcgcga gctgcccgag 480

ctgttcctgg gccagagcga gttcgactgc ttctcggact tggggtccgc gccgcccgcc 540

ggctccgtga gctgcggtgg ttctggtggt ggttctggtg gtggcagcgg gggaggttct 600

ggtcagtccc agctcatcaa acccagccgc atgcgcaagt accccaaccg gcccagcaag 660

acgccccccc acgaacgccc ttacgcttgc ccagtggagt cctgtgatcg ccgcttctcc 720

cgcagcgaca acctggtgag acacatccgc atccacacag gccagaagcc cttccagtgc 780

cgcatctgca tgagaaactt cagccgagag gataacttgc acactcacat ccgcacccac 840

acaggcgaaa agcccttcgc ctgcgacatc tgtggaagaa agtttgcccg gagcgatgaa 900

cttgtccgac ataccaagat ccacttgcgg cagaaggacc gcccttacgc ttgcccagtg 960

gagtcctgtg atcgccgctt ctcccaatca gggaatctga ctgagcacat ccgcatccac 1020

acaggccaga agcccttcca gtgccgcatc tgcatgagaa acttcagcac aagtggacat 1080

ctggtacgcc acatccgcac ccacacaggc gaaaagccct tcgcctgcga catctgtgga 1140

agaaagtttg cccagaatag taccctgacc gaacatacca agatccactt gcggcagaag 1200

gacaag 1206

<210> 205
<211> 402
<212> PRT
<213> Artificial Sequence

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

<400> 205
Met Ala Ala Asp His Leu Met Leu Ala Glu Gly Tyr Arg Leu Val Gln
1 5 10 15

Arg Pro Pro Ser Ala Ala Ala Ala His Gly Pro His Ala Leu Arg Thr
20 25 30

Leu Pro Pro Tyr Ala Gly Pro Gly Leu Asp Ser Gly Leu Arg Pro Arg
35 40 45

Gly Ala Pro Leu Gly Pro Pro Pro Pro Arg Gln Pro Gly Ala Leu Ala
50 55 60

```
Tyr Gly Ala Phe Gly Pro Pro Ser Ser Phe Gln Pro Phe Pro Ala Val
65                  70                  75                  80

Pro Pro Pro Ala Ala Gly Ile Ala His Leu Gln Pro Val Ala Thr Pro
                85                  90                  95

Tyr Pro Gly Arg Ala Ala Ala Pro Pro Asn Ala Pro Gly Gly Pro Pro
            100                 105                 110

Gly Pro Gln Pro Ala Pro Ser Ala Ala Ala Pro Pro Pro Pro Ala His
        115                 120                 125

Ala Leu Gly Gly Met Asp Ala Glu Leu Ile Asp Glu Glu Ala Leu Thr
    130                 135                 140

Ser Leu Glu Leu Glu Leu Gly Leu His Arg Val Arg Glu Leu Pro Glu
145                 150                 155                 160

Leu Phe Leu Gly Gln Ser Glu Phe Asp Cys Phe Ser Asp Leu Gly Ser
                165                 170                 175

Ala Pro Pro Ala Gly Ser Val Ser Cys Gly Gly Ser Gly Gly Gly Ser
            180                 185                 190

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gln Ser Gln Leu Ile Lys Pro
        195                 200                 205

Ser Arg Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Pro His
    210                 215                 220

Glu Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser
225                 230                 235                 240

Arg Ser Asp Asn Leu Val Arg His Ile Arg Ile His Thr Gly Gln Lys
                245                 250                 255

Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Glu Asp Asn
            260                 265                 270
```

```
Leu His Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys
        275                 280                 285


Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Leu Val Arg His
    290                 295                 300


Thr Lys Ile His Leu Arg Gln Lys Asp Arg Pro Tyr Ala Cys Pro Val
305                 310                 315                 320


Glu Ser Cys Asp Arg Arg Phe Ser Gln Ser Gly Asn Leu Thr Glu His
                325                 330                 335


Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met
            340                 345                 350


Arg Asn Phe Ser Thr Ser Gly His Leu Val Arg His Ile Arg Thr His
        355                 360                 365


Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala
    370                 375                 380


Gln Asn Ser Thr Leu Thr Glu His Thr Lys Ile His Leu Arg Gln Lys
385                 390                 395                 400


Asp Lys
```

<210> 206
<211> 1707
<212> DNA
<213> Artificial Sequence

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

<400> 206
atggccgcag atcacctgat gctggctgaa ggctacagac tggtgcagcg gcctccatct 60

gccgctgccg cccacggccc ccacgccctg agaacactgc ccccctacgc cggccctggt 120

cttgatagcg gactcagacc tagaggcgcc cctctgggcc ctccacctcc aagacagcct 180

ggagccctgg cctacggcgc cttcggccct ccttctagct tccagccctt ccccgccgtg 240

cctcctccag ccgctggcat cgcccacctg cagcctgtgg ccacccctta ccccggaaga 300

gccgccgccc ctccaaacgc ccctggcgga cctcctggcc cccagcctgc tccaagcgcc 360

gctgcccctc cacctcctgc tcatgccctg ggcggcatgg acgccgagct gatcgacgag 420

gaagccctga ccagcctgga actggaactg ggcctgcaca gagtgcggga actgcctgag 480

ctgttcctgg gacagagcga gttcgactgc ttcagcgacc tgggcagcgc ccctcctgcc 540

ggctctgtgt cctgcgccga ccacctgatg ctcgccgagg gctaccgcct ggtgcagagg 600

ccgccgtccg ccgccgccgc ccatggccct catgcgctcc ggactctgcc gccgtacgcg 660

ggcccgggcc tggacagtgg gctgaggccg cgggggctc cgctggggcc gccgccgccc 720

cgccaacccg gggccctggc gtacggggcc ttcgggccgc cgtcctcctt ccagcccttt 780

ccggccgtgc ctccgccggc cgcgggcatc gcgcacctgc agcctgtggc gacgccgtac 840

cccggccgcg ccgccgcgcc ccccaacgct ccgggaggcc ccccgggccc gcagccggcc 900

ccaagcgccg cagccccgcc gccgcccgcg cacgccctgg gcggcatgga cgccgaactc 960

atcgacgagg aggcgctgac gtcgctggag ctggagctgg ggctgcaccg cgtgcgcgag 1020

ctgcccgagc tgttcctggg ccagagcgag ttcgactgct tctcggactt ggggtccgcg 1080

ccgcccgccg gctccgtgag ctgccagtcc cagctcatca aacccagccg catgcgcaag 1140

taccccaacc ggcccagcaa gacgcccccc cacgaacgcc cttacgcttg cccagtggag 1200

tcctgtgatc gccgcttctc ccgcagcgac aacctggtga gacacatccg catccacaca 1260

ggccagaagc ccttccagtg ccgcatctgc atgagaaact tcagccgaga ggataacttg 1320

cacactcaca tccgcaccca cacaggcgaa aagcccttcg cctgcgacat ctgtggaaga 1380

aagtttgccc ggagcgatga acttgtccga cataccaaga tccacttgcg gcagaaggac 1440

cgcccttacg cttgcccagt ggagtcctgt gatcgccgct tctcccaatc agggaatctg 1500

actgagcaca tccgcatcca cacaggccag aagcccttcc agtgccgcat ctgcatgaga 1560

aacttcagca caagtggaca tctggtacgc cacatccgca cccacacagg cgaaaagccc 1620

ttcgcctgcg acatctgtgg aagaaagttt gcccagaata gtaccctgac cgaacatacc 1680

aagatccact tgcggcagaa ggacaag 1707

<210> 207
<211> 569
<212> PRT

<213> Artificial Sequence

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

<400> 207
Met Ala Ala Asp His Leu Met Leu Ala Glu Gly Tyr Arg Leu Val Gln
1 5 10 15

Arg Pro Pro Ser Ala Ala Ala Ala His Gly Pro His Ala Leu Arg Thr
20 25 30

Leu Pro Pro Tyr Ala Gly Pro Gly Leu Asp Ser Gly Leu Arg Pro Arg
35 40 45

Gly Ala Pro Leu Gly Pro Pro Pro Pro Arg Gln Pro Gly Ala Leu Ala
50 55 60

Tyr Gly Ala Phe Gly Pro Pro Ser Ser Phe Gln Pro Phe Pro Ala Val
65 70 75 80

Pro Pro Pro Ala Ala Gly Ile Ala His Leu Gln Pro Val Ala Thr Pro
85 90 95

Tyr Pro Gly Arg Ala Ala Ala Pro Pro Asn Ala Pro Gly Gly Pro Pro
100 105 110

Gly Pro Gln Pro Ala Pro Ser Ala Ala Ala Pro Pro Pro Pro Ala His
115 120 125

Ala Leu Gly Gly Met Asp Ala Glu Leu Ile Asp Glu Glu Ala Leu Thr
130 135 140

Ser Leu Glu Leu Glu Leu Gly Leu His Arg Val Arg Glu Leu Pro Glu
145 150 155 160

Leu Phe Leu Gly Gln Ser Glu Phe Asp Cys Phe Ser Asp Leu Gly Ser
165 170 175

Ala Pro Pro Ala Gly Ser Val Ser Cys Ala Asp His Leu Met Leu Ala
180 185 190

```
Glu Gly Tyr Arg Leu Val Gln Arg Pro Pro Ser Ala Ala Ala Ala His
        195                 200                 205

Gly Pro His Ala Leu Arg Thr Leu Pro Pro Tyr Ala Gly Pro Gly Leu
    210                 215                 220

Asp Ser Gly Leu Arg Pro Arg Gly Ala Pro Leu Gly Pro Pro Pro Pro
225                 230                 235                 240

Arg Gln Pro Gly Ala Leu Ala Tyr Gly Ala Phe Gly Pro Pro Ser Ser
                245                 250                 255

Phe Gln Pro Phe Pro Ala Val Pro Pro Pro Ala Ala Gly Ile Ala His
            260                 265                 270

Leu Gln Pro Val Ala Thr Pro Tyr Pro Gly Arg Ala Ala Ala Pro Pro
        275                 280                 285

Asn Ala Pro Gly Gly Pro Pro Gly Pro Gln Pro Ala Pro Ser Ala Ala
    290                 295                 300

Ala Pro Pro Pro Pro Ala His Ala Leu Gly Gly Met Asp Ala Glu Leu
305                 310                 315                 320

Ile Asp Glu Glu Ala Leu Thr Ser Leu Glu Leu Glu Leu Gly Leu His
                325                 330                 335

Arg Val Arg Glu Leu Pro Glu Leu Phe Leu Gly Gln Ser Glu Phe Asp
            340                 345                 350

Cys Phe Ser Asp Leu Gly Ser Ala Pro Pro Ala Gly Ser Val Ser Cys
        355                 360                 365

Gln Ser Gln Leu Ile Lys Pro Ser Arg Met Arg Lys Tyr Pro Asn Arg
    370                 375                 380

Pro Ser Lys Thr Pro Pro His Glu Arg Pro Tyr Ala Cys Pro Val Glu
385                 390                 395                 400

Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Asn Leu Val Arg His Ile
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405 410 415

Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg
420 425 430

Asn Phe Ser Arg Glu Asp Asn Leu His Thr His Ile Arg Thr His Thr
435 440 445

Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg
450 455 460

Ser Asp Glu Leu Val Arg His Thr Lys Ile His Leu Arg Gln Lys Asp
465 470 475 480

Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Gln
485 490 495

Ser Gly Asn Leu Thr Glu His Ile Arg Ile His Thr Gly Gln Lys Pro
500 505 510

Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Thr Ser Gly His Leu
515 520 525

Val Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp
530 535 540

Ile Cys Gly Arg Lys Phe Ala Gln Asn Ser Thr Leu Thr Glu His Thr
545 550 555 560

Lys Ile His Leu Arg Gln Lys Asp Lys
565

<210> 208
<211> 1755
<212> DNA
<213> Artificial Sequence

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

<400> 208
atggccgcag atcacctgat gctggctgaa ggctacagac tggtgcagcg gcctccatct 60

gccgctgccg cccacggccc ccacgccctg agaacactgc ccccctacgc cggccctggt 120

cttgatagcg gactcagacc tagaggcgcc cctctgggcc ctccacctcc aagacagcct 180

ggagccctgg cctacggcgc cttcggccct ccttctagct tccagccctt ccccgccgtg 240

cctcctccag ctgctggcat cgcccacctg cagcctgtgg ccacccctta ccccggaaga 300

gccgccgccc ctccaaacgc ccctggcgga cctcctggcc cccagcctgc tccaagcgcc 360

gctgcccctc cacctcctgc tcatgccctg ggcggcatgg acgccgagct gatcgacgag 420

gaagccctga ccagcctgga actggaactg ggcctgcaca gagtgcggga actgcctgag 480

ctgttcctgg gacagagcga gttcgactgc ttcagcgacc tgggcagcgc ccctcctgcc 540

ggctctgtgt cctgcggcgg cagcggcggc ggaagcggcg ccgaccacct gatgctcgcc 600

gagggctacc gcctggtgca gaggccgccg tccgccgccg ccgcccatgg ccctcatgcg 660

ctccggactc tgccgccgta cgcgggcccg ggcctggaca gtgggctgag gccgcggggg 720

gctccgctgg ggccgccgcc gccccgccaa cccggggccc tggcgtacgg ggccttcggg 780

ccgccgtcct ccttccagcc ctttccggcc gtgcctccgc cggccgcggg catcgcgcac 840

ctgcagcctg tggcgacgcc gtaccccggc cgcgcggccg cgccccccaa cgctccggga 900

ggcccccggg gcccgcagcc ggccccaagc gccgcagccc cgccgccgcc cgcgcacgcc 960

ctgggcggca tggacgccga actcatcgac gaggaggcgc tgacgtcgct ggagctggag 1020

ctggggctgc accgcgtgcg cgagctgccc gagctgttcc tgggccagag cgagttcgac 1080

tgcttctcgg acttggggtc cgcgccgccc gccggctccg tgagctgcgg tggttctggt 1140

ggtggttctg gtcagtccca gctcatcaaa cccagccgca tgcgcaagta ccccaaccgg 1200

cccagcaaga cgccccccca cgaacgccct tacgcttgcc cagtggagtc ctgtgatcgc 1260

cgcttctccc gcagcgacaa cctggtgaga cacatccgca tccacacagg ccagaagccc 1320

ttccagtgcc gcatctgcat gagaaacttc agccgagagg ataacttgca cactcacatc 1380

cgcacccaca caggcgaaaa gcccttcgcc tgcgacatct gtggaagaaa gtttgcccgg 1440

agcgatgaac ttgtccgaca taccaagatc cacttgcggc agaaggaccg cccttacgct 1500

tgcccagtgg agtcctgtga tcgccgcttc tcccaatcag ggaatctgac tgagcacatc 1560

cgcatccaca caggccagaa gcccttccag tgccgcatct gcatgagaaa cttcagcaca 1620

agtggacatc tggtacgcca catccgcacc cacacaggcg aaaagccctt cgcctgcgac 1680

atctgtggaa gaaagtttgc ccagaatagt accctgaccg aacataccaa gatccacttg 1740

cggcagaagg acaag 1755

<210> 209
<211> 585
<212> PRT
<213> Artificial Sequence

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

<400> 209
Met Ala Ala Asp His Leu Met Leu Ala Glu Gly Tyr Arg Leu Val Gln
1 5 10 15

Arg Pro Pro Ser Ala Ala Ala Ala His Gly Pro His Ala Leu Arg Thr
20 25 30

Leu Pro Pro Tyr Ala Gly Pro Gly Leu Asp Ser Gly Leu Arg Pro Arg
35 40 45

Gly Ala Pro Leu Gly Pro Pro Pro Pro Arg Gln Pro Gly Ala Leu Ala
50 55 60

Tyr Gly Ala Phe Gly Pro Pro Ser Ser Phe Gln Pro Phe Pro Ala Val
65 70 75 80

Pro Pro Pro Ala Ala Gly Ile Ala His Leu Gln Pro Val Ala Thr Pro
85 90 95

Tyr Pro Gly Arg Ala Ala Ala Pro Pro Asn Ala Pro Gly Gly Pro Pro
100 105 110

Gly Pro Gln Pro Ala Pro Ser Ala Ala Ala Pro Pro Pro Pro Ala His
115 120 125

Ala Leu Gly Gly Met Asp Ala Glu Leu Ile Asp Glu Glu Ala Leu Thr
130 135 140

Ser Leu Glu Leu Glu Leu Gly Leu His Arg Val Arg Glu Leu Pro Glu
145 150 155 160

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Leu Phe Leu Gly Gln Ser Glu Phe Asp Cys Phe Ser Asp Leu Gly Ser
                165                 170                 175

Ala Pro Pro Ala Gly Ser Val Ser Cys Gly Gly Ser Gly Gly Gly Ser
            180                 185                 190

Gly Ala Asp His Leu Met Leu Ala Glu Gly Tyr Arg Leu Val Gln Arg
        195                 200                 205

Pro Pro Ser Ala Ala Ala Ala His Gly Pro His Ala Leu Arg Thr Leu
    210                 215                 220

Pro Pro Tyr Ala Gly Pro Gly Leu Asp Ser Gly Leu Arg Pro Arg Gly
225                 230                 235                 240

Ala Pro Leu Gly Pro Pro Pro Pro Arg Gln Pro Gly Ala Leu Ala Tyr
                245                 250                 255

Gly Ala Phe Gly Pro Pro Ser Ser Phe Gln Pro Phe Pro Ala Val Pro
            260                 265                 270

Pro Pro Ala Ala Gly Ile Ala His Leu Gln Pro Val Ala Thr Pro Tyr
        275                 280                 285

Pro Gly Arg Ala Ala Ala Pro Pro Asn Ala Pro Gly Gly Pro Pro Gly
    290                 295                 300

Pro Gln Pro Ala Pro Ser Ala Ala Ala Pro Pro Pro Pro Ala His Ala
305                 310                 315                 320

Leu Gly Gly Met Asp Ala Glu Leu Ile Asp Glu Glu Ala Leu Thr Ser
                325                 330                 335

Leu Glu Leu Glu Leu Gly Leu His Arg Val Arg Glu Leu Pro Glu Leu
            340                 345                 350

Phe Leu Gly Gln Ser Glu Phe Asp Cys Phe Ser Asp Leu Gly Ser Ala
        355                 360                 365
```

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Pro Pro Ala Gly Ser Val Ser Cys Gly Gly Ser Gly Gly Gly Ser Gly
    370                 375                 380

Gln Ser Gln Leu Ile Lys Pro Ser Arg Met Arg Lys Tyr Pro Asn Arg
385                 390                 395                 400

Pro Ser Lys Thr Pro Pro His Glu Arg Pro Tyr Ala Cys Pro Val Glu
                405                 410                 415

Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Asn Leu Val Arg His Ile
            420                 425                 430

Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg
        435                 440                 445

Asn Phe Ser Arg Glu Asp Asn Leu His Thr His Ile Arg Thr His Thr
    450                 455                 460

Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg
465                 470                 475                 480

Ser Asp Glu Leu Val Arg His Thr Lys Ile His Leu Arg Gln Lys Asp
                485                 490                 495

Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Gln
            500                 505                 510

Ser Gly Asn Leu Thr Glu His Ile Arg Ile His Thr Gly Gln Lys Pro
        515                 520                 525

Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Thr Ser Gly His Leu
    530                 535                 540

Val Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp
545                 550                 555                 560

Ile Cys Gly Arg Lys Phe Ala Gln Asn Ser Thr Leu Thr Glu His Thr
                565                 570                 575

Lys Ile His Leu Arg Gln Lys Asp Lys
            580                 585
```

<210> 210
<211> 1113
<212> DNA
<213> Homo sapiens

<400> 210
atggagctgg aattggatgc tggtgaccaa gacctgctgg ccttcctgct agaggaaagt 60

ggagatttgg ggacggcacc cgatgaggcc gtgagggccc cactggactg ggcgctgccg 120

ctttctgagg tgccgagcga ctgggaagta gatgatttgc tgtgctccct gctgagtccc 180

ccagcgtcgt tgaacattct cagctcctcc aacccctgcc ttgtccacca tgaccacacc 240

tactccctcc cacgggaaac tgtctctatg gatctagaga gtgagagctg tagaaaagag 300

gggacccaga tgactccaca gcatatggag gagctggcag agcaggagat tgctaggcta 360

gtactgacag atgaggagaa gagtctattg gagaaggagg ggcttattct gcctgagaca 420

cttcctctca ctaagacaga ggaacaaatt ctgaaacgtg tgcggaggaa gattcgaaat 480

aaaagatctg ctcaagagag ccgcaggaaa aagaaggtgt acgttggggg tttagagagc 540

cgggtcttga aatacacagc ccagaatatg gagcttcaga acaaagtaca gcttctggag 600

gaacagaatt tgtcccttct agatcaactg aggaaactcc aggccatggt gattgagatc 660

tcaaacaaaa ccagcagcag cagcacctgc atcttggtcc tgctagtctc cttctgcctc 720

ctccttgtac ctgctatgta ctcctctgac acaaggggga gcctgccagc tgagcatgga 780

gtgttgtccc gccagcttcg tgccctcccc agtgaggacc cttaccagct ggagctgcct 840

gccctgcagt cagaagtgcc gaaagacagc acacaccagt ggttggacgg ctcagactgt 900

gtactccagg cccctggcaa cacttcctgc ctgctgcatt acatgcctca ggctcccagt 960

gcagagcctc ccctggagtg gcccttccct gacctcttct cagagcctct ctgccgaggt 1020

cccatcctcc ccctgcaggc aaatctcaca aggaagggag gatggcttcc tactggtagc 1080

ccctctgtca ttttgcagga cagatactca ggc 1113

<210> 211
<211> 371
<212> PRT
<213> Homo sapiens

<400> 211
Met Glu Leu Glu Leu Asp Ala Gly Asp Gln Asp Leu Leu Ala Phe Leu

```
1               5                   10                  15

Leu Glu Glu Ser Gly Asp Leu Gly Thr Ala Pro Asp Glu Ala Val Arg
            20                  25                  30

Ala Pro Leu Asp Trp Ala Leu Pro Leu Ser Glu Val Pro Ser Asp Trp
        35                  40                  45

Glu Val Asp Asp Leu Leu Cys Ser Leu Leu Ser Pro Pro Ala Ser Leu
    50                  55                  60

Asn Ile Leu Ser Ser Ser Asn Pro Cys Leu Val His His Asp His Thr
65                  70                  75                  80

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

Cys Arg Lys Glu Gly Thr Gln Met Thr Pro Gln His Met Glu Glu Leu
            100                 105                 110

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

Leu Leu Glu Lys Glu Gly Leu Ile Leu Pro Glu Thr Leu Pro Leu Thr
    130                 135                 140

Lys Thr Glu Glu Gln Ile Leu Lys Arg Val Arg Arg Lys Ile Arg Asn
145                 150                 155                 160

Lys Arg Ser Ala Gln Glu Ser Arg Arg Lys Lys Lys Val Tyr Val Gly
                165                 170                 175

Gly Leu Glu Ser Arg Val Leu Lys Tyr Thr Ala Gln Asn Met Glu Leu
            180                 185                 190

Gln Asn Lys Val Gln Leu Leu Glu Glu Gln Asn Leu Ser Leu Leu Asp
        195                 200                 205

Gln Leu Arg Lys Leu Gln Ala Met Val Ile Glu Ile Ser Asn Lys Thr
    210                 215                 220
```

Ser Ser Ser Ser Thr Cys Ile Leu Val Leu Leu Val Ser Phe Cys Leu
225 230 235 240

Leu Leu Val Pro Ala Met Tyr Ser Ser Asp Thr Arg Gly Ser Leu Pro
245 250 255

Ala Glu His Gly Val Leu Ser Arg Gln Leu Arg Ala Leu Pro Ser Glu
260 265 270

Asp Pro Tyr Gln Leu Glu Leu Pro Ala Leu Gln Ser Glu Val Pro Lys
275 280 285

Asp Ser Thr His Gln Trp Leu Asp Gly Ser Asp Cys Val Leu Gln Ala
290 295 300

Pro Gly Asn Thr Ser Cys Leu Leu His Tyr Met Pro Gln Ala Pro Ser
305 310 315 320

Ala Glu Pro Pro Leu Glu Trp Pro Phe Pro Asp Leu Phe Ser Glu Pro
325 330 335

Leu Cys Arg Gly Pro Ile Leu Pro Leu Gln Ala Asn Leu Thr Arg Lys
340 345 350

Gly Gly Trp Leu Pro Thr Gly Ser Pro Ser Val Ile Leu Gln Asp Arg
355 360 365

Tyr Ser Gly
370

<210> 212
<211> 1590
<212> DNA
<213> Artificial Sequence

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

<400> 212
atggagctgg aattggatgc tggtgaccaa gacctgctgg ccttcctgct agaggaaagt 60

ggagatttgg ggacggcacc cgatgaggcc gtgagggccc cactggactg ggcgctgccg 120

ctttctgagg tgccgagcga ctgggaagta gatgatttgc tgtgctccct gctgagtccc 180

ccagcgtcgt tgaacattct cagctcctcc aacccctgcc ttgtccacca tgaccacacc 240

tactccctcc cacgggaaac tgtctctatg gatctagaga gtgagagctg tagaaaagag 300

gggacccaga tgactccaca gcatatggag gagctggcag agcaggagat tgctaggcta 360

gtactgacag atgaggagaa gagtctattg gagaaggagg ggcttattct gcctgagaca 420

cttcctctca ctaagacaga ggaacaaatt ctgaaacgtg tgcggctcga accaggtgaa 480

aaaccttaca aatgtcctga atgtgggaaa tcattcagtc gcagcgacaa cctggtgaga 540

catcaacgca cccatacagg agaaaaacct tataaatgtc cagaatgtgg aaagtccttc 600

tcacgagagg ataacttgca cactcatcaa cgaacacata ctggtgaaaa accatacaag 660

tgtcccgaat gtggtaaaag ttttagccgg agcgatgaac ttgtccgaca ccaacgaacc 720

catacaggcg agaagcctta caaatgtccc gagtgtggca agagcttctc acaatcaggg 780

aatctgactg agcatcaacg aactcatacc ggggaaaaac cttacaagtg tccagagtgt 840

gggaagagct tttccacaag tggacatctg gtacgccacc agaggacaca tacaggggag 900

aagccctaca aatgccccga atgcggtaaa agtttctctc agaatagtac cctgaccgaa 960

caccagcgaa cacacactgg gaaaaaaacg agtgtgtacg ttgggggttt agagagccgg 1020

gtcttgaaat acacagccca gaatatggag cttcagaaca aagtacagct tctggaggaa 1080

cagaatttgt cccttctaga tcaactgagg aaactccagg ccatggtgat tgagatctca 1140

aacaaaacca gcagcagcag cacctgcatc ttggtcctgc tagtctcctt ctgcctcctc 1200

cttgtacctg ctatgtactc ctctgacaca agggggagcc tgccagctga gcatggagtg 1260

ttgtcccgcc agcttcgtgc cctccccagt gaggaccctt accagctgga gctgcctgcc 1320

ctgcagtcag aagtgccgaa agacagcaca caccagtggt tggacggctc agactgtgta 1380

ctccaggccc ctggcaacac ttcctgcctg ctgcattaca tgcctcaggc tcccagtgca 1440

gagcctcccc tggagtggcc cttccctgac ctcttctcag agcctctctg ccgaggtccc 1500

atcctccccc tgcaggcaaa tctcacaagg aagggaggat ggcttcctac tggtagcccc 1560

tctgtcattt tgcaggacag atactcaggc 1590

<210> 213
<211> 530

<212> PRT
<213> Artificial Sequence

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

<400> 213
Met Glu Leu Glu Leu Asp Ala Gly Asp Gln Asp Leu Leu Ala Phe Leu
1 5 10 15

Leu Glu Glu Ser Gly Asp Leu Gly Thr Ala Pro Asp Glu Ala Val Arg
20 25 30

Ala Pro Leu Asp Trp Ala Leu Pro Leu Ser Glu Val Pro Ser Asp Trp
35 40 45

Glu Val Asp Asp Leu Leu Cys Ser Leu Leu Ser Pro Pro Ala Ser Leu
50 55 60

Asn Ile Leu Ser Ser Ser Asn Pro Cys Leu Val His His Asp His Thr
65 70 75 80

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

Cys Arg Lys Glu Gly Thr Gln Met Thr Pro Gln His Met Glu Glu Leu
100 105 110

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

Leu Leu Glu Lys Glu Gly Leu Ile Leu Pro Glu Thr Leu Pro Leu Thr
130 135 140

Lys Thr Glu Glu Gln Ile Leu Lys Arg Val Arg Leu Glu Pro Gly Glu
145 150 155 160

Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Ser Asp
165 170 175

Asn Leu Val Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys
180 185 190

```
Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Glu Asp Asn Leu His Thr
        195                 200                 205

His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys
    210                 215                 220

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

His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe
                245                 250                 255

Ser Gln Ser Gly Asn Leu Thr Glu His Gln Arg Thr His Thr Gly Glu
            260                 265                 270

Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Thr Ser Gly
        275                 280                 285

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

Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Asn Ser Thr Leu Thr Glu
305                 310                 315                 320

His Gln Arg Thr His Thr Gly Lys Lys Thr Ser Val Tyr Val Gly Gly
                325                 330                 335

Leu Glu Ser Arg Val Leu Lys Tyr Thr Ala Gln Asn Met Glu Leu Gln
            340                 345                 350

Asn Lys Val Gln Leu Leu Glu Glu Gln Asn Leu Ser Leu Leu Asp Gln
        355                 360                 365

Leu Arg Lys Leu Gln Ala Met Val Ile Glu Ile Ser Asn Lys Thr Ser
    370                 375                 380

Ser Ser Ser Thr Cys Ile Leu Val Leu Leu Val Ser Phe Cys Leu Leu
385                 390                 395                 400
```

```
Leu Val Pro Ala Met Tyr Ser Ser Asp Thr Arg Gly Ser Leu Pro Ala
                405                 410                 415

Glu His Gly Val Leu Ser Arg Gln Leu Arg Ala Leu Pro Ser Glu Asp
            420                 425                 430

Pro Tyr Gln Leu Glu Leu Pro Ala Leu Gln Ser Glu Val Pro Lys Asp
        435                 440                 445

Ser Thr His Gln Trp Leu Asp Gly Ser Asp Cys Val Leu Gln Ala Pro
    450                 455                 460

Gly Asn Thr Ser Cys Leu Leu His Tyr Met Pro Gln Ala Pro Ser Ala
465                 470                 475                 480

Glu Pro Pro Leu Glu Trp Pro Phe Pro Asp Leu Phe Ser Glu Pro Leu
                485                 490                 495

Cys Arg Gly Pro Ile Leu Pro Leu Gln Ala Asn Leu Thr Arg Lys Gly
            500                 505                 510

Gly Trp Leu Pro Thr Gly Ser Pro Ser Val Ile Leu Gln Asp Arg Tyr
        515                 520                 525

Ser Gly
    530
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<210> 214
<211> 1590
<212> DNA
<213> Artificial Sequence

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

<400> 214
atggagctgg aattggatgc tggtgaccaa gacctgctgg ccttcctgct agaggaaagt 60

ggagatttgg ggacggcacc cgatgaggcc gtgagggccc cactggactg ggcgctgccg 120

ctttctgagg tgccgagcga ctgggaagta gatgatttgc tgtgctccct gctgagtccc 180

ccagcgtcgt tgaacattct cagctcctcc aacccctgcc ttgtccacca tgaccacacc 240

tactccctcc cacgggaaac tgtctctatg gatctagaga gtgagagctg tagaaaagag 300

gggacccaga tgactccaca gcatatggag gagctggcag agcaggagat tgctaggcta 360

gtactgacag atgaggagaa gagtctattg gagaaggagg ggcttattct gcctgagaca 420

cttcctctca ctaagacaga ggaacaaatt ctgaaacgtg tgcggcttga gcccggagag 480

aagccgtaca agtgccctga gtgcggcaag tcttttagca gaagagacga acttaatgtc 540

caccagcgaa cgcatactgg tgaaaagccc tataaatgtc ctgaatgtgg gaaatcattc 600

tccagccgca gaacctgtag ggctcaccag cgaacacaca ccggcgaaaa accatacaaa 660

tgtccagaat gcgggaaatc cttttctcag tcatccaact tggtgagaca tcaacgcacg 720

cacactggag aaaagcctta caaatgcccg gaatgtggaa agtctttttc ccaattggcc 780

catttgcgag cccatcagag gactcacacg ggcgagaaac cttacaaatg cccggaatgc 840

gggaaatctt tttcaacgag tggcaacctc gtaagacacc aaagaacgca tacaggcgaa 900

aagccatata agtgtcctga gtgtggtaaa tcattctcac acaggaccac cctgacaaat 960

caccagcgca cgcacaccgg caagaagaca agcgtgtacg ttgggggttt agagagccgg 1020

gtcttgaaat acacagccca gaatatggag cttcagaaca aagtacagct tctggaggaa 1080

cagaatttgt cccttctaga tcaactgagg aaactccagg ccatggtgat tgagatctca 1140

aacaaaacca gcagcagcag cacctgcatc ttggtcctgc tagtctcctt ctgcctcctc 1200

cttgtacctg ctatgtactc ctctgacaca agggggagcc tgccagctga gcatggagtg 1260

ttgtcccgcc agcttcgtgc cctccccagt gaggaccctt accagctgga gctgcctgcc 1320

ctgcagtcag aagtgccgaa agacagcaca caccagtggt tggacggctc agactgtgta 1380

ctccaggccc ctggcaacac ttcctgcctg ctgcattaca tgcctcaggc tcccagtgca 1440

gagcctcccc tggagtggcc cttccctgac ctcttctcag agcctctctg ccgaggtccc 1500

atcctccccc tgcaggcaaa tctcacaagg aagggaggat ggcttcctac tggtagcccc 1560

tctgtcattt tgcaggacag atactcaggc 1590

<210> 215
<211> 530
<212> PRT
<213> Artificial Sequence

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

polypeptide

<400> 215
Met Glu Leu Glu Leu Asp Ala Gly Asp Gln Asp Leu Leu Ala Phe Leu
1 5 10 15

Leu Glu Glu Ser Gly Asp Leu Gly Thr Ala Pro Asp Glu Ala Val Arg
20 25 30

Ala Pro Leu Asp Trp Ala Leu Pro Leu Ser Glu Val Pro Ser Asp Trp
35 40 45

Glu Val Asp Asp Leu Leu Cys Ser Leu Leu Ser Pro Pro Ala Ser Leu
50 55 60

Asn Ile Leu Ser Ser Ser Asn Pro Cys Leu Val His His Asp His Thr
65 70 75 80

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

Cys Arg Lys Glu Gly Thr Gln Met Thr Pro Gln His Met Glu Glu Leu
100 105 110

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

Leu Leu Glu Lys Glu Gly Leu Ile Leu Pro Glu Thr Leu Pro Leu Thr
130 135 140

Lys Thr Glu Glu Gln Ile Leu Lys Arg Val Arg Leu Glu Pro Gly Glu
145 150 155 160

Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Arg Asp
165 170 175

Glu Leu Asn Val His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys
180 185 190

Cys Pro Glu Cys Gly Lys Ser Phe Ser Ser Arg Arg Thr Cys Arg Ala
195 200 205

```
His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys
    210                 215                 220

Gly Lys Ser Phe Ser Gln Ser Ser Asn Leu Val Arg His Gln Arg Thr
225                 230                 235                 240

His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe
                245                 250                 255

Ser Gln Leu Ala His Leu Arg Ala His Gln Arg Thr His Thr Gly Glu
            260                 265                 270

Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Thr Ser Gly
        275                 280                 285

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

Cys Pro Glu Cys Gly Lys Ser Phe Ser His Arg Thr Thr Leu Thr Asn
305                 310                 315                 320

His Gln Arg Thr His Thr Gly Lys Lys Thr Ser Val Tyr Val Gly Gly
                325                 330                 335

Leu Glu Ser Arg Val Leu Lys Tyr Thr Ala Gln Asn Met Glu Leu Gln
            340                 345                 350

Asn Lys Val Gln Leu Leu Glu Glu Gln Asn Leu Ser Leu Leu Asp Gln
        355                 360                 365

Leu Arg Lys Leu Gln Ala Met Val Ile Glu Ile Ser Asn Lys Thr Ser
    370                 375                 380

Ser Ser Ser Thr Cys Ile Leu Val Leu Leu Val Ser Phe Cys Leu Leu
385                 390                 395                 400

Leu Val Pro Ala Met Tyr Ser Ser Asp Thr Arg Gly Ser Leu Pro Ala
                405                 410                 415

Glu His Gly Val Leu Ser Arg Gln Leu Arg Ala Leu Pro Ser Glu Asp
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420 425 430

Pro Tyr Gln Leu Glu Leu Pro Ala Leu Gln Ser Glu Val Pro Lys Asp
435 440 445

Ser Thr His Gln Trp Leu Asp Gly Ser Asp Cys Val Leu Gln Ala Pro
450 455 460

Gly Asn Thr Ser Cys Leu Leu His Tyr Met Pro Gln Ala Pro Ser Ala
465 470 475 480

Glu Pro Pro Leu Glu Trp Pro Phe Pro Asp Leu Phe Ser Glu Pro Leu
485 490 495

Cys Arg Gly Pro Ile Leu Pro Leu Gln Ala Asn Leu Thr Arg Lys Gly
500 505 510

Gly Trp Leu Pro Thr Gly Ser Pro Ser Val Ile Leu Gln Asp Arg Tyr
515 520 525

Ser Gly
530

<210> 216
<211> 1590
<212> DNA
<213> Artificial Sequence

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

<400> 216
atggagctgg aattggatgc tggtgaccaa gacctgctgg ccttcctgct agaggaaagt 60

ggagatttgg ggacggcacc cgatgaggcc gtgagggccc cactggactg ggcgctgccg 120

ctttctgagg tgccgagcga ctgggaagta gatgatttgc tgtgctccct gctgagtccc 180

ccagcgtcgt tgaacattct cagctcctcc aacccctgcc ttgtccacca tgaccacacc 240

tactccctcc cacgggaaac tgtctctatg gatctagaga gtgagagctg tagaaaagag 300

gggacccaga tgactccaca gcatatggag gagctggcag agcaggagat tgctaggcta 360

gtactgacag atgaggagaa gagtctattg gagaaggagg ggcttattct gcctgagaca 420

cttcctctca ctaagacaga ggaacaaatt ctgaaacgtg tgcggcgccc ttacgcttgc 480

ccagtggagt cctgtgatcg ccgcttctcc cgcagcgaca acctggtgag acacatccgc 540

atccacacag gccagaagcc cttccagtgc cgcatctgca tgagaaactt cagccgagag 600

gataacttgc acactcacat ccgcacccac acaggcgaaa agcccttcgc ctgcgacatc 660

tgtggaagaa agtttgcccg gagcgatgaa cttgtccgac ataccaagat ccacttgcgg 720

cagaaggacc gcccttacgc ttgcccagtg gagtcctgtg atcgccgctt ctcccaatca 780

gggaatctga ctgagcacat ccgcatccac acaggccaga agcccttcca gtgccgcatc 840

tgcatgagaa acttcagcac aagtggacat ctggtacgcc acatccgcac ccacacaggc 900

gaaaagccct tcgcctgcga catctgtgga agaaagtttg cccagaatag taccctgacc 960

gaacatacca agatccactt gcggcagaag gacgtgtacg ttgggggttt agagagccgg 1020

gtcttgaaat acacagccca gaatatggag cttcagaaca aagtacagct tctggaggaa 1080

cagaatttgt cccttctaga tcaactgagg aaactccagg ccatggtgat tgagatctca 1140

aacaaaacca gcagcagcag cacctgcatc ttggtcctgc tagtctcctt ctgcctcctc 1200

cttgtacctg ctatgtactc ctctgacaca agggggagcc tgccagctga gcatggagtg 1260

ttgtcccgcc agcttcgtgc cctccccagt gaggaccctt accagctgga gctgcctgcc 1320

ctgcagtcag aagtgccgaa agacagcaca caccagtggt tggacggctc agactgtgta 1380

ctccaggccc ctggcaacac ttcctgcctg ctgcattaca tgcctcaggc tcccagtgca 1440

gagcctcccc tggagtggcc cttccctgac ctcttctcag agcctctctg ccgaggtccc 1500

atcctccccc tgcaggcaaa tctcacaagg aagggaggat ggcttcctac tggtagcccc 1560

tctgtcattt tgcaggacag atactcaggc 1590

<210> 217
<211> 530
<212> PRT
<213> Artificial Sequence

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

<400> 217
Met Glu Leu Glu Leu Asp Ala Gly Asp Gln Asp Leu Leu Ala Phe Leu
1 5 10 15

```
Leu Glu Glu Ser Gly Asp Leu Gly Thr Ala Pro Asp Glu Ala Val Arg
            20                  25                  30

Ala Pro Leu Asp Trp Ala Leu Pro Leu Ser Glu Val Pro Ser Asp Trp
        35                  40                  45

Glu Val Asp Asp Leu Leu Cys Ser Leu Leu Ser Pro Pro Ala Ser Leu
    50                  55                  60

Asn Ile Leu Ser Ser Ser Asn Pro Cys Leu Val His His Asp His Thr
65                  70                  75                  80

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

Cys Arg Lys Glu Gly Thr Gln Met Thr Pro Gln His Met Glu Glu Leu
            100                 105                 110

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

Leu Leu Glu Lys Glu Gly Leu Ile Leu Pro Glu Thr Leu Pro Leu Thr
    130                 135                 140

Lys Thr Glu Glu Gln Ile Leu Lys Arg Val Arg Arg Pro Tyr Ala Cys
145                 150                 155                 160

Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Asn Leu Val
                165                 170                 175

Arg His Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile
            180                 185                 190

Cys Met Arg Asn Phe Ser Arg Glu Asp Asn Leu His Thr His Ile Arg
        195                 200                 205

Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys
    210                 215                 220
```

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Phe Ala Arg Ser Asp Glu Leu Val Arg His Thr Lys Ile His Leu Arg
225                 230                 235                 240

Gln Lys Asp Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg
                245                 250                 255

Phe Ser Gln Ser Gly Asn Leu Thr Glu His Ile Arg Ile His Thr Gly
            260                 265                 270

Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Thr Ser
        275                 280                 285

Gly His Leu Val Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
    290                 295                 300

Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Gln Asn Ser Thr Leu Thr
305                 310                 315                 320

Glu His Thr Lys Ile His Leu Arg Gln Lys Asp Val Tyr Val Gly Gly
                325                 330                 335

Leu Glu Ser Arg Val Leu Lys Tyr Thr Ala Gln Asn Met Glu Leu Gln
            340                 345                 350

Asn Lys Val Gln Leu Leu Glu Glu Gln Asn Leu Ser Leu Leu Asp Gln
        355                 360                 365

Leu Arg Lys Leu Gln Ala Met Val Ile Glu Ile Ser Asn Lys Thr Ser
    370                 375                 380

Ser Ser Ser Thr Cys Ile Leu Val Leu Leu Val Ser Phe Cys Leu Leu
385                 390                 395                 400

Leu Val Pro Ala Met Tyr Ser Ser Asp Thr Arg Gly Ser Leu Pro Ala
                405                 410                 415

Glu His Gly Val Leu Ser Arg Gln Leu Arg Ala Leu Pro Ser Glu Asp
            420                 425                 430

Pro Tyr Gln Leu Glu Leu Pro Ala Leu Gln Ser Glu Val Pro Lys Asp
        435                 440                 445
```

Ser Thr His Gln Trp Leu Asp Gly Ser Asp Cys Val Leu Gln Ala Pro
450 455 460

Gly Asn Thr Ser Cys Leu Leu His Tyr Met Pro Gln Ala Pro Ser Ala
465 470 475 480

Glu Pro Pro Leu Glu Trp Pro Phe Pro Asp Leu Phe Ser Glu Pro Leu
485 490 495

Cys Arg Gly Pro Ile Leu Pro Leu Gln Ala Asn Leu Thr Arg Lys Gly
500 505 510

Gly Trp Leu Pro Thr Gly Ser Pro Ser Val Ile Leu Gln Asp Arg Tyr
515 520 525

Ser Gly
530

<210> 218
<211> 1590
<212> DNA
<213> Artificial Sequence

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

<400> 218
atggagctgg aattggatgc tggtgaccaa gacctgctgg ccttcctgct agaggaaagt 60

ggagatttgg ggacggcacc cgatgaggcc gtgagggccc cactggactg ggcgctgccg 120

ctttctgagg tgccgagcga ctgggaagta gatgatttgc tgtgctccct gctgagtccc 180

ccagcgtcgt tgaacattct cagctcctcc aacccctgcc ttgtccacca tgaccacacc 240

tactccctcc cacgggaaac tgtctctatg gatctagaga gtgagagctg tagaaaagag 300

gggacccaga tgactccaca gcatatggag gagctggcag agcaggagat tgctaggcta 360

gtactgacag atgaggagaa gagtctattg gagaaggagg ggcttattct gcctgagaca 420

cttcctctca ctaagacaga ggaacaaatt ctgaaacgtg tgcggcgccc ttacgcttgc 480

ccagtggagt cctgtgatcg ccgcttctcc cgctcagaca acctcgttcg acacatccgc 540

atccacacag gccagaagcc cttccagtgc cgcatctgca tgagaaactt cagccaccgg 600

actacactca cgaaccacat ccgcacccac acaggcgaaa agcccttcgc ctgcgacatc 660

tgtggaagaa agtttgccag agaagacaat ctccatactc ataccaagat ccacttgcgg 720

cagaaggacc gcccttacgc ttgcccagtg gagtcctgtg atcgccgctt ctccaccagc 780

cattctctca ctgaacacat ccgcatccac acaggccaga agcccttcca gtgccgcatc 840

tgcatgagaa acttcagcca gtctagctca ctggtgaggc acatccgcac ccacacaggc 900

gaaaagccct tcgcctgcga catctgtgga agaaagtttg ccagggagga taacctgcat 960

acgcatacca agatccactt gcggcagaag gacgtgtacg ttgggggttt agagagccgg 1020

gtcttgaaat acacagccca gaatatggag cttcagaaca aagtacagct tctggaggaa 1080

cagaatttgt cccttctaga tcaactgagg aaactccagg ccatggtgat tgagatctca 1140

aacaaaacca gcagcagcag cacctgcatc ttggtcctgc tagtctcctt ctgcctcctc 1200

cttgtacctg ctatgtactc ctctgacaca agggggagcc tgccagctga gcatggagtg 1260

ttgtcccgcc agcttcgtgc cctccccagt gaggaccctt accagctgga gctgcctgcc 1320

ctgcagtcag aagtgccgaa agacagcaca caccagtggt tggacggctc agactgtgta 1380

ctccaggccc ctggcaacac ttcctgcctg ctgcattaca tgcctcaggc tcccagtgca 1440

gagcctcccc tggagtggcc cttccctgac ctcttctcag agcctctctg ccgaggtccc 1500

atcctccccc tgcaggcaaa tctcacaagg aagggaggat ggcttcctac tggtagcccc 1560

tctgtcattt tgcaggacag atactcaggc 1590

<210> 219
<211> 530
<212> PRT
<213> Artificial Sequence

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

<400> 219
Met Glu Leu Glu Leu Asp Ala Gly Asp Gln Asp Leu Leu Ala Phe Leu
1 5 10 15

Leu Glu Glu Ser Gly Asp Leu Gly Thr Ala Pro Asp Glu Ala Val Arg
20 25 30

```
Ala Pro Leu Asp Trp Ala Leu Pro Leu Ser Glu Val Pro Ser Asp Trp
        35                  40                  45

Glu Val Asp Asp Leu Leu Cys Ser Leu Leu Ser Pro Pro Ala Ser Leu
    50                  55                  60

Asn Ile Leu Ser Ser Ser Asn Pro Cys Leu Val His His Asp His Thr
65                  70                  75                  80

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

Cys Arg Lys Glu Gly Thr Gln Met Thr Pro Gln His Met Glu Glu Leu
            100                 105                 110

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

Leu Leu Glu Lys Glu Gly Leu Ile Leu Pro Glu Thr Leu Pro Leu Thr
    130                 135                 140

Lys Thr Glu Glu Gln Ile Leu Lys Arg Val Arg Arg Pro Tyr Ala Cys
145                 150                 155                 160

Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Asn Leu Val
                165                 170                 175

Arg His Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile
            180                 185                 190

Cys Met Arg Asn Phe Ser His Arg Thr Thr Leu Thr Asn His Ile Arg
        195                 200                 205

Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys
    210                 215                 220

Phe Ala Arg Glu Asp Asn Leu His Thr His Thr Lys Ile His Leu Arg
225                 230                 235                 240

Gln Lys Asp Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg
```

```
               245                 250                 255

Phe Ser Thr Ser His Ser Leu Thr Glu His Ile Arg Ile His Thr Gly
            260                 265                 270

Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Gln Ser
        275                 280                 285

Ser Ser Leu Val Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
    290                 295                 300

Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Glu Asp Asn Leu His
305                 310                 315                 320

Thr His Thr Lys Ile His Leu Arg Gln Lys Asp Val Tyr Val Gly Gly
                325                 330                 335

Leu Glu Ser Arg Val Leu Lys Tyr Thr Ala Gln Asn Met Glu Leu Gln
            340                 345                 350

Asn Lys Val Gln Leu Leu Glu Glu Gln Asn Leu Ser Leu Leu Asp Gln
        355                 360                 365

Leu Arg Lys Leu Gln Ala Met Val Ile Glu Ile Ser Asn Lys Thr Ser
    370                 375                 380

Ser Ser Ser Thr Cys Ile Leu Val Leu Leu Val Ser Phe Cys Leu Leu
385                 390                 395                 400

Leu Val Pro Ala Met Tyr Ser Ser Asp Thr Arg Gly Ser Leu Pro Ala
                405                 410                 415

Glu His Gly Val Leu Ser Arg Gln Leu Arg Ala Leu Pro Ser Glu Asp
            420                 425                 430

Pro Tyr Gln Leu Glu Leu Pro Ala Leu Gln Ser Glu Val Pro Lys Asp
        435                 440                 445

Ser Thr His Gln Trp Leu Asp Gly Ser Asp Cys Val Leu Gln Ala Pro
    450                 455                 460
```

Gly Asn Thr Ser Cys Leu Leu His Tyr Met Pro Gln Ala Pro Ser Ala
465 470 475 480

Glu Pro Pro Leu Glu Trp Pro Phe Pro Asp Leu Phe Ser Glu Pro Leu
485 490 495

Cys Arg Gly Pro Ile Leu Pro Leu Gln Ala Asn Leu Thr Arg Lys Gly
500 505 510

Gly Trp Leu Pro Thr Gly Ser Pro Ser Val Ile Leu Gln Asp Arg Tyr
515 520 525

Ser Gly
530

<210> 220
<211> 1140
<212> DNA
<213> Artificial Sequence

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

<400> 220
atggagctgg aattggatgc tggtgaccaa gacctgctgg ccttcctgct agaggaaagt 60

ggagatttgg ggacggcacc cgatgaggcc gtgagggccc cactggactg ggcgctgccg 120

ctttctgagg tgccgagcga ctgggaagta gatgatttgc tgtgctccct gctgagtccc 180

ccagcgtcgt tgaacattct cagctcctcc aacccctgcc ttgtccacca tgaccacacc 240

tactccctcc cacgggaaac tgtctctatg gatctagaga gtgagagctg tagaaaagag 300

gggacccaga tgactccaca gcatatggag gagctggcag agcaggagat tgctaggcta 360

gtactgacag atgaggagaa gagtctattg gagaaggagg ggcttattct gcctgagaca 420

cttcctctca ctaagacaga ggaacaaatt ctgaaacgtg tgcggctcga accaggtgaa 480

aaaccttaca aatgtcctga atgtgggaaa tcattcagtc gcagcgacaa cctggtgaga 540

catcaacgca cccatacagg agaaaaacct tataaatgtc cagaatgtgg aaagtccttc 600

tcacgagagg ataacttgca cactcatcaa cgaacacata ctggtgaaaa accatacaag 660

tgtcccgaat gtggtaaaag ttttagccgg agcgatgaac ttgtccgaca ccaacgaacc 720

catacaggcg agaagcctta caaatgtccc gagtgtggca agagcttctc acaatcaggg 780

aatctgactg agcatcaacg aactcatacc ggggaaaaac cttacaagtg tccagagtgt 840

gggaagagct tttccacaag tggacatctg gtacgccacc agaggacaca tacaggggag 900

aagccctaca aatgccccga atgcggtaaa agtttctctc agaatagtac cctgaccgaa 960

caccagcgaa cacacactgg gaaaaaaacg agtgtgtacg ttgggggttt agagagccgg 1020

gtcttgaaat acacagccca gaatatggag cttcagaaca aagtacagct tctggaggaa 1080

cagaatttgt cccttctaga tcaactgagg aaactccagg ccatggtgat tgagatatca 1140

<210> 221
<211> 380
<212> PRT
<213> Artificial Sequence

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

<400> 221
Met Glu Leu Glu Leu Asp Ala Gly Asp Gln Asp Leu Leu Ala Phe Leu
1 5 10 15

Leu Glu Glu Ser Gly Asp Leu Gly Thr Ala Pro Asp Glu Ala Val Arg
20 25 30

Ala Pro Leu Asp Trp Ala Leu Pro Leu Ser Glu Val Pro Ser Asp Trp
35 40 45

Glu Val Asp Asp Leu Leu Cys Ser Leu Leu Ser Pro Pro Ala Ser Leu
50 55 60

Asn Ile Leu Ser Ser Ser Asn Pro Cys Leu Val His His Asp His Thr
65 70 75 80

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

Cys Arg Lys Glu Gly Thr Gln Met Thr Pro Gln His Met Glu Glu Leu
100 105 110

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

Leu Leu Glu Lys Glu Gly Leu Ile Leu Pro Glu Thr Leu Pro Leu Thr
    130                 135                 140

Lys Thr Glu Glu Gln Ile Leu Lys Arg Val Arg Leu Glu Pro Gly Glu
145                 150                 155                 160

Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Ser Asp
                165                 170                 175

Asn Leu Val Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys
            180                 185                 190

Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Glu Asp Asn Leu His Thr
        195                 200                 205

His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys
    210                 215                 220

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

His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe
                245                 250                 255

Ser Gln Ser Gly Asn Leu Thr Glu His Gln Arg Thr His Thr Gly Glu
            260                 265                 270

Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Thr Ser Gly
        275                 280                 285

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

Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Asn Ser Thr Leu Thr Glu
305                 310                 315                 320

His Gln Arg Thr His Thr Gly Lys Lys Thr Ser Val Tyr Val Gly Gly
                325                 330                 335
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Leu Glu Ser Arg Val Leu Lys Tyr Thr Ala Gln Asn Met Glu Leu Gln
340 345 350

Asn Lys Val Gln Leu Leu Glu Glu Gln Asn Leu Ser Leu Leu Asp Gln
355 360 365

Leu Arg Lys Leu Gln Ala Met Val Ile Glu Ile Ser
370 375 380

<210> 222
<211> 1140
<212> DNA
<213> Artificial Sequence

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

<400> 222
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ggagatttgg ggacggcacc cgatgaggcc gtgagggccc cactggactg ggcgctgccg 120

ctttctgagg tgccgagcga ctgggaagta gatgatttgc tgtgctccct gctgagtccc 180

ccagcgtcgt tgaacattct cagctcctcc aacccctgcc ttgtccacca tgaccacacc 240

tactccctcc cacgggaaac tgtctctatg gatctagaga gtgagagctg tagaaaagag 300

gggacccaga tgactccaca gcatatggag gagctggcag agcaggagat tgctaggcta 360

gtactgacag atgaggagaa gagtctattg gagaaggagg ggcttattct gcctgagaca 420

cttcctctca ctaagacaga ggaacaaatt ctgaaacgtg tgcggcgccc ttacgcttgc 480

ccagtggagt cctgtgatcg ccgcttctcc cgcagcgaca acctggtgag acacatccgc 540

atccacacag gccagaagcc cttccagtgc cgcatctgca tgagaaactt cagccgagag 600

gataacttgc acactcacat ccgcacccac acaggcgaaa agcccttcgc ctgcgacatc 660

tgtggaagaa agtttgcccg gagcgatgaa cttgtccgac ataccaagat ccacttgcgg 720

cagaaggacc gcccttacgc ttgcccagtg gagtcctgtg atcgccgctt ctcccaatca 780

gggaatctga ctgagcacat ccgcatccac acaggccaga agcccttcca gtgccgcatc 840

tgcatgagaa acttcagcac aagtggacat ctggtacgcc acatccgcac ccacacaggc 900

gaaaagccct tcgcctgcga catctgtgga agaaagtttg cccagaatag taccctgacc 960

gaacatacca agatccactt gcggcagaag gacgtgtacg ttgggggttt agagagccgg 1020

gtcttgaaat acacagccca gaatatggag cttcagaaca aagtacagct tctggaggaa 1080

cagaatttgt cccttctaga tcaactgagg aaactccagg ccatggtgat tgagatctca 1140

<210> 223
<211> 380
<212> PRT
<213> Artificial Sequence

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

<400> 223
Met Glu Leu Glu Leu Asp Ala Gly Asp Gln Asp Leu Leu Ala Phe Leu
1 5 10 15

Leu Glu Glu Ser Gly Asp Leu Gly Thr Ala Pro Asp Glu Ala Val Arg
20 25 30

Ala Pro Leu Asp Trp Ala Leu Pro Leu Ser Glu Val Pro Ser Asp Trp
35 40 45

Glu Val Asp Asp Leu Leu Cys Ser Leu Leu Ser Pro Pro Ala Ser Leu
50 55 60

Asn Ile Leu Ser Ser Ser Asn Pro Cys Leu Val His His Asp His Thr
65 70 75 80

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

Cys Arg Lys Glu Gly Thr Gln Met Thr Pro Gln His Met Glu Glu Leu
100 105 110

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

Leu Leu Glu Lys Glu Gly Leu Ile Leu Pro Glu Thr Leu Pro Leu Thr
130 135 140

```
Lys Thr Glu Glu Gln Ile Leu Lys Arg Val Arg Arg Pro Tyr Ala Cys
145                 150                 155                 160

Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Asn Leu Val
                165                 170                 175

Arg His Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile
            180                 185                 190

Cys Met Arg Asn Phe Ser Arg Glu Asp Asn Leu His Thr His Ile Arg
        195                 200                 205

Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys
    210                 215                 220

Phe Ala Arg Ser Asp Glu Leu Val Arg His Thr Lys Ile His Leu Arg
225                 230                 235                 240

Gln Lys Asp Arg Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg
                245                 250                 255

Phe Ser Gln Ser Gly Asn Leu Thr Glu His Ile Arg Ile His Thr Gly
            260                 265                 270

Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Thr Ser
        275                 280                 285

Gly His Leu Val Arg His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
    290                 295                 300

Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Gln Asn Ser Thr Leu Thr
305                 310                 315                 320

Glu His Thr Lys Ile His Leu Arg Gln Lys Asp Val Tyr Val Gly Gly
                325                 330                 335

Leu Glu Ser Arg Val Leu Lys Tyr Thr Ala Gln Asn Met Glu Leu Gln
            340                 345                 350

Asn Lys Val Gln Leu Leu Glu Glu Gln Asn Leu Ser Leu Leu Asp Gln
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        355                 360                 365

Leu Arg Lys Leu Gln Ala Met Val Ile Glu Ile Ser
    370                 375                 380


<210> 224
<211> 155
<212> PRT
<213> Artificial Sequence

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

<400> 224
Met Glu Leu Glu Leu Asp Ala Gly Asp Gln Asp Leu Leu Ala Phe Leu
1               5                   10                  15


Leu Glu Glu Ser Gly Asp Leu Gly Thr Ala Pro Asp Glu Ala Val Arg
            20                  25                  30


Ala Pro Leu Asp Trp Ala Leu Pro Leu Ser Glu Val Pro Ser Asp Trp
        35                  40                  45


Glu Val Asp Asp Leu Leu Cys Ser Leu Leu Ser Pro Pro Ala Ser Leu
    50                  55                  60


Asn Ile Leu Ser Ser Ser Asn Pro Cys Leu Val His His Asp His Thr
65                  70                  75                  80


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


Cys Arg Lys Glu Gly Thr Gln Met Thr Pro Gln His Met Glu Glu Leu
            100                 105                 110


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


Leu Leu Glu Lys Glu Gly Leu Ile Leu Pro Glu Thr Leu Pro Leu Thr
    130                 135                 140


Lys Thr Glu Glu Gln Ile Leu Lys Arg Val Arg
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145 150 155

<210> 225
<211> 199
<212> PRT
<213> Artificial Sequence

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

<400> 225
Val Tyr Val Gly Gly Leu Glu Ser Arg Val Leu Lys Tyr Thr Ala Gln
1 5 10 15

Asn Met Glu Leu Gln Asn Lys Val Gln Leu Leu Glu Glu Gln Asn Leu
20 25 30

Ser Leu Leu Asp Gln Leu Arg Lys Leu Gln Ala Met Val Ile Glu Ile
35 40 45

Ser Asn Lys Thr Ser Ser Ser Ser Thr Cys Ile Leu Val Leu Leu Val
50 55 60

Ser Phe Cys Leu Leu Leu Val Pro Ala Met Tyr Ser Ser Asp Thr Arg
65 70 75 80

Gly Ser Leu Pro Ala Glu His Gly Val Leu Ser Arg Gln Leu Arg Ala
85 90 95

Leu Pro Ser Glu Asp Pro Tyr Gln Leu Glu Leu Pro Ala Leu Gln Ser
100 105 110

Glu Val Pro Lys Asp Ser Thr His Gln Trp Leu Asp Gly Ser Asp Cys
115 120 125

Val Leu Gln Ala Pro Gly Asn Thr Ser Cys Leu Leu His Tyr Met Pro
130 135 140

Gln Ala Pro Ser Ala Glu Pro Pro Leu Glu Trp Pro Phe Pro Asp Leu
145 150 155 160

Phe Ser Glu Pro Leu Cys Arg Gly Pro Ile Leu Pro Leu Gln Ala Asn

165 170 175

Leu Thr Arg Lys Gly Gly Trp Leu Pro Thr Gly Ser Pro Ser Val Ile
180 185 190

Leu Gln Asp Arg Tyr Ser Gly
195

<210> 226
<211> 49
<212> PRT
<213> Artificial Sequence

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

<400> 226
Val Tyr Val Gly Gly Leu Glu Ser Arg Val Leu Lys Tyr Thr Ala Gln
1 5 10 15

Asn Met Glu Leu Gln Asn Lys Val Gln Leu Leu Glu Glu Gln Asn Leu
20 25 30

Ser Leu Leu Asp Gln Leu Arg Lys Leu Gln Ala Met Val Ile Glu Ile
35 40 45

Ser