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<150> 62/419,947

<151> 2016-11-09

<160> 65

<170> PatentIn version 3.5

<210> 1

<211> 3171

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

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<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

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<212> DNA

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<221> source

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

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<211> 2928

<212> DNA

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

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<212> DNA

<213> Artificial Sequence

<220>

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

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<210> 6

<211> 2928

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

polynucleotide"

<400> 6

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<210> 7

<211> 3165

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 7

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<210> 8

<211> 2925

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 8

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<210> 9

<211> 1554

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 9

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acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc	1140
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aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctcgtcagc	1440
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<210> 10

<211> 1554

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 10

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tcaggaggtg gaagcggcgg ctctggggac acccgaccac gtttcttgga gtactctacg	180
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aaccaggagg agaacgtgcg cttcgacagc gacgtggggg agttccgggc ggtgacggag	300
ctggggcggc ctgatgccga gtactggaac agccagaagg acctcctgga gcagaagcgg	360
ggccgggtgg acaactactg cagacacaac tacgggggtg tggagagctt cacagtgcag	420
cggcgagtcc atcctaaggt gactgtgtat cttcaaaga cccagcccct gcagcaccat	480
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cggaatggcc aggaagagaa gactgggggtg gtgtccacag gcctgatcca caatggagac	600
tggaccttcc agaccctggg gatgctggaa acagttcctc ggagtggaga ggtttacacc	660
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tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccc aaaaccaag	960
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<210> 11

<211> 1434

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 11

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tttgatggatg atgagatddd ccatgtggat atggcaaaga aggagacggc ctggcggctt	180
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gacaaagcca acctggaaat catgacaaag cgctccaact atactccgat caccaatgta	300
cctccagagg taactgtgct cacaaacagc cctgtggaac tgagagagcc caacgtcctc	360
atctgtttca tagacaagtt caccacacca gtggtcaatg tcacgtggct tcgaaatgga	420
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cgcaagttcc actatctccc cttcctgccc tcaactgagg acgtttacga ctgcagggtg	540
gagcactggg gcttggatga gcctcttctc aagcactggg agtttgatgc tccaagccct	600
ctcccagaga ctacagagtc cggaggcgga ggcggaactga cagatacact ccaagcggag	660
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acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc	1020
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aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc	1320
aagctcaccg tggacaagag cagggtggcag caggggaacg tcttctcatg ctccgtgatg	1380
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<210> 12

<211> 1434

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 12

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tttgatgggtg atgagatfff ccatgtggat atggcaaaga aggagacggg ctggcggctt	180
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gacaaagcca acctggaaat catgacaaag cgctccaact atactccgat caccaatgta	300
cctccagagg taactgtgct cacaacacagc cctgtggaac tgagagagcc caacgtcctc	360
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cgcaagttcc actatctccc cttcctgccc tcaactgagg acgtttacga ctgcagggtg	540
gagcactggg gcttggtatga gcctcttctc aagcactggg agttttgatgc tccaagccct	600
ctcccagaga ctacagagtc cggaggcgga ggcggtactga cagatacact ccaagcggag	660

acagatcaac ttgaagacga gaagtctgcg ttgcagaccg agattgccaa tctactgaaa	720
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gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaa	960
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aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg	1380
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<210> 13

<211> 1434

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 13

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tcaggagggtg gaagcggcgg ctctggggac acccgaccac gtttcttggg gtactctacg	180
tctgagtgtc atttcttcaa tgggacggag cgggtgcggt acctggacag atacttccat	240
aaccaggagg agaacgtgcg cttcgacagc gacgtggggg agttccgggc ggtgacggag	300
ctggggcggc ctgatgccga gtactggaac agccagaagg acctcctgga gcagaagcgg	360

ggccgggtgg acaactactg cagacacaac tacggggttg tggagagctt cacagtgcag	420
cggcgagtcc atcctaaggt gactgtgtat ccttcaaaga cccagcccct gcagcaccat	480
aacctcctgg tctgttctgt gagtggtttc tatccaggca gcattgaagt caggtggttc	540
cggaatggcc aggaagagaa gactgggggtg gtgtccacag gcctgatcca caatggagac	600
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gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag	960
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aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg	1380
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<210> 14

<211> 1434

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 14

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tcaggagggtg gaagcggcgg ctctggggac acccgaccac gtttcttgga gtactctacg	180
tctgagtgtc atttcttcaa tgggacggag cgggtgcggt acctggacag atacttccat	240
aaccaggagg agaacgtgcg cttcgacagc gacgtggggg agttccgggc ggtgacggag	300
ctggggcggc ctgatgccga gtactggaac agccagaagg acctcctgga gcagaagcgg	360
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gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag	960
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aagctcaccg tggacaagag cagggtggcag caggggaacg tcttctcatg ctccgtgatg	1380
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<210> 15

<211> 1314

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 15

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tttgatgggtg atgagatttt ccatgtggat atggcaaaga aggagacggc ctggcggcctt	180
gaagaatttg gacgatttgc cagctttgag gctcaagggtg cattggccaa catagctgtg	240
gacaaaagcca acctggaaat catgacaaaag cgctccaact atactccgat caccaatgta	300
cctccagagg taactgtgct cacaacagc cctgtggaac tgagagagcc caacgtcctc	360
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aaacctgtca ccacaggagt gtcagagaca gtcttcctgc ccagggaaga ccaccttttc	480
cgcaagttcc actatctccc ctctctgccc tcaactgagg acgtttacga ctgcagggtg	540
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ctcccagaga ctacagagtc cggaggcgga ggaggagaca aaactcacac atgcccaccg	660
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<210> 16

<211> 1314

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 16

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tttgatgggtg atgagatfff ccatgtggat atggcaaaga aggagacggg ctggcggcctt 180

gaagaatttg gacgatttgc cagctttgag gctcaagggt cattggccaa catagctgtg 240

gacaaaagcca acctggaaat catgacaaaag cgctccaact atactccgat caccaatgta 300

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cgcaagttcc actatctccc cttcctgccc tcaactgagg acgtttacga ctgcagggtg 540

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ctcccagaga ctacagagtc cggaggcgga ggaggagaca aaactcacac atgcccaccg 660

tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccc aaaaccaag 720

gacaccctca tgatctcccg gaccctgag gtcacatgcg tgggtggtgga cgtgagccac 780

gaagaccctg aggtcaagtt caactggtac gtggacggcg tggagggtgca taatgccaag 840

acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc 900

ctgcaccagg actggctgaa tggcaaggag tacaagtgca aagtctccaa caaagccctc 960

ccagccccca tcgagaaaac catctccaaa gccaaagggc agccccgaga accacaggtg 1020

tgcaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gagctgcgcg 1080

gtcaaaggct tctatcccag cgacatcgcc gtggagtggg agagcaatgg gcagccggag	1140
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aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg	1260
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<210> 17

<211> 1539

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 17

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ggtggagggt ctggagactc cgaaaggcat ttcgtgcacc agttcaagggt cgagtgtctac	180
ttcaccaacg ggacgcagcg catacggctc gtgaccagat acatctacaa ccgggaggag	240
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tcagccgagt actacaataa gcagtacctg gagcgaacgc gggccgagct ggacacggcg	360
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gcgcaaaaact ccgagctggc gtccacggcc aacatgctca gggaacagggt ggcacagctt	840
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cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc	1380
acgcctcccg tgctggactc cgacgggtcc ttcttcctcg tcagcaagct caccgtggac	1440
aagagtaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac	1500
aaccactaca cacagaagag cctctccctg tctcccggc	1539

<210> 18

<211> 1539

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 18

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cccatctggg cccgaatgga cgccggagggt ggaggctcac tagtgccccg aggctctgga	120
ggtggagggt ctggagactc cgaaaggcat ttcgtgcacc agttcaaggg cgagtgtctac	180
ttcaccaacg ggacgcagcg catacggctc gtgaccagat acatctacaa ccgggaggag	240
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tcagccgagt actacaataa gcagtacctg gagcgaacgc gggccgagct ggacacggcg	360
tgcagacaca actacgagga gacggagggtc cccacctccc tgcggcggct tgaacagccc	420
aatgtcgcca tctccctgtc caggacagag gccctcaacc accacaacac tctggtctgt	480

tcggtgacag atttctaccc agccaagatc aaagtgcgct ggttcaggaa tggccaggag	540
gagacagtgg ggggtctcatc cacacagctt attaggaatg gggactggac cttccaggtc	600
ctgggtcatgc tggagatgac ccctcatcag ggagagggtct atacctgcca tgtggagcat	660
cccagcctga agagcccat cactgtggag tggagggcac agtccgagtc tgcccggagc	720
aagtccggag gcgaggcg acggatcgct cggctagagg aaaaagtga aaccttgaaa	780
gcgcaaaact ccgagctggc gtccacggcc aacatgctca gggaacagggt ggcacagctt	840
aagcagaaag tcatgaacca cgacaaaact cacacatgcc caccgtgccc agcacctgaa	900
ctcctggggg gaccgtcagt cttcctcttc ccccaaaac ccaaggacac cctcatgac	960
tcccggaccc ctgaggtcac atgcgtgggtg gtggacgtga gccacgaaga ccctgaggtc	1020
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acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac	1440
aagagtaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac	1500
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<210> 19

<211> 1446

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 19

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gccgaccacg taggcttcta tggtaacaact gtttatcagt ctcttgagga cattggccag	120
tacacacatg aatttgatgg tgatgagttg ttctatgtgg acttggataa gaagaaaact	180
gtctggaggc ttcctgagtt tggccaattg atactctttg agccccaagg tggactgcaa	240
aacatagctg cagaaaaaca caacttggga atcttgacta agaggtcaaa tttcacccca	300
gctaccaatg aggctcctca agcgactgtg ttccccaagt cccctgtgct gctgggtcag	360
cccaacaccc ttatctgctt tgttgacaac atcttccac ctgtgatcaa catcacatgg	420
ctcagaaata gcaagtcagt cacagacggc gtttatgaga ccagcttcct cgtcaaccgt	480
gaccattcct tccacaagct gtcttatctc accttcatcc cttctgatga tgacatttat	540
gactgcaagg tggagcactg gggcctggag gagccggttc tgaaacactg ggaacctgag	600
attccagccc ccatgtcaga gctgacagag tccggaggcg gaggcggact gacagataca	660
ctccaagcgg agacagatca acttgaagac gagaagtctg cgttgacagac cgagattgcc	720
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acatgcccac cgtgcccagc acctgaactc ctggggggac cgtcagtctt cctcttcccc	840
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cataatgcca agacaaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc	1020
gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggctctcc	1080
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga	1140
gaaccacagg tgtacaccct gccccatgc cgggatgagc tgaccaagaa ccaggtcagc	1200
ctgtggtgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat	1260
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc	1320
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tgctccgtga tgcatgaggc tctgcacaac cactacacac agaagagcct ctccctgtct	1440
ccgggc	1446

<210> 20
<211> 1446
<212> DNA
<213> Artificial Sequence

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

<400> 20
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tacacacatg aatttgatgg tgatgagttg ttctatgtgg acttgataa gaagaaaact 180
gtctggaggc ttcctgagtt tggccaattg atactctttg agccccaagg tggactgcaa 240
aacatagctg cagaaaaaca caacttggga atcttgacta agaggatcaa tttcacccca 300
gctaccaatg aggctcctca agcgactgtg ttccccaagt cccctgtgct gctgggtcag 360
cccaacaccc ttatctgctt tgtggacaac atcttccac ctgtgatcaa catcacatgg 420
ctcagaaata gcaagtcagt cacagacggc gtttatgaga ccagcttcct cgtcaaccgt 480
gaccattcct tccacaagct gtcttatctc accttcatcc cttctgatga tgacatttat 540
gactgcaagg tggagcactg gggcctggag gagccggttc tgaaacactg ggaacctgag 600
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ctccaagcgg agacagatca acttgaagac gagaagtctg cgttgacagac cgagattgcc 720
aatctactga aagagaagga aaaactggag tttattttgg cagcccacga caaaactcac 780
acatgcccac cgtgcccagc acctgaactc ctggggggac cgtcagtctt cctcttcccc 840
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aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1140
gaaccacagg tgtgcaccct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1200

ctgagctgcg cgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat	1260
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc	1320
ttcctcgtca gcaagctcac cgtggacaag agtaggtggc agcaggggaa cgtcttctca	1380
tgctccgtga tgcatgaggc tctgcacaac cactacacac agaagagcct ctccctgtct	1440
cccggc	1446

<210> 21

<211> 1419

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 21

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cccatctggg cccgaatgga cgccggagggt ggaggctcac tagtgccccg aggctctgga	120
ggtggagggt ctggagactc cgaaaggcat ttcgtgcacc agttcaagggt cgagtgtctac	180
ttcaccaacg ggacgcagcg catacggctc gtgaccagat acatctacaa ccgggaggag	240
tacctgcgct tcgacagcga cgtgggcgag taccgcgcgg tgaccgagct ggggcggcac	300
tcagccgagt actacaataa gcagtacctg gagcgaacgc gggccgagct ggacacggcg	360
tgacagacac actacgagga gacggagggt cccacctccc tgcggcggct tgaacagccc	420
aatgtcgcca tctccctgtc caggacagag gccctcaacc accacaacac tctggtctgt	480
tcggtgacag atttctaccc agccaagatc aaagtgcgct gggtcaggaa tggccaggag	540
gagacagtgg ggggtctcatc cacacagctt attaggaatg gggactggac cttccagggtc	600
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cccagcctga agagccccc cactgtggag tggagggcac agtccgagtc tgcccggagc	720
aagtccggag gcggaggcgg agacaaaact cacacatgcc caccgtgccc agcacctgaa	780
ctcctggggg gaccgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgatc	840

tccccgaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc	900
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gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg	1020
ctgaatggca aggagtacaa gtgcaaggct tccaacaaag ccctcccagc ccccatcgag	1080
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtgcac cctgccccca	1140
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cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc	1260
acgcctcccg tgctggactc cgacggctcc ttcttcctcg tcagcaagct caccgtggac	1320
aagagtaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac	1380
aaccactaca cacagaagag cctctccctg tctcccggc	1419

<210> 22

<211> 1419

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 22

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cccatctggg cccgaatgga cgccggagggt ggaggctcac tagtgccccg aggctctgga	120
ggtggaggct ctggagactc cgaaaggcat ttcgtgcacc agttcaaggg cgagtgtac	180
ttcaccaacg ggacgcagcg catacggctc gtgaccagat acatctacaa ccgggaggag	240
tacctgcgct tcgacagcga cgtgggagag taccgcgcgg tgaccgagct ggggcggcac	300
tcagccgagt actacaataa gcagtacctg gagcgaacgc gggccgagct ggacacggcg	360
tgcagacaca actacgagga gacggaggct cccacctccc tgcggcggct tgaacagccc	420
aatgtcgcca tctccctgtc caggacagag gccctcaacc accacaacac tctgggtctgt	480
tcggtgacag atttctaccc agccaagatc aaagtgcgct ggttcaggaa tggccaggag	540

gagacagtgg gggctctcatc cacacagctt attaggaatg gggactggac cttccaggtc	600
ctgggtcatgc tggagatgac ccctcatcag ggagaggtct atacctgcca tgttgagcat	660
cccagcctga agagcccat cactgtggag tggagggcac agtccgagtc tgcccggagc	720
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aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag	960
gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg	1020
ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag	1080
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca	1140
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cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc	1260
acgcctcccc tgctggactc cgacggctcc ttcttctctt acagcaagct caccgtggac	1320
aagagtaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac	1380
aaccactaca cacagaagag cctctccctg tctccgggc	1419

<210> 23

<211> 1326

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 23

atggctatca tctacctcat cctcctgttc accgctgtgc ggggcgaaga cgacattgag	60
gccgaccacg taggcttcta tggtaacaact gtttatcagt ctcttgaga cattggccag	120
tacacacatg aatttgatgg tgatgagttg ttctatgtgg acttgataa gaagaaaact	180
gtctggaggc ttcctgagtt tggccaattg atactctttg agccccaagg tggactgcaa	240

aacatagctg cagaaaaaca caacttgga atcttgacta agaggtcaaa tttcacccca	300
gctaccaatg aggctcctca agcgactgtg ttccccaagt cccctgtgct gctgggtcag	360
cccaacaccc ttatctgctt tgtggacaac atcttccac ctgtgatcaa catcacatgg	420
ctcagaaata gcaagtcagt cacagacggc gtttatgaga ccagcttcct cgtcaaccgt	480
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gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagt caaggtctcc	960
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga	1020
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gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc	1200
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tgctccgtga tgcatgaggc tctgcacaac cactacacac agaagagcct ctccctgtct	1320
ccgggc	1326

<210> 24

<211> 1326

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 24

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tacacacatg aatttgatgg tgatgagttg ttctatgtgg acttgagataa gaagaaaact	180
gtctggaggc ttcctgagtt tggccaattg atactctttg agccccaagg tggactgcaa	240
aacatagctg cagaaaaaca caacttggga atcttgacta agagggtcaaa tttcacccca	300
gctaccaatg aggctcctca agcgactgtg ttccccaagt cccctgtgct gctgggtcag	360
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cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc	900
gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggctctcc	960
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga	1020
gaaccacagg tgtgcaccct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc	1080
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ttcctcgtca gcaagctcac cgtggacaag agtaggtggc agcaggggaa cgtcttctca	1260
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cccggc	1326

<210> 25

<211> 678

<212> DNA
<213> Artificial Sequence

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

<400> 25
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gacggctcct tcttcctcgt cagcaagctc accgtggaca agagcagggtg gcagcagggg 600
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac acagaagagc 660
ctctccctgt ctcccggc 678

<210> 26
<211> 678
<212> DNA
<213> Artificial Sequence

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

<400> 26
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tgcgtggtgg tggacgtgag ccacgaagac cctgagggtca agttcaactg gtacgtggac 180

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ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac      240
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag      300
tgcaaagtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa      360
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat gccgggatga gctgaccaag      420
aaccaggtca gcctgtggtg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag      480
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc      540
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg      600
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac acagaagagc      660
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<210> 27

<211> 1056

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 27

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Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly Met Leu
1           5           10          15

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Val Ala Ser Ser Leu Gly Gln His Leu Gln Lys Asp Tyr Arg Ala Tyr
          20          25          30

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```

Tyr Thr Phe Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser
          35          40          45

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Gly Asp Thr Arg Pro Arg Phe Leu Glu Tyr Ser Thr Ser Glu Cys His
          50          55          60

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Phe Phe Asn Gly Thr Glu Arg Val Arg Tyr Leu Asp Arg Tyr Phe His
65          70          75          80

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Asn Gln Glu Glu Asn Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg
85 90 95

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

Lys Asp Leu Leu Glu Gln Lys Arg Gly Arg Val Asp Asn Tyr Cys Arg
115 120 125

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

Pro Lys Val Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His
145 150 155 160

Asn Leu Leu Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu
165 170 175

Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser
180 185 190

Thr Gly Leu Ile His Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met
195 200 205

Leu Glu Thr Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu
210 215 220

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

Glu Ser Ala Gln Ser Lys Ser Gly Gly Gly Gly Gly Arg Ile Ala Arg
245 250 255

Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn Ser Glu Leu Ala
260 265 270

Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala Gln Leu Lys Gln Lys

275

280

285

Val Met Asn His Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 290 295 300

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 305 310 315 320

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 325 330 335

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 340 345 350

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 355 360 365

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 370 375 380

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 385 390 395 400

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 405 410 415

Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
 420 425 430

Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp
 435 440 445

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 450 455 460

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

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
485 490 495

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
500 505 510

Leu Ser Leu Ser Pro Gly Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu
515 520 525

Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Ile Ile
530 535 540

Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Ile Lys Glu Glu His
545 550 555 560

Val Ile Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu
565 570 575

Phe Met Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala
580 585 590

Lys Lys Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser
595 600 605

Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn
610 615 620

Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val
625 630 635 640

Pro Pro Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu
645 650 655

Pro Asn Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val
660 665 670

Asn Val Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser

675

680

685

Glu Thr Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His
 690 695 700

Tyr Leu Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val
 705 710 715 720

Glu His Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp
 725 730 735

Ala Pro Ser Pro Leu Pro Glu Thr Thr Glu Ser Gly Gly Gly Gly Gly
 740 745 750

Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys
 755 760 765

Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys
 770 775 780

Leu Glu Phe Ile Leu Ala Ala His Asp Lys Thr His Thr Cys Pro Pro
 785 790 795 800

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 805 810 815

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 820 825 830

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 835 840 845

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 850 855 860

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 865 870 875 880

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
885 890 895

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
900 905 910

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp
915 920 925

Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
930 935 940

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
945 950 955 960

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
965 970 975

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
980 985 990

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
995 1000 1005

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Ser Gly Ser Gly
1010 1015 1020

Ser Gly Ser Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu
1025 1030 1035

Arg Asp His His His His His His Asn Trp Ser His Pro Gln Phe
1040 1045 1050

Glu Lys Cys
1055

<210> 28

<211> 976
<212> PRT
<213> Artificial Sequence

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

<400> 28
Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly Met Leu
1 5 10 15

Val Ala Ser Ser Leu Gly Gln His Leu Gln Lys Asp Tyr Arg Ala Tyr
20 25 30

Tyr Thr Phe Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser
35 40 45

Gly Asp Thr Arg Pro Arg Phe Leu Glu Tyr Ser Thr Ser Glu Cys His
50 55 60

Phe Phe Asn Gly Thr Glu Arg Val Arg Tyr Leu Asp Arg Tyr Phe His
65 70 75 80

Asn Gln Glu Glu Asn Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg
85 90 95

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

Lys Asp Leu Leu Glu Gln Lys Arg Gly Arg Val Asp Asn Tyr Cys Arg
115 120 125

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

Pro Lys Val Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His
145 150 155 160

Asn Leu Leu Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu
165 170 175

Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser
180 185 190

Thr Gly Leu Ile His Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met
195 200 205

Leu Glu Thr Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu
210 215 220

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

Glu Ser Ala Gln Ser Lys Ser Gly Gly Gly Gly Gly Asp Lys Thr His
245 250 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

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

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro
370 375 380

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala
385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

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

Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Ser
465 470 475 480

Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu
485 490 495

Asn Pro Gly Pro Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala
500 505 510

Val Arg Gly Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr
515 520 525

Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp Gly Asp
530 535 540

Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu
545 550 555 560

Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala
565 570 575

Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser
580 585 590

Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val Leu Thr
595 600 605

Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys Phe Ile
610 615 620

Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg Asn Gly
625 630 635 640

Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe Leu Pro Arg Glu
645 650 655

Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro Ser Thr
660 665 670

Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp Glu Pro
675 680 685

Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro Glu Thr
690 695 700

Thr Glu Ser Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro
705 710 715 720

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
725 730 735

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
740 745 750

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
755 760 765

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
770 775 780

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
785 790 795 800

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
805 810 815

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
820 825 830

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp
835 840 845

Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
850 855 860

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
865 870 875 880

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
885 890 895

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
900 905 910

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
915 920 925

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Ser Gly Ser Gly Ser
930 935 940

Gly Ser Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp
945 950 955 960

His His His His His His Asn Trp Ser His Pro Gln Phe Glu Lys Cys
965 970 975

<210> 29

<211> 1055

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 29

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Arg
1 5 10 15

Ser Ala His His Pro Ile Trp Ala Arg Met Asp Ala Gly Gly Gly Gly
20 25 30

Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Gly Ser Gly Asp Ser Glu
35 40 45

Arg His Phe Val His Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly
50 55 60

Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu Glu
65 70 75 80

Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu
85 90 95

Leu Gly Arg His Ser Ala Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Arg
100 105 110

Thr Arg Ala Glu Leu Asp Thr Ala Cys Arg His Asn Tyr Glu Glu Thr
115 120 125

Glu Val Pro Thr Ser Leu Arg Arg Leu Glu Gln Pro Asn Val Ala Ile
130 135 140

Ser Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr Leu Val Cys
145 150 155 160

Ser Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg Trp Phe Arg
165 170 175

Asn Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln Leu Ile Arg
180 185 190

Asn Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu Met Thr Pro
195 200 205

His Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro Ser Leu Lys
210 215 220

Ser Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser Ala Arg Ser
225 230 235 240

Lys Ser Gly Gly Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val
245 250 255

Lys Thr Leu Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met
260 265 270

Leu Arg Glu Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His Asp
275 280 285

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
290 295 300

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
305 310 315 320

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
325 330 335

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

340

345

350

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 355 360 365

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 370 375 380

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 385 390 395 400

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys
 405 410 415

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 420 425 430

Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 435 440 445

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 450 455 460

Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp
 465 470 475 480

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 485 490 495

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 500 505 510

Gly Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp
 515 520 525

Val Glu Glu Asn Pro Gly Pro Met Ala Ile Ile Tyr Leu Ile Leu Leu
 530 535 540

Phe Thr Ala Val Arg Gly Glu Asp Asp Ile Glu Ala Asp His Val Gly
545 550 555 560

Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr
565 570 575

Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys
580 585 590

Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe
595 600 605

Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn Leu
610 615 620

Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu Ala
625 630 635 640

Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln Pro
645 650 655

Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile Asn
660 665 670

Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr Glu
675 680 685

Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser Tyr
690 695 700

Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu
705 710 715 720

His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu Ile
725 730 735

Pro Ala Pro Met Ser Glu Leu Thr Glu Ser Gly Gly Gly Gly Leu

740

745

750

Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser
 755 760 765

Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu
 770 775 780

Glu Phe Ile Leu Ala Ala His Asp Lys Thr His Thr Cys Pro Pro Cys
 785 790 795 800

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 805 810 815

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 820 825 830

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 835 840 845

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 850 855 860

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 865 870 875 880

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 885 890 895

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 900 905 910

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu
 915 920 925

Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr
 930 935 940

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
945 950 955 960

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
965 970 975

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
980 985 990

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
995 1000 1005

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Ser Gly Ser Gly Ser
1010 1015 1020

Gly Ser Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg
1025 1030 1035

Asp His His His His His His Asn Trp Ser His Pro Gln Phe Glu
1040 1045 1050

Lys Cys
1055

<210> 30

<211> 975

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 30

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Arg
1 5 10 15

Ser Ala His His Pro Ile Trp Ala Arg Met Asp Ala Gly Gly Gly Gly
20 25 30

Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Gly Ser Gly Asp Ser Glu
35 40 45

Arg His Phe Val His Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly
50 55 60

Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu Glu
65 70 75 80

Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu
85 90 95

Leu Gly Arg His Ser Ala Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Arg
100 105 110

Thr Arg Ala Glu Leu Asp Thr Ala Cys Arg His Asn Tyr Glu Glu Thr
115 120 125

Glu Val Pro Thr Ser Leu Arg Arg Leu Glu Gln Pro Asn Val Ala Ile
130 135 140

Ser Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr Leu Val Cys
145 150 155 160

Ser Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg Trp Phe Arg
165 170 175

Asn Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln Leu Ile Arg
180 185 190

Asn Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu Met Thr Pro
195 200 205

His Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro Ser Leu Lys
210 215 220

Ser Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser Ala Arg Ser
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Ser Gly Ala Thr Asn Phe
465 470 475 480

Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met
485 490 495

Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Glu Asp
500 505 510

Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr Gln
515 520 525

Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu
530 535 540

Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu Pro
545 550 555 560

Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln Asn
565 570 575

Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser Asn
580 585 590

Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys
595 600 605

Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp
610 615 620

Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys
625 630 635 640

Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp
645 650 655

His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp
660 665 670

Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val
675 680 685

Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr
690 695 700

Glu Ser Gly Gly Gly Gly Glu Asp Lys Thr His Thr Cys Pro Pro Cys
705 710 715 720

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
725 730 735

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
740 745 750

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
755 760 765

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
770 775 780

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
785 790 795 800

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
805 810 815

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
820 825 830

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu
835 840 845

Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr
850 855 860

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
865 870 875 880

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
885 890 895

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
900 905 910

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
915 920 925

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Ser Gly Ser Gly Ser Gly
930 935 940

Ser Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp His
945 950 955 960

His His His His His Asn Trp Ser His Pro Gln Phe Glu Lys Cys
965 970 975

<210> 31

<211> 1056

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 31

Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly Met Leu

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

Leu Glu Thr Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu
210 215 220

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

Glu Ser Ala Gln Ser Lys Ser Gly Gly Gly Gly Gly Arg Ile Ala Arg
245 250 255

Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn Ser Glu Leu Ala
260 265 270

Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala Gln Leu Lys Gln Lys
275 280 285

Val Met Asn His Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
290 295 300

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
305 310 315 320

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
325 330 335

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
340 345 350

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
355 360 365

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
370 375 380

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
385 390 395 400

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg

405

410

415

Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys
 420 425 430

Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 435 440 445

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 450 455 460

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

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 485 490 495

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 500 505 510

Leu Ser Leu Ser Pro Gly Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu
 515 520 525

Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Ile Ile
 530 535 540

Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Ile Lys Glu Glu His
 545 550 555 560

Val Ile Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu
 565 570 575

Phe Met Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala
 580 585 590

Lys Lys Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser
 595 600 605

Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn
610 615 620

Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val
625 630 635 640

Pro Pro Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu
645 650 655

Pro Asn Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val
660 665 670

Asn Val Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser
675 680 685

Glu Thr Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His
690 695 700

Tyr Leu Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val
705 710 715 720

Glu His Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp
725 730 735

Ala Pro Ser Pro Leu Pro Glu Thr Thr Glu Ser Gly Gly Gly Gly Gly
740 745 750

Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys
755 760 765

Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys
770 775 780

Leu Glu Phe Ile Leu Ala Ala His Asp Lys Thr His Thr Cys Pro Pro
785 790 795 800

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro

805

810

815

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 820 825 830

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 835 840 845

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 850 855 860

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 865 870 875 880

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 885 890 895

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 900 905 910

Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp
 915 920 925

Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe
 930 935 940

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 945 950 955 960

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 965 970 975

Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 980 985 990

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 995 1000 1005

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Ser Gly Ser Gly
1010 1015 1020

Ser Gly Ser Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu
1025 1030 1035

Arg Asp His His His His His His Asn Trp Ser His Pro Gln Phe
1040 1045 1050

Glu Lys Cys
1055

<210> 32

<211> 976

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 32

Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly Met Leu
1 5 10 15

Val Ala Ser Ser Leu Gly Gln His Leu Gln Lys Asp Tyr Arg Ala Tyr
20 25 30

Tyr Thr Phe Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser
35 40 45

Gly Asp Thr Arg Pro Arg Phe Leu Glu Tyr Ser Thr Ser Glu Cys His
50 55 60

Phe Phe Asn Gly Thr Glu Arg Val Arg Tyr Leu Asp Arg Tyr Phe His
65 70 75 80

Asn Gln Glu Glu Asn Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg
85 90 95

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

Lys Asp Leu Leu Glu Gln Lys Arg Gly Arg Val Asp Asn Tyr Cys Arg
115 120 125

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

Pro Lys Val Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His
145 150 155 160

Asn Leu Leu Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu
165 170 175

Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser
180 185 190

Thr Gly Leu Ile His Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met
195 200 205

Leu Glu Thr Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu
210 215 220

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

Glu Ser Ala Gln Ser Lys Ser Gly Gly Gly Gly Gly Asp Lys Thr His
245 250 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

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

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
370 375 380

Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu
385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Ser
465 470 475 480

Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu
485 490 495

Asn Pro Gly Pro Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala
500 505 510

Val Arg Gly Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr
515 520 525

Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp Gly Asp
530 535 540

Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu
545 550 555 560

Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala
565 570 575

Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser
580 585 590

Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val Leu Thr
595 600 605

Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys Phe Ile
610 615 620

Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg Asn Gly
625 630 635 640

Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe Leu Pro Arg Glu
645 650 655

Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro Ser Thr
660 665 670

Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp Glu Pro
675 680 685

Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro Glu Thr
690 695 700

Thr Glu Ser Gly Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro
705 710 715 720

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
725 730 735

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
740 745 750

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
755 760 765

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
770 775 780

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
785 790 795 800

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
805 810 815

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
820 825 830

Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp
835 840 845

Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe
850 855 860

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
865 870 875 880

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
885 890 895

Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
900 905 910

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
915 920 925

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Ser Gly Ser Gly Ser
930 935 940

Gly Ser Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp
945 950 955 960

His His His His His Asn Trp Ser His Pro Gln Phe Glu Lys Cys
965 970 975

<210> 33

<211> 1055

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 33

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Arg
1 5 10 15

Ser Ala His His Pro Ile Trp Ala Arg Met Asp Ala Gly Gly Gly Gly
20 25 30

Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Gly Ser Gly Asp Ser Glu
35 40 45

Arg His Phe Val His Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly
50 55 60

Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu Glu

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

Leu Arg Glu Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His Asp
275 280 285

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
290 295 300

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
305 310 315 320

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
325 330 335

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
340 345 350

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
355 360 365

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
370 375 380

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
385 390 395 400

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
405 410 415

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
420 425 430

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
435 440 445

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
450 455 460

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp

465		470		475		480
Lys Ser Arg Trp	Gln Gln Gly Asn Val	Phe Ser Cys Ser Val	Met His			
	485	490	495			
Glu Ala Leu His	Asn His Tyr Thr	Gln Lys Ser Leu Ser	Leu Ser Pro			
	500	505	510			
Gly Gly Ser Gly	Ala Thr Asn Phe Ser	Leu Leu Lys Gln	Ala Gly Asp			
	515	520	525			
Val Glu Glu Asn	Pro Gly Pro Met	Ala Ile Ile Tyr	Leu Ile Leu Leu			
	530	535	540			
Phe Thr Ala Val	Arg Gly Glu Asp	Asp Ile Glu Ala	Asp His Val Gly			
545	550	555	560			
Phe Tyr Gly Thr	Thr Val Tyr Gln	Ser Pro Gly Asp	Ile Gly Gln Tyr			
	565	570	575			
Thr His Glu Phe	Asp Gly Asp Glu	Leu Phe Tyr Val	Asp Leu Asp Lys			
	580	585	590			
Lys Lys Thr Val	Trp Arg Leu Pro	Glu Phe Gly Gln	Leu Ile Leu Phe			
	595	600	605			
Glu Pro Gln Gly	Gly Leu Gln Asn	Ile Ala Ala Glu	Lys His Asn Leu			
	610	615	620			
Gly Ile Leu Thr	Lys Arg Ser Asn	Phe Thr Pro Ala	Thr Asn Glu Ala			
625	630	635	640			
Pro Gln Ala Thr	Val Phe Pro Lys	Ser Pro Val Leu	Leu Gly Gln Pro			
	645	650	655			
Asn Thr Leu Ile	Cys Phe Val Asp	Asn Ile Phe Pro	Pro Val Ile Asn			
	660	665	670			

Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr Glu
675 680 685

Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser Tyr
690 695 700

Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu
705 710 715 720

His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu Ile
725 730 735

Pro Ala Pro Met Ser Glu Leu Thr Glu Ser Gly Gly Gly Gly Gly Leu
740 745 750

Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser
755 760 765

Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu
770 775 780

Glu Phe Ile Leu Ala Ala His Asp Lys Thr His Thr Cys Pro Pro Cys
785 790 795 800

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
805 810 815

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
820 825 830

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
835 840 845

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
850 855 860

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu

[illegible]

<210> 34
<211> 975
<212> PRT
<213> Artificial Sequence

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

<400> 34
Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Arg
1 5 10 15

Ser Ala His His Pro Ile Trp Ala Arg Met Asp Ala Gly Gly Gly Gly
20 25 30

Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Gly Ser Gly Asp Ser Glu
35 40 45

Arg His Phe Val His Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly
50 55 60

Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu Glu
65 70 75 80

Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu
85 90 95

Leu Gly Arg His Ser Ala Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Arg
100 105 110

Thr Arg Ala Glu Leu Asp Thr Ala Cys Arg His Asn Tyr Glu Glu Thr
115 120 125

Glu Val Pro Thr Ser Leu Arg Arg Leu Glu Gln Pro Asn Val Ala Ile
130 135 140

Ser Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr Leu Val Cys
145 150 155 160

Ser Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg Trp Phe Arg
165 170 175

Asn Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln Leu Ile Arg
180 185 190

Asn Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu Met Thr Pro
195 200 205

His Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro Ser Leu Lys
210 215 220

Ser Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser Ala Arg Ser
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Ser Gly Ala Thr Asn Phe
465 470 475 480

Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met
485 490 495

Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Glu Asp
500 505 510

Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr Gln
515 520 525

Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu
530 535 540

Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu Pro
545 550 555 560

Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln Asn
565 570 575

Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser Asn
580 585 590

Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys
595 600 605

Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp
610 615 620

Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys
625 630 635 640

Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp
645 650 655

His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp
660 665 670

Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val
675 680 685

Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr
690 695 700

Glu Ser Gly Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys
705 710 715 720

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
725 730 735

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
740 745 750

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
755 760 765

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
770 775 780

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
785 790 795 800

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
805 810 815

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
820 825 830

Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu
835 840 845

Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr
850 855 860

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
865 870 875 880

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
885 890 895

Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
900 905 910

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
915 920 925

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Ser Gly Ser Gly Ser Gly
930 935 940

Ser Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp His
945 950 955 960

His His His His His Asn Trp Ser His Pro Gln Phe Glu Lys Cys
965 970 975

<210> 35

<211> 518

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 35

Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly Met Leu
1 5 10 15

Val Ala Ser Ser Leu Gly Gln His Leu Gln Lys Asp Tyr Arg Ala Tyr
20 25 30

Tyr Thr Phe Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser
35 40 45

Gly Asp Thr Arg Pro Arg Phe Leu Glu Tyr Ser Thr Ser Glu Cys His
50 55 60

Phe Phe Asn Gly Thr Glu Arg Val Arg Tyr Leu Asp Arg Tyr Phe His
65 70 75 80

Asn Gln Glu Glu Asn Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg
85 90 95

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

Lys Asp Leu Leu Glu Gln Lys Arg Gly Arg Val Asp Asn Tyr Cys Arg
115 120 125

His Asn Tyr Gly Val Val Glu Ser Phe Thr Val Gln Arg Arg Val His

130

135

140

Pro Lys Val Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His
 145 150 155 160

Asn Leu Leu Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu
 165 170 175

Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser
 180 185 190

Thr Gly Leu Ile His Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met
 195 200 205

Leu Glu Thr Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu
 210 215 220

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

Glu Ser Ala Gln Ser Lys Ser Gly Gly Gly Gly Gly Arg Ile Ala Arg
 245 250 255

Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn Ser Glu Leu Ala
 260 265 270

Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala Gln Leu Lys Gln Lys
 275 280 285

Val Met Asn His Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 290 295 300

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 305 310 315 320

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 325 330 335

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
340 345 350

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
355 360 365

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
370 375 380

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
385 390 395 400

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
405 410 415

Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
420 425 430

Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp
435 440 445

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
450 455 460

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

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
485 490 495

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
500 505 510

Leu Ser Leu Ser Pro Gly
515

<211> 518
<212> PRT
<213> Artificial Sequence

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

<400> 36
Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly Met Leu
1 5 10 15

Val Ala Ser Ser Leu Gly Gln His Leu Gln Lys Asp Tyr Arg Ala Tyr
20 25 30

Tyr Thr Phe Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser
35 40 45

Gly Asp Thr Arg Pro Arg Phe Leu Glu Tyr Ser Thr Ser Glu Cys His
50 55 60

Phe Phe Asn Gly Thr Glu Arg Val Arg Tyr Leu Asp Arg Tyr Phe His
65 70 75 80

Asn Gln Glu Glu Asn Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg
85 90 95

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

Lys Asp Leu Leu Glu Gln Lys Arg Gly Arg Val Asp Asn Tyr Cys Arg
115 120 125

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

Pro Lys Val Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His
145 150 155 160

Asn Leu Leu Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu
165 170 175

Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser
180 185 190

Thr Gly Leu Ile His Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met
195 200 205

Leu Glu Thr Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu
210 215 220

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

Glu Ser Ala Gln Ser Lys Ser Gly Gly Gly Gly Gly Arg Ile Ala Arg
245 250 255

Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn Ser Glu Leu Ala
260 265 270

Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala Gln Leu Lys Gln Lys
275 280 285

Val Met Asn His Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
290 295 300

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
305 310 315 320

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
325 330 335

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
340 345 350

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
355 360 365

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
370 375 380

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
385 390 395 400

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
405 410 415

Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys
420 425 430

Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
435 440 445

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
450 455 460

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

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
485 490 495

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
500 505 510

Leu Ser Leu Ser Pro Gly
515

<210> 37

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

polypeptide"

<400> 37

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Ile
1 5 10 15

Lys Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp
20 25 30

Gln Ser Gly Glu Phe Met Phe Asp Phe Asp Gly Asp Glu Ile Phe His
35 40 45

Val Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu Glu Glu Phe Gly
50 55 60

Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val
65 70 75 80

Asp Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro
85 90 95

Ile Thr Asn Val Pro Pro Glu Val Thr Val Leu Thr Asn Ser Pro Val
100 105 110

Glu Leu Arg Glu Pro Asn Val Leu Ile Cys Phe Ile Asp Lys Phe Thr
115 120 125

Pro Pro Val Val Asn Val Thr Trp Leu Arg Asn Gly Lys Pro Val Thr
130 135 140

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

Arg Lys Phe His Tyr Leu Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr
165 170 175

Asp Cys Arg Val Glu His Trp Gly Leu Asp Glu Pro Leu Leu Lys His
180 185 190

Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro Glu Thr Thr Glu Ser Gly
195 200 205

Gly Gly Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu
210 215 220

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

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

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
370 375 380

Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu

385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465 470 475

<210> 38

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 38

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Ile
1 5 10 15

Lys Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp
20 25 30

Gln Ser Gly Glu Phe Met Phe Asp Phe Asp Gly Asp Glu Ile Phe His
35 40 45

Val Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu Glu Glu Phe Gly
50 55 60

Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val
65 70 75 80

Asp Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro
85 90 95

Ile Thr Asn Val Pro Pro Glu Val Thr Val Leu Thr Asn Ser Pro Val
100 105 110

Glu Leu Arg Glu Pro Asn Val Leu Ile Cys Phe Ile Asp Lys Phe Thr
115 120 125

Pro Pro Val Val Asn Val Thr Trp Leu Arg Asn Gly Lys Pro Val Thr
130 135 140

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

Arg Lys Phe His Tyr Leu Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr
165 170 175

Asp Cys Arg Val Glu His Trp Gly Leu Asp Glu Pro Leu Leu Lys His
180 185 190

Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro Glu Thr Thr Glu Ser Gly
195 200 205

Gly Gly Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu
210 215 220

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

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

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro
370 375 380

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala
385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

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

Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465 470 475

<210> 39

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 39

Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly Met Leu
1 5 10 15

Val Ala Ser Ser Leu Gly Gln His Leu Gln Lys Asp Tyr Arg Ala Tyr
20 25 30

Tyr Thr Phe Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser
35 40 45

Gly Asp Thr Arg Pro Arg Phe Leu Glu Tyr Ser Thr Ser Glu Cys His
50 55 60

Phe Phe Asn Gly Thr Glu Arg Val Arg Tyr Leu Asp Arg Tyr Phe His
65 70 75 80

Asn Gln Glu Glu Asn Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg
85 90 95

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

Lys Asp Leu Leu Glu Gln Lys Arg Gly Arg Val Asp Asn Tyr Cys Arg
115 120 125

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

Pro Lys Val Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His
145 150 155 160

Asn Leu Leu Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu
165 170 175

Val Arg Trp Phe Arg Asn Gly Gln Glu Lys Thr Gly Val Val Ser
180 185 190

Thr Gly Leu Ile His Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met
195 200 205

Leu Glu Thr Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu
210 215 220

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

Glu Ser Ala Gln Ser Lys Ser Gly Gly Gly Gly Gly Asp Lys Thr His
245 250 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys

340

345

350

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
 355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro
 370 375 380

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala
 385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 405 410 415

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

Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg
 435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 465 470 475

<210> 40

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 40

Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly Met Leu
 1 5 10 15

Val Ala Ser Ser Leu Gly Gln His Leu Gln Lys Asp Tyr Arg Ala Tyr
20 25 30

Tyr Thr Phe Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser
35 40 45

Gly Asp Thr Arg Pro Arg Phe Leu Glu Tyr Ser Thr Ser Glu Cys His
50 55 60

Phe Phe Asn Gly Thr Glu Arg Val Arg Tyr Leu Asp Arg Tyr Phe His
65 70 75 80

Asn Gln Glu Glu Asn Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg
85 90 95

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

Lys Asp Leu Leu Glu Gln Lys Arg Gly Arg Val Asp Asn Tyr Cys Arg
115 120 125

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

Pro Lys Val Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His
145 150 155 160

Asn Leu Leu Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu
165 170 175

Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser
180 185 190

Thr Gly Leu Ile His Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met
195 200 205

Leu Glu Thr Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu
210 215 220

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

Glu Ser Ala Gln Ser Lys Ser Gly Gly Gly Gly Gly Asp Lys Thr His
245 250 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

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

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
370 375 380

Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu
385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465 470 475

<210> 41

<211> 438

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 41

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Ile
1 5 10 15

Lys Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp
20 25 30

Gln Ser Gly Glu Phe Met Phe Asp Phe Asp Gly Asp Glu Ile Phe His
35 40 45

Val Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu Glu Glu Phe Gly
50 55 60

Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val
65 70 75 80

Asp Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro
85 90 95

Ile Thr Asn Val Pro Pro Glu Val Thr Val Leu Thr Asn Ser Pro Val
100 105 110

Glu Leu Arg Glu Pro Asn Val Leu Ile Cys Phe Ile Asp Lys Phe Thr
115 120 125

Pro Pro Val Val Asn Val Thr Trp Leu Arg Asn Gly Lys Pro Val Thr
130 135 140

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

Arg Lys Phe His Tyr Leu Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr
165 170 175

Asp Cys Arg Val Glu His Trp Gly Leu Asp Glu Pro Leu Leu Lys His
180 185 190

Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro Glu Thr Thr Glu Ser Gly
195 200 205

Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
210 215 220

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
225 230 235 240

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
245 250 255

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
260 265 270

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
275 280 285

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp

290

295

300

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
305 310 315 320

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
325 330 335

Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys
340 345 350

Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
355 360 365

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

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
385 390 395 400

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
405 410 415

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
420 425 430

Leu Ser Leu Ser Pro Gly
435

<210> 42

<211> 438

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 42

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Ile
1 5 10 15

Lys Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp
20 25 30

Gln Ser Gly Glu Phe Met Phe Asp Phe Asp Gly Asp Glu Ile Phe His
35 40 45

Val Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu Glu Glu Phe Gly
50 55 60

Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val
65 70 75 80

Asp Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro
85 90 95

Ile Thr Asn Val Pro Pro Glu Val Thr Val Leu Thr Asn Ser Pro Val
100 105 110

Glu Leu Arg Glu Pro Asn Val Leu Ile Cys Phe Ile Asp Lys Phe Thr
115 120 125

Pro Pro Val Val Asn Val Thr Trp Leu Arg Asn Gly Lys Pro Val Thr
130 135 140

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

Arg Lys Phe His Tyr Leu Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr
165 170 175

Asp Cys Arg Val Glu His Trp Gly Leu Asp Glu Pro Leu Leu Lys His
180 185 190

Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro Glu Thr Thr Glu Ser Gly
195 200 205

Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
210 215 220

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
225 230 235 240

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
245 250 255

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
260 265 270

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
275 280 285

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
290 295 300

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
305 310 315 320

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
325 330 335

Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
340 345 350

Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp
355 360 365

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

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser
385 390 395 400

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
405 410 415

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
420 425 430

Leu Ser Leu Ser Pro Gly
435

<210> 43

<211> 513

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 43

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Arg
1 5 10 15

Ser Ala His His Pro Ile Trp Ala Arg Met Asp Ala Gly Gly Gly Gly
20 25 30

Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Gly Ser Gly Asp Ser Glu
35 40 45

Arg His Phe Val His Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly
50 55 60

Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu Glu
65 70 75 80

Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu
85 90 95

Leu Gly Arg His Ser Ala Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Arg
100 105 110

Thr Arg Ala Glu Leu Asp Thr Ala Cys Arg His Asn Tyr Glu Glu Thr
115 120 125

Glu Val Pro Thr Ser Leu Arg Arg Leu Glu Gln Pro Asn Val Ala Ile
130 135 140

Ser Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr Leu Val Cys
145 150 155 160

Ser Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg Trp Phe Arg
165 170 175

Asn Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln Leu Ile Arg
180 185 190

Asn Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu Met Thr Pro
195 200 205

His Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro Ser Leu Lys
210 215 220

Ser Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser Ala Arg Ser
225 230 235 240

Lys Ser Gly Gly Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val
245 250 255

Lys Thr Leu Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met
260 265 270

Leu Arg Glu Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His Asp
275 280 285

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
290 295 300

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile

305		310		315		320
Ser Arg Thr Pro	Glu Val Thr Cys Val Val Val Asp Val Ser His Glu					
	325		330			335
Asp Pro Glu Val	Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His					
	340		345			350
Asn Ala Lys Thr	Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg					
	355		360			365
Val Val Ser Val	Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys					
	370		375			380
Glu Tyr Lys Cys	Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu					
385		390		395		400
Lys Thr Ile Ser	Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys					
	405		410			415
Thr Leu Pro Pro	Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu					
	420		425			430
Ser Cys Ala Val	Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp					
	435		440			445
Glu Ser Asn Gly	Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val					
	450		455			460
Leu Asp Ser Asp	Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp					
465		470		475		480
Lys Ser Arg Trp	Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His					
	485		490			495
Glu Ala Leu His	Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro					
	500		505			510

Gly

<210> 44

<211> 513

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 44

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Arg
1 5 10 15

Ser Ala His His Pro Ile Trp Ala Arg Met Asp Ala Gly Gly Gly Gly
20 25 30

Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Gly Ser Gly Asp Ser Glu
35 40 45

Arg His Phe Val His Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly
50 55 60

Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu Glu
65 70 75 80

Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu
85 90 95

Leu Gly Arg His Ser Ala Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Arg
100 105 110

Thr Arg Ala Glu Leu Asp Thr Ala Cys Arg His Asn Tyr Glu Glu Thr
115 120 125

Glu Val Pro Thr Ser Leu Arg Arg Leu Glu Gln Pro Asn Val Ala Ile
130 135 140

Ser Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr Leu Val Cys
145 150 155 160

Ser Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg Trp Phe Arg
165 170 175

Asn Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln Leu Ile Arg
180 185 190

Asn Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu Met Thr Pro
195 200 205

His Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro Ser Leu Lys
210 215 220

Ser Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser Ala Arg Ser
225 230 235 240

Lys Ser Gly Gly Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val
245 250 255

Lys Thr Leu Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met
260 265 270

Leu Arg Glu Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His Asp
275 280 285

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
290 295 300

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
305 310 315 320

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
325 330 335

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
340 345 350

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
355 360 365

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
370 375 380

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
385 390 395 400

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
405 410 415

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
420 425 430

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
435 440 445

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
450 455 460

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
465 470 475 480

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
485 490 495

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
500 505 510

Gly

<210> 45
<211> 482

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 45

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Glu
1 5 10 15

Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr
20 25 30

Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp
35 40 45

Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu
50 55 60

Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln
65 70 75 80

Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser
85 90 95

Asn Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro
100 105 110

Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val
115 120 125

Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser
130 135 140

Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg
145 150 155 160

Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp

165

170

175

Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro
 180 185 190

Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu
 195 200 205

Thr Glu Ser Gly Gly Gly Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu
 210 215 220

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

Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His
 245 250 255

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 260 265 270

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 275 280 285

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 290 295 300

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 305 310 315 320

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 325 330 335

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 340 345 350

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 355 360 365

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
370 375 380

Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
385 390 395 400

Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
405 410 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
420 425 430

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
435 440 445

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
450 455 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465 470 475 480

Pro Gly

<210> 46

<211> 482

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 46

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Glu
1 5 10 15

Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr
20 25 30

Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp
35 40 45

Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu
50 55 60

Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln
65 70 75 80

Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser
85 90 95

Asn Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro
100 105 110

Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val
115 120 125

Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser
130 135 140

Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg
145 150 155 160

Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp
165 170 175

Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro
180 185 190

Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu
195 200 205

Thr Glu Ser Gly Gly Gly Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu
210 215 220

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

Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His
245 250 255

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
260 265 270

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
275 280 285

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
290 295 300

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
305 310 315 320

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
325 330 335

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
340 345 350

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
355 360 365

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
370 375 380

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
385 390 395 400

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
405 410 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
420 425 430

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
435 440 445

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
450 455 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465 470 475 480

Pro Gly

<210> 47

<211> 473

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 47

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Arg
1 5 10 15

Ser Ala His His Pro Ile Trp Ala Arg Met Asp Ala Gly Gly Gly Gly
20 25 30

Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Gly Ser Gly Asp Ser Glu
35 40 45

Arg His Phe Val His Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly
50 55 60

Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu Glu
65 70 75 80

Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu

85

90

95

Leu Gly Arg His Ser Ala Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Arg
 100 105 110

Thr Arg Ala Glu Leu Asp Thr Ala Cys Arg His Asn Tyr Glu Glu Thr
 115 120 125

Glu Val Pro Thr Ser Leu Arg Arg Leu Glu Gln Pro Asn Val Ala Ile
 130 135 140

Ser Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr Leu Val Cys
 145 150 155 160

Ser Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg Trp Phe Arg
 165 170 175

Asn Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln Leu Ile Arg
 180 185 190

Asn Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu Met Thr Pro
 195 200 205

His Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro Ser Leu Lys
 210 215 220

Ser Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser Ala Arg Ser
 225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly
465 470

<210> 48

<211> 473
<212> PRT
<213> Artificial Sequence

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

<400> 48
Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Arg
1 5 10 15

Ser Ala His His Pro Ile Trp Ala Arg Met Asp Ala Gly Gly Gly Gly
20 25 30

Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Gly Ser Gly Asp Ser Glu
35 40 45

Arg His Phe Val His Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly
50 55 60

Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu Glu
65 70 75 80

Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu
85 90 95

Leu Gly Arg His Ser Ala Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Arg
100 105 110

Thr Arg Ala Glu Leu Asp Thr Ala Cys Arg His Asn Tyr Glu Glu Thr
115 120 125

Glu Val Pro Thr Ser Leu Arg Arg Leu Glu Gln Pro Asn Val Ala Ile
130 135 140

Ser Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr Leu Val Cys
145 150 155 160

Ser Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg Trp Phe Arg
165 170 175

Asn Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln Leu Ile Arg
180 185 190

Asn Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu Met Thr Pro
195 200 205

His Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro Ser Leu Lys
210 215 220

Ser Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser Ala Arg Ser
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly
465 470

<210> 49

<211> 442

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 49

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Glu
1 5 10 15

Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr
20 25 30

Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp

35

40

45

Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu
 50 55 60

Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln
 65 70 75 80

Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser
 85 90 95

Asn Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro
 100 105 110

Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val
 115 120 125

Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser
 130 135 140

Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg
 145 150 155 160

Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp
 165 170 175

Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro
 180 185 190

Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu
 195 200 205

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

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

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

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
260 265 270

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

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

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

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

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp
340 345 350

Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
355 360 365

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

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385 390 395 400

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

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

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

435

440

<210> 50

<211> 442

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 50

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Glu
1 5 10 15

Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr
20 25 30

Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp
35 40 45

Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu
50 55 60

Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln
65 70 75 80

Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser
85 90 95

Asn Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro
100 105 110

Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val
115 120 125

Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser
130 135 140

Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg
145 150 155 160

Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp
165 170 175

Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro
180 185 190

Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu
195 200 205

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

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

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

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
260 265 270

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

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

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

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

Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp
340 345 350

Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe
355 360 365

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

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385 390 395 400

Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
405 410 415

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

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440

<210> 51

<211> 226

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 51

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

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

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

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

50

55

60

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

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

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

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

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

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

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

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

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

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

Pro Gly
 225

<210> 52
 <211> 106
 <212> PRT

<213> Homo sapiens

<400> 52

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

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

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

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

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
100 105

<210> 53

<211> 226

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 53

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly
225

<210> 54
<211> 106
<212> PRT
<213> Homo sapiens

<400> 54
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp
1 5 10 15

Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
100 105

<210> 55
<211> 113
<212> PRT
<213> Homo sapiens

<400> 55
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
1 5 10 15

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
20 25 30

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
35 40 45

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
50 55 60

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
65 70 75 80

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
85 90 95

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
100 105 110

Lys

<210> 56

<211> 224

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 56

Gln His Leu Gln Lys Asp Tyr Arg Ala Tyr Tyr Thr Phe Gly Gly Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Gly Asp Thr Arg Pro Arg
20 25 30

Phe Leu Glu Tyr Ser Thr Ser Glu Cys His Phe Phe Asn Gly Thr Glu
35 40 45

Arg Val Arg Tyr Leu Asp Arg Tyr Phe His Asn Gln Glu Glu Asn Val
50 55 60

Arg Phe Asp Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly
65 70 75 80

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

Lys Arg Gly Arg Val Asp Asn Tyr Cys Arg His Asn Tyr Gly Val Val
100 105 110

Glu Ser Phe Thr Val Gln Arg Arg Val His Pro Lys Val Thr Val Tyr
115 120 125

Pro Ser Lys Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser
130 135 140

Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Arg Asn
145 150 155 160

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

Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg
180 185 190

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

Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys
210 215 220

<210> 57
<211> 191
<212> PRT
<213> Homo sapiens

<400> 57
Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr Leu Asn Pro
1 5 10 15

Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp Gly Asp Glu Ile Phe
20 25 30

His Val Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu Glu Glu Phe
35 40 45

Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala
50 55 60

Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Thr
65 70 75 80

Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val Leu Thr Asn Ser Pro
85 90 95

Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys Phe Ile Asp Lys Phe
100 105 110

Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg Asn Gly Lys Pro Val
115 120 125

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

Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro Ser Thr Glu Asp Val
145 150 155 160

Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp Glu Pro Leu Leu Lys
165 170 175

His Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro Glu Thr Thr Glu
180 185 190

<210> 58

<211> 198

<212> PRT

<213> Mus musculus

<400> 58

Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly Glu Cys Tyr
1 5 10 15

Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr
20 25 30

Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg
35 40 45

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

Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys Arg His Asn
65 70 75 80

Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg Arg Leu Glu Gln Pro
85 90 95

Asn Val Ala Ile Ser Leu Ser Arg Thr Glu Ala Leu Asn His His Asn
100 105 110

Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val
115 120 125

Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr
130 135 140

Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu
145 150 155 160

Glu Met Thr Pro His Gln Gly Glu Val Tyr Thr Cys His Val Glu His
165 170 175

Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu
180 185 190

Ser Ala Arg Ser Lys Ser

195

<210> 59

<211> 196

<212> PRT

<213> Mus musculus

<400> 59

Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val
1 5 10 15

Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly
20 25 30

Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg
35 40 45

Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu
50 55 60

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

Ser Asn Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe
85 90 95

Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe
100 105 110

Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn
115 120 125

Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn
130 135 140

Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser
145 150 155 160

Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu

165

170

175

Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu
 180 185 190

Leu Thr Glu Ser
 195

<210> 60

<211> 476

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 60

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Ile
 1 5 10 15

Lys Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp
 20 25 30

Gln Ser Gly Glu Phe Met Phe Asp Phe Asp Gly Asp Glu Ile Phe His
 35 40 45

Val Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu Glu Glu Phe Gly
 50 55 60

Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val
 65 70 75 80

Asp Lys Ala Asn Leu Glu Cys Met Thr Lys Arg Ser Asn Tyr Thr Pro
 85 90 95

Ile Thr Asn Val Pro Pro Glu Val Thr Val Leu Thr Asn Ser Pro Val
 100 105 110

Glu Leu Arg Glu Pro Asn Val Leu Ile Cys Phe Ile Asp Lys Phe Thr
115 120 125

Pro Pro Val Val Asn Val Thr Trp Leu Arg Asn Gly Lys Pro Val Thr
130 135 140

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

Arg Lys Phe His Tyr Leu Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr
165 170 175

Asp Cys Arg Val Glu His Trp Gly Leu Asp Glu Pro Leu Leu Lys His
180 185 190

Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro Glu Thr Thr Glu Ser Gly
195 200 205

Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
210 215 220

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
225 230 235 240

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
245 250 255

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
260 265 270

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
275 280 285

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
290 295 300

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
305 310 315 320

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
325 330 335

Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys
340 345 350

Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
355 360 365

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

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
385 390 395 400

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
405 410 415

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
420 425 430

Leu Ser Leu Ser Pro Gly Gly Ser Gly Ser Gly Ser Gly Ser Leu Gly
435 440 445

Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp His His His His
450 455 460

His His Asn Trp Ser His Pro Gln Phe Glu Lys Cys
465 470 475

<210> 61

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

polypeptide"

<400> 61

Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly Met Leu
1 5 10 15

Val Ala Ser Ser Leu Gly Gln His Leu Gln Lys Asp Tyr Arg Ala Tyr
20 25 30

Tyr Thr Cys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser
35 40 45

Gly Asp Thr Arg Pro Arg Phe Leu Glu Tyr Ser Thr Ser Glu Cys His
50 55 60

Phe Phe Asn Gly Thr Glu Arg Val Arg Tyr Leu Asp Arg Tyr Phe His
65 70 75 80

Asn Gln Glu Glu Asn Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg
85 90 95

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

Lys Asp Leu Leu Glu Gln Lys Arg Gly Arg Val Asp Asn Tyr Cys Arg
115 120 125

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

Pro Lys Val Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His
145 150 155 160

Asn Leu Leu Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu
165 170 175

Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser
180 185 190

Thr Gly Leu Ile His Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met
195 200 205

Leu Glu Thr Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu
210 215 220

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

Glu Ser Ala Gln Ser Lys Ser Gly Gly Gly Gly Gly Asp Lys Thr His
245 250 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

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

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro
370 375 380

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala

385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

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

Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465 470 475

<210> 62
<211> 443
<212> PRT
<213> Artificial Sequence

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

<400> 62
Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala
1 5 10 15

Thr Gln Ala Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr
20 25 30

Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp Gly Asp
35 40 45

Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu
50 55 60

Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala
65 70 75 80

Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Met Thr Lys Arg Ser Asn
85 90 95

Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val Leu Thr Asn
100 105 110

Ser Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys Phe Ile Asp Lys
115 120 125

Phe Thr Pro Val Val Asn Val Thr Trp Leu Arg Asn Gly Lys Pro Val
130 135 140

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

Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro Ser Thr Glu Asp Val
165 170 175

Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp Glu Pro Leu Leu Lys
180 185 190

His Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro Glu Thr Thr Glu Ser
195 200 205

Gly Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Cys Pro Ala Pro
210 215 220

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

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
245 250 255

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
260 265 270

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
275 280 285

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
290 295 300

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
305 310 315 320

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
325 330 335

Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys
340 345 350

Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
355 360 365

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

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
385 390 395 400

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
405 410 415

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
420 425 430

Leu Ser Leu Ser Pro Gly Gly Ser Gly Ser Cys
435 440

<210> 63

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 63

Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly Met Leu
1 5 10 15

Val Ala Ser Ser Leu Gly Gln His Leu Gln Lys Asp Tyr Arg Ala Tyr
20 25 30

Tyr Thr Cys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser
35 40 45

Gly Asp Thr Arg Pro Arg Phe Leu Glu Tyr Ser Thr Ser Glu Cys His
50 55 60

Phe Phe Asn Gly Thr Glu Arg Val Arg Tyr Leu Asp Arg Tyr Phe His
65 70 75 80

Asn Gln Glu Glu Asn Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg
85 90 95

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

Lys Asp Leu Leu Glu Gln Lys Arg Gly Arg Val Asp Asn Tyr Cys Arg
115 120 125

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

Pro Lys Val Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His
145 150 155 160

Asn Leu Leu Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu
165 170 175

Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser
180 185 190

Thr Gly Leu Ile His Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met
195 200 205

Leu Glu Thr Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu
210 215 220

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

Glu Ser Ala Gln Ser Lys Ser Gly Gly Gly Gly Gly Asp Lys Thr His
245 250 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

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

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro

370

375

380

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala
 385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 405 410 415

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

Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg
 435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 465 470 475

<210> 64

<211> 1344

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 64

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aaagaagaac atgtgatcat ccaggccgag ttctatctga atcctgacca atcaggcgag 120

tttatgtttg actttgatgg tgatgagatt ttccatgtgg atatggcaaa gaaggagacg 180

gtctggcggc ttgaagaatt tggacgattt gccagctttg aggctcaagg tgcattggcc 240

aacatagctg tggacaaaagc caacctggaa tgcatgacaa agcgctccaa ctatactccg 300

atcaccaatg tacctccaga ggtaactgtg ctacaaaaca gccctgtgga actgagagag 360

cccaacgtcc tcatctgttt catagacaag ttcacccccac cagtgggtcaa tgtcacgtgg	420
cttcgaaatg gaaaacctgt caccacagga gtgtcagaga cagtcttcct gcccagggaa	480
gaccaccttt tccgcaagtt ccactatctc cccttcctgc cctcaactga ggacgtttac	540
gactgcaggg tggagcactg gggcttggat gagcctcttc tcaagcactg ggagtttgat	600
gctccaagcc ctctcccaga gactacagag tccggaggcg gaggcggaga caaaactcac	660
acatgcccac cgtgcccagc acctgaagcc gcgggggggac cgtcagtcctt cctcttcccc	720
ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtgggtggtg	780
gacgtgagcc acgaagaccc tgagggtcaag ttcaactggt acgtggacgg cgtggagggtg	840
cataatgcca agacaaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc	900
gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc	960
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga	1020
gaaccacagg tgtacaccct gccccatgc cgggatgagc tgaccaagaa ccaggtcagc	1080
ctgtgggtgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat	1140
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc	1200
ttcctctaca gcaagctcac cgtggacaag agtaggtggc agcaggggaa cgtcttctca	1260
tgctccgtga tgcatgaggc tctgcacaac cactacacac agaagagcct ctccctgtct	1320
ccgggcggtg gtggtagttg ttga	1344

<210> 65

<211> 1437

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 65

atgggttctc tgcaaccgct ggccaccttg tacctgctgg gtatgctggt cgctagcagc	60
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ctcggacagc acctgcagaa ggactacaga gcctactaca cctgtggagg tggaggcggc	120
---	-----

tcaggaggtg gaagcggcgg ctctggggac acccgaccac gtttcttgga gtactctacg	180
tctgagtgtc atttcttcaa tgggacggag cgggtgcggt acctggacag atacttccat	240
aaccaggagg agaacgtgcg cttcgacagc gacgtggggg agttccgggc ggtgacggag	300
ctggggcggc ctgatgccga gtactggaac agccagaagg acctcctgga gcagaagcgg	360
ggccgggtgg acaactactg cagacacaac tacggggttg tggagagctt cacagtgcag	420
cggcgagtcc atcctaaggt gactgtgtat cttcaaaga cccagcccct gcagcaccat	480
aacctcctgg tctgttctgt gagtggtttc tatccaggca gcattgaagt caggtggttc	540
cggaatggcc aggaagagaa gactgggggtg gtgtccacag gcctgatcca caatggagac	600
tggaccttcc agaccttggg gatgctggaa acagttcctc ggagtggaga ggtttacacc	660
tgccaagtgg agcacccaag cgtgacaagc cctctcacag tggaatggag agcacgggtct	720
gaatctgcac agagcaagtc cggaggcgga ggcgagaca aaactcacac atgcccaccg	780
tgcccagcac ctgaagccgc ggggggaccg tcagtcttcc tcttcccccc aaaaccaag	840
gacaccctca tgatctcccg gaccctgag gtcacatgcg tggtggtgga cgtgagccac	900
gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag	960
acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc	1020
ctgcaccagg actggctgaa tggcaaggag tacaagtgca aagtctcaa caaagccctc	1080
ccagccccca tcgagaaaac catctccaaa gccaaagggc agccccgaga accacaggtg	1140
tgcaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gagctgcgcg	1200
gtcaaaggct tctatcccag cgacatcgcc gtggagtggg agagcaatgg gcagccggag	1260
aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctcgtcagc	1320
aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg	1380
catgaggctc tgcacaacca ctacacacag aagagcctct ccctgtctcc cggctga	1437