

SEQUENCE LISTING

<110> REGENERON PHARMACEUTICALS, INC.

<120> METHODS AND SYSTEMS FOR IDENTIFYING, CLASSIFYING, AND/OR RANKING
GENETIC SEQUENCES

<130> 2010794-2132

<140>

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<150> 62/993,567

<151> 2020-03-23

<150> 62/934,323

<151> 2019-11-12

<160> 108

<170> PatentIn version 3.5

<210> 1

<211> 1751

<212> DNA

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
HA_1755_bp_B_Lee_1940 sequence"

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gtgactggcg tgataccact gacaacaaca ccaacaaaat cttattttgc aaatctcaaa 180

ggaacaagga ccagagggaa actatgcccc gactgtctca actgtacaga tctggatgtg 240

gccttgggca ggccaatgtg tgtggggacc acaccttctg ctaaagcttc aatactccat 300

gaggtcagac ctgttacatc cgggtgcttt cctataatgc acgacagaac aaaaatcaga 360

caactaccca atcttctcag aggatatgaa aagatcaggt tatcaaccca aaacgttatc 420

gatgcagaaa aagcaccagg aggaccctac agacttggaa cctcaggatc ttgccctaac 480

gctaccagta aaattggatt ttttgcaaca atggcttggg ctgttccaaa ggacaactac 540

aaaaatgcaa cgaaccacaca aacagtggaa gtaccataca tttgtacaga aggggaagac	600
caaattactg tttgggggtt tcattcggat aacaaaaccc aaatgaagag cctctatgga	660
gactcaaatc ctcaaaagtt cacctcatct gctaattggag tgaccacaca ttatgtttct	720
cagattggcg acttcccaga tcaaacagaa gacggaggac taccacaaag cggcagaatt	780
gttggtgatt acatggtgca aaaacctggg aaaacaggaa caattgtcta tcaaaggggt	840
gttttgttgc ctcaaaaggt gtggtgcgcg agtggccgga gcaaagtaat aaaaggggtca	900
ttgcctttta ttggtgaagc agattgcctt catgaagaat atggtggatt aaacaaaagc	960
aagccttact acacaggaaa acatgcaaaa gccataggaa attgcccaat atgggtaaaa	1020
acacctttga agcttgccaa tggaacacaaa tatagacctc ctgcaaaaact attgaaggaa	1080
aggggtttct tcggagctat tgctggtttc ctagaaggag gatgggaagg aatgattgca	1140
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agtacacaag aagctataaa caagataaca aaaaatctca attctttgag tgaactagaa	1260
gtaaagaacc ttcaaagact aagtgggtgcc atggatgaac tccacaacga aatacttgag	1320
ctggatgaaa aagtggatga cctcagagct gacactataa gctcacaat agaacttgca	1380
gtcttgcttt ccaacgaagg aataataaac agtgaagatg agcatctatt ggcacttgag	1440
agaaaaactaa agaaaatgct ggggtccctct gctgtagaca taggaaacgg atgcttcgaa	1500
accaaacaca aatgcaacca gacctgctta gacaggatag ctgctggcac ctttaatgca	1560
ggagaatttt ctctccccac ttttgactca ttgaacatta ctgctgcac tttaaatgat	1620
gatggattgg ataaccatac tatactgctc tattactcaa ctgctgcttc tagtttggct	1680
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<210> 2

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<212> DNA

<213> Unknown

<220>

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<223> /note="Description of Unknown:

HA_1755_bp_B_Alabama_02_2018 sequence"

<400> 2

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gtgactggcg tgataccact gacaacaaca ccaacaaaat cttattttgc aaatctcaaa	180
ggaacaagga ccagagggaa actgtgccccg gactgtctca attgtacaga tctggatgtg	240
gccttgggca ggccaatgtg tgtgggggacc acaccttctg ctaaagcttc aatactccat	300
gaggtcagac ctgttacatc cgggtgcttt cctataatgc acgacagaac aaaaatcaga	360
caactaccca atcttctcag aggatatgaa aagatcaggt tatcaaccca aaacgttatc	420
gatgcagaaa aagcaccagg aggaccctac agacttgga cctcaggatc ttgccctaac	480
gctaccagta aaattggatt ttttgcaaca atggcttggg ctgttccgaa ggacaactat	540
aaaaatgcaa cgaaccacaca aacagtggaa gtaccataca tctgtacaga aggggaagac	600
caaattactg tttgggggtt tcattcggat aacaaaaccc aaatgaagag cctctatgga	660
gactcaaatc ctcaaaagtt cacctcatct gccaatggag tgaccacaca ttatgtttct	720
cagattggcg acttcccaga tcaaacagaa gacggaggac taccacaaag cggcagaatt	780
gttgttgatt acatggtgca aaaacctggg aaaacaggaa caattgtcta tcaaaggggt	840
gttttgttgc ctcaaaaggt gtggtgcgcg agtggcagga gcaaagtaat aaaaggggtca	900
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aagccttact acacaggaaa acatgcaaaa gccataggaa attgcccaat atgggtaaaa	1020
acacctttga agcttgccaa tggaacccaaa tatagacctc ctgcaaaaact attgaaagaa	1080
aggggtttct tcggagctat tgctggtttc ctagaaggag gatgggaagg aatgattgca	1140
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gtaaagaacc ttcaaagact aagtgggtgcc atggatgaac tccacaacga aatacttgag	1320
ctggatgaaa aagtggatga cctcagagct gacactataa gctcacaat agaacttgca	1380

gtcttgcttt ccaacgaagg aataataaac agtgaagatg agcatctatt ggcacttgag	1440
agaaaaactaa agaaaaatgct ggggtccctct gctgtagaca taggaaacgg atgcttcgaa	1500
accaaacaca aatgcaacca gacctgctta gacaggatag ctgctggcac ctttaatgca	1560
ggagaatfff ctctccccac ttttgactca ttgaacatta ctgctgcatc tttaaatgat	1620
gatggattgg ataaccatac tatactgctc tattactcaa ctgctgcttc tagtttggct	1680
gtaacattaa tgctagctat ttttattgtt tatatggctc ccagagacaa cgtttcatgc	1740
tccatctgtc t	1751

<210> 3

<211> 1751

<212> DNA

<213> Unknown

<220>

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<223> /note="Description of Unknown:

HA_1755_bp_B_Alabama_04_2018 sequence"

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gtgactggcg tgataccact gacaacaaca ccaacaaaat cttatffffc aaatctcaaa	180
ggaacaagga ccagagggaa actatgcccc gactgtctca actgtacaga tctggatgtg	240
gccttgggca ggccaatgtg tgtggggacc acaccttctg ctaaagcttc aatactccat	300
gaggtcagac ctgttacatc cgggtgcttt cctataatgc acgacagaac aaaaatcaga	360
caactaccca atcttctcag aggatatgaa aagatcaggt tgtcaaccca aaacgttatc	420
gatgcagaaa aagcaccagg aggaccctac agacttggaa cctcaggatc ttgccctaac	480
gctaccagta aaattggatt ttttgcaaca atggcttggg ctgttccaaa ggacaactac	540
aaaaatgcaa cgaaccacaca aacagtggaa gtaccataca tttgtacaga aggggaagac	600
caaattactg tttggggggtt ccattcggat aacaaaaccc aaatgaagag cctctatgga	660
gactcaaadc ctcaaaagt t cacctcatct gctaattggag tgaccacaca ttatgtttct	720

cagattggcg acttcccaga tcaaacagaa gacggagggc taccacaaag cggcagaatt	780
gttgttgatt acatgggtgca aaaacctggg aaaacaggaa caattgtcta tcaaaggggt	840
gttttgttgc ctcaaaaggt gtgggtgcgcg agtggcagga gcaaagtaat aaaaggggtca	900
ttgcctttta ttggtgaagc agattgcctt catgaagaat acggtggatt aaacaaaagc	960
aagccttact acacaggaaa acatgcaaaa gccataggaa attgcccaat atgggtaaaaa	1020
acacctttga agcttgctaa tggaacaaaa tatagacctc ctgcaaaact attgaaggaa	1080
aggggtttct tcggagctat tgctggtttc ctagaaggag gatgggaagg aatgattgca	1140
ggctggcacg gatacacatc tcacggagca catggagtgg cagtggcggc agaccttaag	1200
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ctggatgaaa aagtggatga cctcagagct gacactataa gctcaciaat agaacttgca	1380
gtcttgcttt ccaacgaagg aataataaac agtgaagatg agcatctatt ggcacttgag	1440
agaaaactaa agaaaatgct ggggtccctct gctgtagaca taggaaacgg atgcttcgaa	1500
accaaacaca aatgcaacca gacctgctta gacaggatag ctgctggcac ctttaatgca	1560
ggagaatfff ctctccccac ttttgactca ttgaacatta ctgctgcac tttaaatgat	1620
gatggattgg ataaccatac tatactgctc tattactcaa ctgctgcttc tagtttggct	1680
gtaacattaa tgctagctat ttttattgtt tatatgggtc ccagagacaa cgtttcatgc	1740
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<210> 4

<211> 1751

<212> DNA

<213> Unknown

<220>

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<223> /note="Description of Unknown:

HA_1755_bp_B_Alabama_05_2018 sequence"

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gtgactggcg tgataccact gacaacaaca ccaacaaaat cttattttgc aaatctcaaa	180
ggaacaagga ccagagggaa actatgcccc gactgtctca actgtacaga tctggatgtg	240
gccttgggca ggccaatgtg tgtggggacc acaccttctg ctaaagcttc aatactccat	300
gaggtcagac ctgttacatc cgggtgcttt cctataatgc acgacagaac aaaaatcaga	360
caactaccca atcttctcag aggatatgaa aagatcaggt tatcaaccca aaacgttatc	420
gatgcagaaa aagcaccagg aggaccctac agacttggaa cctcaggatc ttgccctaac	480
gctaccagta aaattggatt ttttgcaaca atggcttggg ctgttcctaaa ggacaactac	540
aaaaatgcaa cgaacccaca aacagtggaa gtaccataca tttgtacaga aggggaagac	600
caaattactg tttggggggt tcattcggat aacaaaaccc aaatgaagag cctctatgga	660
gactcaaatc ctcaaaagtt cacctcatct gctaattggag tgaccacaca ttatgtttct	720
cagattggcg acttcccaga tcaaacagaa gacggaggac taccacaaag cggcagaatt	780
gttggtgatt acatggtgca aaaacctggg aaaacaggaa caattgtcta tcaaaggggt	840
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ttgcctttaa ttggtgaagc agattgcctt catgaagaat atggtggatt aaacaaaagc	960
aagccttact acacaggaaa acatgcaaaa gccataggaa attgccaat atgggtaaaa	1020
acacctttga agcttgccaa tggaaccaa tatagacctc ctgcaaaact attgaaggaa	1080
aggggtttct tcggagctat tgctggtttc ctagaaggag gatgggaagg aatgattgca	1140
ggttggcacg gatacacatc tcacggagca catggagtgg cagtggcggc agaccttaaa	1200
agtacacaag aagctataaa caagataaca aaaaatctca attctttgag tgaactagaa	1260
gtaaagaacc ttcaaagact aagtgggtgcc atggatgaac tccacaacga aataattgag	1320
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gtcttgcttt ccaacgaggg aataataaac agtgaagatg agcatctatt ggcaacttgag	1440
agaaaactaa agaaaatgct gggtcctct gctgtagaca taggaaacgg atgcttcgaa	1500
accaaacaca aatgcaacca gacctgctta gacaggatag ctgctggcac ctttaatgca	1560

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ggagaatttt ctctccccac ttttgactca ttgaacatta ctgctgcatc tttaaatgat      1620
gatgggttgg ataaccatac tatactgctc tattactcaa ctgctgcttc tagtttggct      1680
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tccatctgtc t                                                                1751

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<210> 5
<211> 584
<212> PRT
<213> Unknown

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<220>
<221> source
<223> /note="Description of Unknown:
      HA_1755_bp_B_Lee_1940 sequence"

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

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Thr Ala Thr Gln Gly Glu Val Asn Val Thr Gly Val Ile Pro Leu Thr
15           40           45

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Thr Thr Pro Thr Lys Ser His Phe Ala Asn Leu Lys Gly Thr Gln Thr
50           55           60

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

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Ala Leu Gly Arg Pro Lys Cys Met Gly Asn Thr Pro Ser Ala Lys Val
          85           90           95

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Ser Ile Leu His Glu Val Lys Pro Ala Thr Ser Gly Cys Phe Pro Ile
100          105          110

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Met His Asp Arg Thr Lys Ile Arg Gln Leu Pro Asn Leu Leu Arg Gly

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115

120

125

Tyr Glu Asn Ile Arg Leu Ser Thr Ser Asn Val Ile Asn Thr Glu Thr
 130 135 140

Ala Pro Gly Gly Pro Tyr Lys Val Gly Thr Ser Gly Ser Cys Pro Asn
 145 150 155 160

Val Ala Asn Gly Asn Gly Phe Phe Asn Thr Met Ala Trp Val Ile Pro
 165 170 175

Lys Asp Asn Asn Lys Thr Ala Ile Asn Pro Val Thr Val Glu Val Pro
 180 185 190

Tyr Ile Cys Ser Glu Gly Glu Asp Gln Ile Thr Val Trp Gly Phe His
 195 200 205

Ser Asp Asp Lys Thr Gln Met Glu Arg Leu Tyr Gly Asp Ser Asn Pro
 210 215 220

Gln Lys Phe Thr Ser Ser Ala Asn Gly Val Thr Thr His Tyr Val Ser
 225 230 235 240

Gln Ile Gly Gly Phe Pro Asn Gln Thr Glu Asp Glu Gly Leu Lys Gln
 245 250 255

Ser Gly Arg Ile Val Val Asp Tyr Met Val Gln Lys Pro Gly Lys Thr
 260 265 270

Gly Thr Ile Val Tyr Gln Arg Gly Ile Leu Leu Pro Gln Lys Val Trp
 275 280 285

Cys Ala Ser Gly Arg Ser Lys Val Ile Lys Gly Ser Leu Pro Leu Ile
 290 295 300

Gly Glu Ala Asp Cys Leu His Glu Lys Tyr Gly Gly Leu Asn Lys Ser
 305 310 315 320

Lys Pro Tyr Tyr Thr Gly Glu His Ala Lys Ala Ile Gly Asn Cys Pro
325 330 335

Ile Trp Val Lys Thr Pro Leu Lys Leu Ala Asn Gly Thr Lys Tyr Arg
340 345 350

Pro Pro Ala Lys Leu Leu Lys Glu Arg Gly Phe Phe Gly Ala Ile Ala
355 360 365

Gly Phe Leu Glu Gly Gly Trp Glu Gly Met Ile Ala Gly Trp His Gly
370 375 380

Tyr Thr Ser His Gly Ala His Gly Val Ala Val Ala Ala Asp Leu Lys
385 390 395 400

Ser Thr Gln Glu Ala Ile Asn Lys Ile Thr Lys Asn Leu Asn Tyr Leu
405 410 415

Ser Glu Leu Glu Val Lys Asn Leu Gln Arg Leu Ser Gly Ala Met Asn
420 425 430

Glu Leu His Asp Glu Ile Leu Glu Leu Asp Glu Lys Val Asp Asp Leu
435 440 445

Arg Ala Asp Thr Ile Ser Ser Gln Ile Glu Leu Ala Val Leu Leu Ser
450 455 460

Asn Glu Gly Ile Ile Asn Ser Glu Asp Glu His Leu Leu Ala Leu Glu
465 470 475 480

Arg Lys Leu Lys Lys Met Leu Gly Pro Ser Ala Val Glu Ile Gly Asn
485 490 495

Gly Cys Phe Glu Thr Lys His Lys Cys Asn Gln Thr Cys Leu Asp Arg
500 505 510

Ile Ala Ala Gly Thr Phe Asn Ala Gly Asp Phe Ser Leu Pro Thr Phe

515

520

525

Asp Ser Leu Asn Ile Thr Ala Ala Ser Leu Asn Asp Asp Gly Leu Asp
 530 535 540

Asn His Thr Ile Leu Leu Tyr Tyr Ser Thr Ala Ala Ser Ser Leu Ala
 545 550 555 560

Val Thr Leu Met Ile Ala Ile Phe Ile Val Tyr Met Val Ser Arg Asp
 565 570 575

Asn Val Ser Cys Ser Ile Cys Leu
 580

<210> 6

<211> 583

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
 HA_1755_bp_B_Alabama_02_2018 sequence"

<400> 6

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

Thr Ala Thr Gln Gly Glu Val Asn Val Thr Gly Val Ile Pro Leu Thr
 35 40 45

Thr Thr Pro Thr Lys Ser Tyr Phe Ala Asn Leu Lys Gly Thr Arg Thr
 50 55 60

Arg Gly Lys Leu Cys Pro Asp Cys Leu Asn Cys Thr Asp Leu Asp Val
 65 70 75 80

Ala Leu Gly Arg Pro Met Cys Val Gly Thr Thr Pro Ser Ala Lys Ala
85 90 95

Ser Ile Leu His Glu Val Arg Pro Val Thr Ser Gly Cys Phe Pro Ile
100 105 110

Met His Asp Arg Thr Lys Ile Arg Gln Leu Pro Asn Leu Leu Arg Gly
115 120 125

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

Ala Pro Gly Gly Pro Tyr Arg Leu Gly Thr Ser Gly Ser Cys Pro Asn
145 150 155 160

Ala Thr Ser Lys Ile Gly Phe Phe Ala Thr Met Ala Trp Ala Val Pro
165 170 175

Lys Asp Asn Tyr Lys Asn Ala Thr Asn Pro Gln Thr Val Glu Val Pro
180 185 190

Tyr Ile Cys Thr Glu Gly Glu Asp Gln Ile Thr Val Trp Gly Phe His
195 200 205

Ser Asp Asn Lys Thr Gln Met Lys Ser Leu Tyr Gly Asp Ser Asn Pro
210 215 220

Gln Lys Phe Thr Ser Ser Ala Asn Gly Val Thr Thr His Tyr Val Ser
225 230 235 240

Gln Ile Gly Asp Phe Pro Asp Gln Thr Glu Asp Gly Gly Leu Pro Gln
245 250 255

Ser Gly Arg Ile Val Val Asp Tyr Met Val Gln Lys Pro Gly Lys Thr
260 265 270

Gly Thr Ile Val Tyr Gln Arg Gly Val Leu Leu Pro Gln Lys Val Trp
275 280 285

Cys Ala Ser Gly Arg Ser Lys Val Ile Lys Gly Ser Leu Pro Leu Ile
290 295 300

Gly Glu Ala Asp Cys Leu His Glu Glu Tyr Gly Gly Leu Asn Lys Ser
305 310 315 320

Lys Pro Tyr Tyr Thr Gly Lys His Ala Lys Ala Ile Gly Asn Cys Pro
325 330 335

Ile Trp Val Lys Thr Pro Leu Lys Leu Ala Asn Gly Thr Lys Tyr Arg
340 345 350

Pro Pro Ala Lys Leu Leu Lys Glu Arg Gly Phe Phe Gly Ala Ile Ala
355 360 365

Gly Phe Leu Glu Gly Gly Trp Glu Gly Met Ile Ala Gly Trp His Gly
370 375 380

Tyr Thr Ser His Gly Ala His Gly Val Ala Val Ala Ala Asp Leu Lys
385 390 395 400

Ser Thr Gln Glu Ala Ile Asn Lys Ile Thr Lys Asn Leu Asn Ser Leu
405 410 415

Ser Glu Leu Glu Val Lys Asn Leu Gln Arg Leu Ser Gly Ala Met Asp
420 425 430

Glu Leu His Asn Glu Ile Leu Glu Leu Asp Glu Lys Val Asp Asp Leu
435 440 445

Arg Ala Asp Thr Ile Ser Ser Gln Ile Glu Leu Ala Val Leu Leu Ser
450 455 460

Asn Glu Gly Ile Ile Asn Ser Glu Asp Glu His Leu Leu Ala Leu Glu
465 470 475 480

Arg Lys Leu Lys Lys Met Leu Gly Pro Ser Ala Val Asp Ile Gly Asn
485 490 495

Gly Cys Phe Glu Thr Lys His Lys Cys Asn Gln Thr Cys Leu Asp Arg
500 505 510

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

Asp Ser Leu Asn Ile Thr Ala Ala Ser Leu Asn Asp Asp Gly Leu Asp
530 535 540

Asn His Thr Ile Leu Leu Tyr Tyr Ser Thr Ala Ala Ser Ser Leu Ala
545 550 555 560

Val Thr Leu Met Leu Ala Ile Phe Ile Val Tyr Met Val Ser Arg Asp
565 570 575

Asn Val Ser Cys Ser Ile Cys
580

<210> 7

<211> 583

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
HA_1755_bp_B_Alabama_04_2018 sequence"

<400> 7

Met Lys Thr Ile Ile Val Leu Leu Met Val Val Thr Ser Asn Ala Asp
1 5 10 15

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

Thr Ala Thr Gln Gly Glu Val Asn Val Thr Gly Val Ile Pro Leu Thr
35 40 45

Thr Thr Pro Thr Lys Ser Tyr Phe Ala Asn Leu Lys Gly Thr Arg Thr
50 55 60

Arg Gly Lys Leu Cys Pro Asp Cys Leu Asn Cys Thr Asp Leu Asp Val
65 70 75 80

Ala Leu Gly Arg Pro Met Cys Val Gly Thr Thr Pro Ser Ala Lys Ala
85 90 95

Ser Ile Leu His Glu Val Arg Pro Val Thr Ser Gly Cys Phe Pro Ile
100 105 110

Met His Asp Arg Thr Lys Ile Arg Gln Leu Pro Asn Leu Leu Arg Gly
115 120 125

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

Ala Pro Gly Gly Pro Tyr Arg Leu Gly Thr Ser Gly Ser Cys Pro Asn
145 150 155 160

Ala Thr Ser Lys Ile Gly Phe Phe Ala Thr Met Ala Trp Ala Val Pro
165 170 175

Lys Asp Asn Tyr Lys Asn Ala Thr Asn Pro Gln Thr Val Glu Val Pro
180 185 190

Tyr Ile Cys Thr Glu Gly Glu Asp Gln Ile Thr Val Trp Gly Phe His
195 200 205

Ser Asp Asn Lys Thr Gln Met Lys Ser Leu Tyr Gly Asp Ser Asn Pro
210 215 220

Gln Lys Phe Thr Ser Ser Ala Asn Gly Val Thr Thr His Tyr Val Ser
225 230 235 240

Gln Ile Gly Asp Phe Pro Asp Gln Thr Glu Asp Gly Gly Leu Pro Gln

245

250

255

Ser Gly Arg Ile Val Val Asp Tyr Met Val Gln Lys Pro Gly Lys Thr
 260 265 270

Gly Thr Ile Val Tyr Gln Arg Gly Val Leu Leu Pro Gln Lys Val Trp
 275 280 285

Cys Ala Ser Gly Arg Ser Lys Val Ile Lys Gly Ser Leu Pro Leu Ile
 290 295 300

Gly Glu Ala Asp Cys Leu His Glu Glu Tyr Gly Gly Leu Asn Lys Ser
 305 310 315 320

Lys Pro Tyr Tyr Thr Gly Lys His Ala Lys Ala Ile Gly Asn Cys Pro
 325 330 335

Ile Trp Val Lys Thr Pro Leu Lys Leu Ala Asn Gly Thr Lys Tyr Arg
 340 345 350

Pro Pro Ala Lys Leu Leu Lys Glu Arg Gly Phe Phe Gly Ala Ile Ala
 355 360 365

Gly Phe Leu Glu Gly Gly Trp Glu Gly Met Ile Ala Gly Trp His Gly
 370 375 380

Tyr Thr Ser His Gly Ala His Gly Val Ala Val Ala Ala Asp Leu Lys
 385 390 395 400

Ser Thr Gln Glu Ala Ile Asn Lys Ile Thr Lys Asn Leu Asn Ser Leu
 405 410 415

Ser Glu Leu Glu Val Lys Asn Leu Gln Arg Leu Ser Gly Ala Met Asp
 420 425 430

Glu Leu His Asn Glu Ile Leu Glu Leu Asp Glu Lys Val Asp Asp Leu
 435 440 445

Arg Ala Asp Thr Ile Ser Ser Gln Ile Glu Leu Ala Val Leu Leu Ser
450 455 460

Asn Glu Gly Ile Ile Asn Ser Glu Asp Glu His Leu Leu Ala Leu Glu
465 470 475 480

Arg Lys Leu Lys Lys Met Leu Gly Pro Ser Ala Val Asp Ile Gly Asn
485 490 495

Gly Cys Phe Glu Thr Lys His Lys Cys Asn Gln Thr Cys Leu Asp Arg
500 505 510

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

Asp Ser Leu Asn Ile Thr Ala Ala Ser Leu Asn Asp Asp Gly Leu Asp
530 535 540

Asn His Thr Ile Leu Leu Tyr Tyr Ser Thr Ala Ala Ser Ser Leu Ala
545 550 555 560

Val Thr Leu Met Leu Ala Ile Phe Ile Val Tyr Met Val Ser Arg Asp
565 570 575

Asn Val Ser Cys Ser Ile Cys
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<210> 8

<211> 583

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
HA_1755_bp_B_Alabama_05_2018 sequence"

<400> 8

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

Thr Ala Thr Gln Gly Glu Val Asn Val Thr Gly Val Ile Pro Leu Thr
35 40 45

Thr Thr Pro Thr Lys Ser Tyr Phe Ala Asn Leu Lys Gly Thr Arg Thr
50 55 60

Arg Gly Lys Leu Cys Pro Asp Cys Leu Asn Cys Thr Asp Leu Asp Val
65 70 75 80

Ala Leu Gly Arg Pro Met Cys Val Gly Thr Thr Pro Ser Ala Lys Ala
85 90 95

Ser Ile Leu His Glu Val Arg Pro Val Thr Ser Gly Cys Phe Pro Ile
100 105 110

Met His Asp Arg Thr Lys Ile Arg Gln Leu Pro Asn Leu Leu Arg Gly
115 120 125

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

Ala Pro Gly Gly Pro Tyr Arg Leu Gly Thr Ser Gly Ser Cys Pro Asn
145 150 155 160

Ala Thr Ser Lys Ile Gly Phe Phe Ala Thr Met Ala Trp Ala Val Pro
165 170 175

Lys Asp Asn Tyr Lys Asn Ala Thr Asn Pro Gln Thr Val Glu Val Pro
180 185 190

Tyr Ile Cys Thr Glu Gly Glu Asp Gln Ile Thr Val Trp Gly Phe His
195 200 205

Ser Asp Asn Lys Thr Gln Met Lys Ser Leu Tyr Gly Asp Ser Asn Pro
210 215 220

Gln Lys Phe Thr Ser Ser Ala Asn Gly Val Thr Thr His Tyr Val Ser
225 230 235 240

Gln Ile Gly Asp Phe Pro Asp Gln Thr Glu Asp Gly Gly Leu Pro Gln
245 250 255

Ser Gly Arg Ile Val Val Asp Tyr Met Val Gln Lys Pro Gly Lys Thr
260 265 270

Gly Thr Ile Val Tyr Gln Arg Gly Val Leu Leu Pro Gln Lys Val Trp
275 280 285

Cys Ala Ser Gly Arg Ser Lys Val Ile Lys Gly Ser Leu Pro Leu Ile
290 295 300

Gly Glu Ala Asp Cys Leu His Glu Glu Tyr Gly Gly Leu Asn Lys Ser
305 310 315 320

Lys Pro Tyr Tyr Thr Gly Lys His Ala Lys Ala Ile Gly Asn Cys Pro
325 330 335

Ile Trp Val Lys Thr Pro Leu Lys Leu Ala Asn Gly Thr Lys Tyr Arg
340 345 350

Pro Pro Ala Lys Leu Leu Lys Glu Arg Gly Phe Phe Gly Ala Ile Ala
355 360 365

Gly Phe Leu Glu Gly Gly Trp Glu Gly Met Ile Ala Gly Trp His Gly
370 375 380

Tyr Thr Ser His Gly Ala His Gly Val Ala Val Ala Ala Asp Leu Lys
385 390 395 400

Ser Thr Gln Glu Ala Ile Asn Lys Ile Thr Lys Asn Leu Asn Ser Leu
405 410 415

Ser Glu Leu Glu Val Lys Asn Leu Gln Arg Leu Ser Gly Ala Met Asp
420 425 430

Glu Leu His Asn Glu Ile Ile Glu Leu Asp Glu Lys Val Asp Asp Leu
435 440 445

Arg Ala Asp Thr Ile Ser Ser Gln Ile Glu Leu Ala Val Leu Leu Ser
450 455 460

Asn Glu Gly Ile Ile Asn Ser Glu Asp Glu His Leu Leu Ala Leu Glu
465 470 475 480

Arg Lys Leu Lys Lys Met Leu Gly Pro Ser Ala Val Asp Ile Gly Asn
485 490 495

Gly Cys Phe Glu Thr Lys His Lys Cys Asn Gln Thr Cys Leu Asp Arg
500 505 510

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

Asp Ser Leu Asn Ile Thr Ala Ala Ser Leu Asn Asp Asp Gly Leu Asp
530 535 540

Asn His Thr Ile Leu Leu Tyr Tyr Ser Thr Ala Ala Ser Ser Leu Ala
545 550 555 560

Val Thr Leu Met Leu Ala Ile Phe Ile Val Tyr Met Val Ser Arg Asp
565 570 575

Asn Val Ser Cys Ser Ile Cys
580

<210> 9

<211> 14

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
Hepatitis B amino acid sequence"

<400> 9

Met Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn
1 5 10

<210> 10

<211> 14

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
Hepatitis B amino acid sequence"

<400> 10

Met Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn
1 5 10

<210> 11

<211> 14

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
Hepatitis B amino acid sequence"

<400> 11

Met Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Ser
1 5 10

<210> 12

<211> 14

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
Hepatitis B amino acid sequence"

<400> 12

Met Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn
1 5 10

<210> 13

<211> 14

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
Hepatitis B amino acid sequence"

<400> 13

Met Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn
1 5 10

<210> 14

<211> 14

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
Hepatitis B amino acid sequence"

<400> 14

Met Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn
1 5 10

<210> 15

<211> 14

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
Hepatitis B amino acid sequence"

<400> 15

Met Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asp
1 5 10

<210> 16
<211> 14
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Hepatitis B amino acid sequence"

<400> 16
Met Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn
1 5 10

<210> 17
<211> 14
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Hepatitis B amino acid sequence"

<400> 17
Met Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn
1 5 10

<210> 18
<211> 14
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Hepatitis B amino acid sequence"

<400> 18
Met Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn
1 5 10

<210> 19
<211> 14
<212> PRT
<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
Hepatitis B amino acid sequence"

<400> 19

Met Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn
1 5 10

<210> 20

<211> 14

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
Hepatitis B amino acid sequence"

<400> 20

Met Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn
1 5 10

<210> 21

<211> 584

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
Lee/1940 sequence"

<400> 21

Met Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn Ala Asp
1 5 10 15

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

Thr Ala Thr Gln Gly Glu Val Asn Val Thr Gly Val Ile Pro Leu Thr
35 40 45

Thr Thr Pro Thr Lys Ser His Phe Ala Asn Leu Lys Gly Thr Gln Thr

50

55

60

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

Ala Leu Gly Arg Pro Lys Cys Met Gly Asn Thr Pro Ser Ala Lys Val
85 90 95

Ser Ile Leu His Glu Val Lys Pro Ala Thr Ser Gly Cys Phe Pro Ile
100 105 110

Met His Asp Arg Thr Lys Ile Arg Gln Leu Pro Asn Leu Leu Arg Gly
115 120 125

Tyr Glu Asn Ile Arg Leu Ser Thr Ser Asn Val Ile Asn Thr Glu Thr
130 135 140

Ala Pro Gly Gly Pro Tyr Lys Val Gly Thr Ser Gly Ser Cys Pro Asn
145 150 155 160

Val Ala Asn Gly Asn Gly Phe Phe Asn Thr Met Ala Trp Val Ile Pro
165 170 175

Lys Asp Asn Asn Lys Thr Ala Ile Asn Pro Val Thr Val Glu Val Pro
180 185 190

Tyr Ile Cys Ser Glu Gly Glu Asp Gln Ile Thr Val Trp Gly Phe His
195 200 205

Ser Asp Asp Lys Thr Gln Met Glu Arg Leu Tyr Gly Asp Ser Asn Pro
210 215 220

Gln Lys Phe Thr Ser Ser Ala Asn Gly Val Thr Thr His Tyr Val Ser
225 230 235 240

Gln Ile Gly Gly Phe Pro Asn Gln Thr Glu Asp Glu Gly Leu Lys Gln
245 250 255

Ser Gly Arg Ile Val Val Asp Tyr Met Val Gln Lys Pro Gly Lys Thr
260 265 270

Gly Thr Ile Val Tyr Gln Arg Gly Ile Leu Leu Pro Gln Lys Val Trp
275 280 285

Cys Ala Ser Gly Arg Ser Lys Val Ile Lys Gly Ser Leu Pro Leu Ile
290 295 300

Gly Glu Ala Asp Cys Leu His Glu Lys Tyr Gly Gly Leu Asn Lys Ser
305 310 315 320

Lys Pro Tyr Tyr Thr Gly Glu His Ala Lys Ala Ile Gly Asn Cys Pro
325 330 335

Ile Trp Val Lys Thr Pro Leu Lys Leu Ala Asn Gly Thr Lys Tyr Arg
340 345 350

Pro Pro Ala Lys Leu Leu Lys Glu Arg Gly Phe Phe Gly Ala Ile Ala
355 360 365

Gly Phe Leu Glu Gly Gly Trp Glu Gly Met Ile Ala Gly Trp His Gly
370 375 380

Tyr Thr Ser His Gly Ala His Gly Val Ala Val Ala Ala Asp Leu Lys
385 390 395 400

Ser Thr Gln Glu Ala Ile Asn Lys Ile Thr Lys Asn Leu Asn Tyr Leu
405 410 415

Ser Glu Leu Glu Val Lys Asn Leu Gln Arg Leu Ser Gly Ala Met Asn
420 425 430

Glu Leu His Asp Glu Ile Leu Glu Leu Asp Glu Lys Val Asp Asp Leu
435 440 445

Arg Ala Asp Thr Ile Ser Ser Gln Ile Glu Leu Ala Val Leu Leu Ser

450

455

460

Asn Glu Gly Ile Ile Asn Ser Glu Asp Glu His Leu Leu Ala Leu Glu
 465 470 475 480

Arg Lys Leu Lys Lys Met Leu Gly Pro Ser Ala Val Glu Ile Gly Asn
 485 490 495

Gly Cys Phe Glu Thr Lys His Lys Cys Asn Gln Thr Cys Leu Asp Arg
 500 505 510

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

Asp Ser Leu Asn Ile Thr Ala Ala Ser Leu Asn Asp Asp Gly Leu Asp
 530 535 540

Asn His Thr Ile Leu Leu Tyr Tyr Ser Thr Ala Ala Ser Ser Leu Ala
 545 550 555 560

Val Thr Leu Met Ile Ala Ile Phe Ile Val Tyr Met Val Ser Arg Asp
 565 570 575

Asn Val Ser Cys Ser Ile Cys Leu
 580

<210> 22

<211> 345

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
 Russia/1960 sequence"

<400> 22

Asp Arg Ile Cys Thr Gly Ile Thr Ser Ser Asn Ser Pro His Val Val
 1 5 10 15

Lys Thr Ala Thr Gln Gly Glu Val Asn Val Thr Gly Val Ile Pro Leu
20 25 30

Thr Thr Thr Pro Thr Lys Ser His Phe Ala Asn Leu Lys Gly Thr Gln
35 40 45

Thr Arg Gly Lys Leu Cys Pro Asn Cys Leu Asn Cys Thr Asp Leu Asp
50 55 60

Val Ala Leu Gly Arg Pro Lys Cys Ser Gly Thr Ile Pro Ser Ala Lys
65 70 75 80

Val Ser Ile Leu His Glu Val Lys Pro Val Thr Ser Gly Cys Phe Pro
85 90 95

Ile Met His Asp Arg Thr Lys Ile Arg Gln Leu Pro Asn Leu Leu Arg
100 105 110

Gly Tyr Glu Asn Ile Arg Leu Ser Thr Arg Asn Val Ile Asn Ala Glu
115 120 125

Thr Ala Pro Gly Gly Pro Tyr Thr Val Gly Thr Ser Gly Ser Cys Pro
130 135 140

Asn Val Thr Asn Gly Lys Gly Phe Phe Glu Thr Met Ala Trp Ala Val
145 150 155 160

Pro Lys Asn Lys Asn Lys Thr Ala Thr Asn Pro Leu Thr Val Glu Val
165 170 175

Pro Tyr Ile Cys Thr Lys Gly Glu Asp Gln Ile Thr Val Trp Gly Phe
180 185 190

His Ser Asp Asp Glu Thr Gln Met Val Ile Leu Tyr Gly Asp Ser Lys
195 200 205

Pro Gln Lys Phe Thr Ser Ser Ala Asn Gly Val Thr Thr His Tyr Val
210 215 220

Ser Gln Ile Gly Gly Phe Pro Asn Gln Thr Glu Asp Glu Gly Leu Lys
225 230 235 240

Gln Ser Gly Arg Ile Val Val Asp Tyr Ile Val Gln Lys Pro Gly Lys
245 250 255

Thr Gly Thr Ile Val Tyr Gln Arg Gly Val Leu Leu Pro Gln Lys Val
260 265 270

Trp Cys Ala Ser Gly Arg Ser Lys Val Ile Lys Gly Ser Leu Pro Leu
275 280 285

Ile Gly Glu Ala Asp Cys Leu His Glu Lys Tyr Gly Gly Leu Asn Lys
290 295 300

Ser Lys Pro Tyr Tyr Thr Gly Glu His Ala Lys Ala Ile Gly Asn Cys
305 310 315 320

Pro Ile Trp Val Lys Thr Pro Leu Lys Leu Ala Asn Gly Thr Lys Tyr
325 330 335

Arg Pro Pro Ala Lys Leu Leu Lys Glu
340 345

<210> 23
<211> 581
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
HongKong/1972 sequence"

<400> 23
Met Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn Ala Asp
1 5 10 15

Arg Ile Cys Thr Gly Ile Thr Ser Ser Asn Ser Pro His Val Val Lys

20

25

30

Thr Ala Thr Gln Gly Glu Val Asn Val Thr Gly Val Ile Pro Leu Thr
 35 40 45

Thr Thr Pro Thr Lys Ser His Phe Ala Asn Leu Lys Gly Thr Gln Thr
 50 55 60

Arg Gly Lys Leu Cys Pro Asn Cys Leu Asn Cys Thr Asp Leu Asp Val
 65 70 75 80

Ala Leu Gly Arg Pro Lys Cys Met Gly Thr Ile Pro Ser Ala Lys Ala
 85 90 95

Ser Ile Leu His Glu Val Lys Pro Val Thr Ser Gly Cys Phe Pro Ile
 100 105 110

Met His Asp Arg Thr Lys Ile Arg Gln Leu Pro Asn Leu Leu Arg Gly
 115 120 125

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

Ala Pro Gly Gly Pro Tyr Ile Val Gly Ile Ser Gly Ser Cys Pro Asn
 145 150 155 160

Val Thr Asn Gly Asn Gly Phe Phe Ala Thr Met Ala Trp Ala Val Pro
 165 170 175

Lys Asn Lys Thr Ala Thr Asn Pro Leu Thr Val Glu Val Pro Tyr Ile
 180 185 190

Cys Ala Lys Gly Glu Asp Gln Ile Thr Val Trp Gly Phe His Ser Asp
 195 200 205

Asn Glu Ile Gln Met Val Lys Leu Tyr Gly Asp Ser Lys Pro Gln Lys
 210 215 220

Phe Thr Ser Ser Ala Asn Gly Val Thr Thr His Tyr Val Ser Gln Ile
225 230 235 240

Gly Gly Phe Pro Asn Gln Ala Glu Asp Glu Gly Leu Pro Gln Ser Gly
245 250 255

Arg Ile Val Val Asp Tyr Met Val Gln Lys Pro Gly Lys Thr Gly Thr
260 265 270

Ile Ala Tyr Gln Arg Gly Val Leu Leu Pro Gln Lys Val Trp Cys Ala
275 280 285

Ser Gly Arg Ser Lys Val Ile Lys Gly Ser Leu Pro Leu Ile Gly Glu
290 295 300

Ala Asp Cys Leu His Glu Lys Tyr Gly Gly Leu Asn Lys Ser Lys Pro
305 310 315 320

Tyr Tyr Thr Gly Glu His Ala Lys Ala Ile Gly Asn Cys Pro Ile Trp
325 330 335

Val Lys Thr Pro Leu Lys Leu Ala Asn Gly Thr Lys Tyr Arg Pro Pro
340 345 350

Ala Lys Leu Leu Lys Glu Arg Gly Phe Phe Gly Ala Ile Ala Gly Phe
355 360 365

Leu Glu Gly Gly Trp Glu Gly Met Ile Ala Gly Trp His Gly Tyr Thr
370 375 380

Ser His Gly Ala His Gly Val Ala Val Ala Ala Asp Leu Lys Ser Thr
385 390 395 400

Gln Glu Ala Ile Asn Lys Ile Thr Lys Asn Leu Asn Ser Leu Ser Glu
405 410 415

Leu Glu Val Lys Asn Leu Gln Arg Leu Ser Gly Ala Met Asp Glu Leu

420

425

430

His Asn Glu Ile Leu Glu Leu Asp Glu Lys Val Asp Asp Leu Arg Ala
435 440 445

Asp Thr Ile Ser Ser Gln Ile Glu Leu Ala Val Leu Leu Ser Asn Glu
450 455 460

Gly Ile Ile Asn Ser Glu Asp Glu His Leu Leu Ala Leu Glu Arg Lys
465 470 475 480

Leu Lys Lys Met Leu Gly Pro Ser Ala Val Asp Ile Gly Asn Gly Cys
485 490 495

Phe Glu Thr Lys His Lys Cys Asn Gln Thr Cys Leu Asp Arg Ile Ala
500 505 510

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

Leu Asn Ile Thr Ala Ala Ser Leu Asn Asp Asp Gly Leu Asp Asn His
530 535 540

Thr Ile Leu Leu Tyr Tyr Ser Thr Ala Ala Ser Ser Leu Ala Val Thr
545 550 555 560

Leu Met Ile Ala Ile Phe Ile Val Tyr Met Val Ser Arg Asp Asn Val
565 570 575

Ser Cys Ser Ile Cys
580

<210> 24

<211> 582

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
Singapore/1979 sequence"

<400> 24

Met Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn Ala Asp
1 5 10 15

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

Thr Ala Thr Gln Gly Glu Val Asn Val Thr Gly Val Ile Pro Leu Thr
35 40 45

Thr Thr Pro Thr Lys Ser His Phe Ala Asn Leu Lys Gly Thr Lys Thr
50 55 60

Arg Gly Lys Leu Cys Pro Asn Cys Leu Asn Cys Thr Asp Leu Asp Val
65 70 75 80

Ala Leu Gly Arg Pro Lys Cys Met Gly Thr Ile Pro Ser Ala Lys Ala
85 90 95

Ser Ile Leu His Glu Val Lys Pro Val Thr Ser Gly Cys Phe Pro Ile
100 105 110

Met His Asp Arg Thr Lys Ile Arg Gln Leu Pro Asn Leu Leu Arg Gly
115 120 125

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

Ala Pro Gly Gly Pro Tyr Ile Ile Gly Thr Ser Gly Ser Cys Pro Asn
145 150 155 160

Val Thr Asn Gly Asn Gly Phe Phe Ala Thr Met Ala Trp Ala Val Pro
165 170 175

Lys Asp Asn Lys Thr Ala Thr Asn Pro Leu Thr Val Glu Val Pro Tyr
180 185 190

Ile Cys Thr Lys Gly Glu Asp Gln Ile Thr Val Trp Gly Phe His Ser
195 200 205

Asp Thr Glu Thr Gln Met Val Lys Leu Tyr Gly Asp Ser Lys Pro Gln
210 215 220

Lys Phe Thr Ser Ser Ala Asn Gly Val Thr Thr His Tyr Val Ser Gln
225 230 235 240

Ile Gly Gly Phe Pro Asn Gln Thr Glu Asp Gly Gly Leu Pro Gln Ser
245 250 255

Gly Arg Ile Val Val Asp Tyr Met Val Gln Lys Pro Gly Lys Thr Gly
260 265 270

Thr Ile Val Tyr Gln Arg Gly Val Leu Leu Pro Gln Lys Val Trp Cys
275 280 285

Ala Ser Gly Arg Ser Lys Val Ile Lys Gly Ser Leu Pro Leu Ile Gly
290 295 300

Glu Ala Asp Cys Leu His Glu Lys Tyr Gly Gly Leu Asn Lys Ser Lys
305 310 315 320

Pro Tyr Tyr Thr Gly Glu His Ala Lys Ala Ile Gly Asn Cys Pro Ile
325 330 335

Trp Val Lys Thr Pro Leu Lys Leu Ala Asn Gly Thr Lys Tyr Arg Pro
340 345 350

Pro Ala Lys Leu Leu Lys Glu Arg Gly Phe Phe Gly Ala Ile Ala Gly
355 360 365

Phe Leu Glu Gly Gly Trp Glu Gly Met Ile Ala Gly Trp His Gly Tyr
370 375 380

Thr Ser His Gly Ala His Gly Val Ala Val Ala Ala Asp Leu Lys Ser
385 390 395 400

Thr Gln Glu Ala Ile Asn Lys Ile Thr Lys Asn Leu Asn Ser Leu Ser
405 410 415

Glu Leu Glu Val Lys Asn Leu Gln Arg Leu Ser Gly Ala Met Asp Glu
420 425 430

Leu His Asn Glu Ile Leu Glu Leu Asp Glu Lys Val Asp Asp Leu Arg
435 440 445

Ala Asp Thr Ile Ser Ser Gln Ile Glu Leu Ala Val Leu Leu Ser Asn
450 455 460

Glu Gly Ile Ile Asn Ser Glu Asp Glu His Leu Leu Ala Leu Glu Arg
465 470 475 480

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

Cys Phe Glu Thr Lys His Lys Cys Asn Gln Thr Cys Leu Asp Arg Ile
500 505 510

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

Ser Leu Asn Ile Thr Ala Ala Ser Leu Asn Asp Asp Gly Leu Asp Asn
530 535 540

His Thr Ile Leu Leu Tyr Tyr Ser Thr Ala Ala Ser Ser Leu Ala Val
545 550 555 560

Thr Leu Met Ile Ala Ile Phe Ile Val Tyr Met Val Ser Arg Asp Asn
565 570 575

Val Ser Cys Ser Ile Cys
580

<210> 25
<211> 582
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Yamagata/1988 sequence"

<400> 25
Met Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn Ala Asp
1 5 10 15

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

Thr Ala Thr Gln Gly Glu Val Asn Val Thr Gly Val Ile Pro Leu Thr
35 40 45

Thr Thr Pro Thr Lys Ser His Phe Ala Asn Leu Lys Gly Thr Lys Thr
50 55 60

Arg Gly Lys Leu Cys Pro Asn Cys Leu Asn Cys Thr Asp Leu Asp Val
65 70 75 80

Ala Leu Gly Arg Pro Met Cys Met Gly Thr Ile Pro Ser Ala Lys Ala
85 90 95

Ser Ile Leu His Glu Val Arg Pro Val Thr Ser Gly Cys Phe Pro Ile
100 105 110

Met His Asp Arg Thr Lys Ile Arg Gln Leu Pro Asn Leu Leu Arg Gly
115 120 125

Tyr Glu Asn Ile Arg Leu Ser Thr His Asn Val Ile Asn Ala Glu Arg
130 135 140

Ala Pro Gly Gly Pro Tyr Arg Leu Gly Thr Ser Gly Ser Cys Pro Asn

145		150		155		160
Val Thr Ser Arg Asn Gly Phe Phe Ala Thr Met Ala Trp Ala Val Pro						
		165		170		175
Arg Asp Asn Lys Thr Ala Thr Asn Pro Leu Thr Val Glu Val Pro Tyr						
		180		185		190
Ile Cys Thr Lys Gly Glu Asp Gln Ile Thr Val Trp Gly Phe His Ser						
		195		200		205
Asp Asp Lys Thr Gln Met Lys Asn Leu Tyr Gly Asp Ser Asn Pro Gln						
		210		215		220
Lys Phe Thr Ser Ser Ala Asn Gly Val Thr Thr His Tyr Val Ser Gln						
		225		230		235
						240
Ile Gly Asp Phe Pro Asn Gln Thr Glu Asp Gly Gly Leu Pro Gln Ser						
		245		250		255
Gly Arg Ile Val Val Asp Tyr Met Val Gln Lys Pro Gly Lys Thr Gly						
		260		265		270
Thr Ile Val Tyr Gln Arg Gly Val Leu Leu Pro Gln Lys Val Trp Cys						
		275		280		285
Ala Ser Gly Arg Ser Lys Val Ile Lys Gly Ser Leu Pro Leu Ile Gly						
		290		295		300
Glu Ala Asp Cys Leu His Glu Lys Tyr Gly Gly Leu Asn Lys Ser Lys						
		305		310		315
						320
Pro Tyr Tyr Thr Gly Glu His Ala Lys Ala Ile Gly Asn Cys Pro Ile						
		325		330		335
Trp Val Lys Thr Pro Leu Lys Leu Ala Asn Gly Thr Lys Tyr Arg Pro						
		340		345		350

Pro Ala Lys Leu Leu Lys Glu Arg Gly Phe Phe Gly Ala Ile Ala Gly
355 360 365

Phe Leu Glu Gly Gly Trp Glu Gly Met Ile Ala Gly Trp His Gly Tyr
370 375 380

Thr Ser His Gly Ala His Gly Val Ala Val Ala Ala Asp Leu Lys Ser
385 390 395 400

Thr Gln Glu Ala Ile Asn Lys Ile Thr Lys Asn Leu Asn Ser Leu Ser
405 410 415

Glu Leu Glu Val Lys Asn Leu Gln Arg Leu Ser Gly Ala Met Asp Glu
420 425 430

Leu His Asn Glu Ile Leu Glu Leu Asp Glu Lys Val Asp Asp Leu Arg
435 440 445

Ala Asp Thr Ile Ser Ser Gln Ile Glu Leu Ala Val Leu Leu Ser Asn
450 455 460

Glu Gly Ile Ile Asn Ser Glu Asp Glu His Leu Leu Ala Leu Glu Arg
465 470 475 480

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

Cys Phe Glu Thr Lys His Lys Cys Asn Gln Thr Cys Leu Asp Arg Ile
500 505 510

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

Ser Leu Asn Ile Thr Ala Ala Ser Leu Asn Asp Asp Gly Leu Asp Asn
530 535 540

His Thr Ile Leu Leu Tyr Tyr Ser Thr Ala Ala Ser Ser Leu Ala Val

545 550 555 560

Thr Leu Met Ile Ala Ile Phe Ile Val Tyr Met Val Ser Arg Asp Asn
565 570 575

Val Ser Cys Ser Ile Cys
580

<210> 26
<211> 584
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Malaysia/2004 sequence"

<220>
<221> MOD_RES
<222> (214)..(214)
<223> Any amino acid

<400> 26
Met Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn Ala Asp
1 5 10 15

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

Thr Ala Thr Gln Gly Glu Val Asn Val Thr Gly Val Ile Pro Leu Thr
35 40 45

Thr Thr Pro Thr Lys Ser His Phe Ala Asn Leu Lys Gly Thr Glu Thr
50 55 60

Arg Gly Lys Leu Cys Pro Lys Cys Leu Asn Cys Thr Asp Leu Asp Val
65 70 75 80

Ala Leu Gly Arg Pro Lys Cys Thr Gly Asn Ile Pro Ser Ala Arg Val
85 90 95

Ser Ile Leu His Glu Val Arg Pro Val Thr Ser Gly Cys Phe Pro Ile
100 105 110

Met His Asp Arg Thr Lys Ile Arg Gln Leu Pro Asn Leu Leu Arg Gly
115 120 125

Tyr Glu His Ile Arg Leu Ser Thr His Asn Val Ile Asn Ala Glu Asn
130 135 140

Ala Pro Gly Gly Pro Tyr Lys Ile Gly Thr Ser Gly Ser Cys Pro Asn
145 150 155 160

Val Thr Asn Gly Asn Gly Phe Phe Ala Thr Met Ala Trp Ala Val Pro
165 170 175

Lys Asn Asp Asn Asn Lys Thr Ala Thr Asn Ser Leu Thr Ile Glu Val
180 185 190

Pro Tyr Ile Cys Thr Glu Gly Glu Asp Gln Ile Thr Val Trp Gly Phe
195 200 205

His Ser Asp Asn Glu Xaa Gln Met Ala Lys Leu Tyr Gly Asp Ser Lys
210 215 220

Pro Gln Lys Phe Thr Ser Ser Ala Asn Gly Val Thr Thr His Tyr Val
225 230 235 240

Ser Gln Ile Gly Gly Phe Pro Asn Gln Thr Glu Asp Gly Gly Leu Pro
245 250 255

Gln Ser Gly Arg Ile Val Val Asp Tyr Met Val Gln Lys Ser Gly Lys
260 265 270

Thr Gly Thr Ile Thr Tyr Gln Arg Gly Ile Leu Leu Pro Gln Lys Val
275 280 285

Trp Cys Ala Ser Gly Arg Ser Lys Val Ile Lys Gly Ser Leu Pro Leu
290 295 300

Ile Gly Glu Ala Asp Cys Leu His Glu Lys Tyr Gly Gly Leu Asn Lys
305 310 315 320

Ser Lys Pro Tyr Tyr Thr Gly Glu His Ala Lys Ala Ile Gly Asn Cys
325 330 335

Pro Ile Trp Val Lys Thr Pro Leu Lys Leu Ala Asn Gly Thr Lys Tyr
340 345 350

Arg Pro Pro Ala Lys Leu Leu Lys Glu Arg Gly Phe Phe Gly Ala Ile
355 360 365

Ala Gly Phe Leu Glu Gly Gly Trp Glu Gly Met Ile Ala Gly Trp His
370 375 380

Gly Tyr Thr Ser His Gly Ala His Gly Val Ala Val Ala Ala Asp Leu
385 390 395 400

Lys Ser Thr Gln Glu Ala Ile Asn Lys Ile Thr Lys Asn Leu Asn Ser
405 410 415

Leu Ser Glu Leu Glu Val Lys Asn Leu Gln Arg Leu Ser Gly Ala Met
420 425 430

Asp Glu Leu His Asn Glu Ile Leu Glu Leu Asp Glu Lys Val Asp Asp
435 440 445

Leu Arg Ala Asp Thr Ile Ser Ser Gln Ile Glu Leu Ala Val Leu Leu
450 455 460

Ser Asn Glu Gly Ile Ile Asn Ser Glu Asp Glu His Leu Leu Ala Leu
465 470 475 480

Glu Arg Lys Leu Lys Lys Met Leu Gly Pro Ser Ala Val Glu Ile Gly
485 490 495

Asn Gly Cys Phe Glu Thr Lys His Lys Cys Asn Gln Thr Cys Leu Asp
500 505 510

Arg Ile Ala Ala Gly Thr Phe Asp Ala Gly Glu Phe Ser Leu Pro Thr
515 520 525

Phe Asp Ser Leu Asn Ile Thr Ala Ala Ser Leu Asn Asp Asp Gly Leu
530 535 540

Asp Asn His Thr Ile Leu Leu Tyr Tyr Ser Thr Ala Ala Ser Ser Leu
545 550 555 560

Ala Val Thr Leu Met Ile Ala Ile Phe Val Val Tyr Met Val Ser Arg
565 570 575

Asp Asn Val Ser Cys Ser Ile Cys
580

<210> 27

<211> 583

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
Florida/2006 sequence"

<400> 27

Met Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn Ala Asp
1 5 10 15

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

Thr Ala Thr Gln Gly Glu Val Asn Val Thr Gly Val Ile Pro Leu Thr
35 40 45

Thr Thr Pro Thr Lys Ser Tyr Phe Ala Asn Leu Lys Gly Thr Arg Thr

50

55

60

Arg Gly Lys Leu Cys Pro Asp Cys Leu Asn Cys Thr Asp Leu Asp Val
65 70 75 80

Ala Leu Gly Arg Pro Met Cys Val Gly Thr Thr Pro Ser Ala Lys Ala
85 90 95

Ser Ile Leu His Glu Val Lys Pro Val Thr Ser Gly Cys Phe Pro Ile
100 105 110

Met His Asp Arg Thr Lys Ile Arg Gln Leu Pro Asn Leu Leu Arg Gly
115 120 125

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

Ala Pro Gly Gly Pro Tyr Arg Leu Gly Thr Ser Gly Ser Cys Pro Asn
145 150 155 160

Ala Thr Ser Lys Ser Gly Phe Phe Ala Thr Met Ala Trp Ala Val Pro
165 170 175

Lys Asp Asn Asn Lys Asn Ala Thr Asn Pro Leu Thr Val Glu Val Pro
180 185 190

Tyr Ile Cys Thr Glu Gly Glu Asp Gln Ile Thr Val Trp Gly Phe His
195 200 205

Ser Asp Asp Lys Thr Gln Met Lys Asn Leu Tyr Gly Asp Ser Asn Pro
210 215 220

Gln Lys Phe Thr Ser Ser Ala Asn Gly Val Thr Thr His Tyr Val Ser
225 230 235 240

Gln Ile Gly Ser Phe Pro Asp Gln Thr Glu Asp Gly Gly Leu Pro Gln
245 250 255

Ser Gly Arg Ile Val Val Asp Tyr Met Met Gln Lys Pro Gly Lys Thr
260 265 270

Gly Thr Ile Val Tyr Gln Arg Gly Val Leu Leu Pro Gln Lys Val Trp
275 280 285

Cys Ala Ser Gly Arg Ser Lys Val Ile Lys Gly Ser Leu Pro Leu Ile
290 295 300

Gly Glu Ala Asp Cys Leu His Glu Lys Tyr Gly Gly Leu Asn Lys Ser
305 310 315 320

Lys Pro Tyr Tyr Thr Gly Glu His Ala Lys Ala Ile Gly Asn Cys Pro
325 330 335

Ile Trp Val Lys Thr Pro Leu Lys Leu Ala Asn Gly Thr Lys Tyr Arg
340 345 350

Pro Pro Ala Lys Leu Leu Lys Glu Arg Gly Phe Phe Gly Ala Ile Ala
355 360 365

Gly Phe Leu Glu Gly Gly Trp Glu Gly Met Ile Ala Gly Trp His Gly
370 375 380

Tyr Thr Ser His Gly Ala His Gly Val Ala Val Ala Ala Asp Leu Lys
385 390 395 400

Ser Thr Gln Glu Ala Ile Asn Lys Ile Thr Lys Asn Leu Asn Ser Leu
405 410 415

Ser Glu Leu Glu Val Lys Asn Leu Gln Arg Leu Ser Gly Ala Met Asp
420 425 430

Glu Leu His Asn Glu Ile Leu Glu Leu Asp Glu Lys Val Asp Asp Leu
435 440 445

Arg Ala Asp Thr Ile Ser Ser Gln Ile Glu Leu Ala Val Leu Leu Ser

450

455

460

Asn Glu Gly Ile Ile Asn Ser Glu Asp Glu His Leu Leu Ala Leu Glu
 465 470 475 480

Arg Lys Leu Lys Lys Met Leu Gly Pro Ser Ala Val Glu Ile Gly Asn
 485 490 495

Gly Cys Phe Glu Thr Lys His Lys Cys Asn Gln Thr Cys Leu Asp Arg
 500 505 510

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

Asp Ser Leu Asn Ile Thr Ala Ala Ser Leu Asn Asp Asp Gly Leu Asp
 530 535 540

Asn His Thr Ile Leu Leu Tyr Tyr Ser Thr Ala Ala Ser Ser Leu Ala
 545 550 555 560

Val Thr Leu Met Leu Ala Ile Phe Ile Val Tyr Met Val Ser Arg Asp
 565 570 575

Asn Val Ser Cys Ser Ile Cys
 580

<210> 28

<211> 585

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
 FluB/2018 & 2019 consensus sequence "

<400> 28

Met Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn Ala Asp
 1 5 10 15

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

Thr Ala Thr Gln Gly Glu Val Asn Val Thr Gly Val Ile Pro Leu Thr
35 40 45

Thr Thr Pro Thr Lys Ser Tyr Phe Ala Asn Leu Lys Gly Thr Arg Thr
50 55 60

Arg Gly Lys Leu Cys Pro Asp Cys Leu Asn Cys Thr Asp Leu Asp Val
65 70 75 80

Ala Leu Gly Arg Pro Met Cys Val Gly Thr Thr Pro Ser Ala Lys Ala
85 90 95

Ser Ile Leu His Glu Val Arg Pro Val Thr Ser Gly Cys Phe Pro Ile
100 105 110

Met His Asp Arg Thr Lys Ile Arg Gln Leu Pro Asn Leu Leu Arg Gly
115 120 125

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

Ala Pro Gly Gly Pro Tyr Arg Leu Gly Thr Ser Gly Ser Cys Pro Asn
145 150 155 160

Ala Thr Ser Lys Ile Gly Phe Phe Ala Thr Met Ala Trp Ala Val Pro
165 170 175

Lys Asp Asn Lys Tyr Lys Asn Ala Thr Asn Pro Gln Thr Val Glu Val
180 185 190

Pro Tyr Ile Cys Thr Glu Gly Glu Asp Gln Ile Thr Val Trp Gly Phe
195 200 205

His Ser Asp Asn Lys Thr Gln Met Lys Ser Leu Tyr Gly Asp Ser Asn
210 215 220

Pro Gln Lys Phe Thr Ser Ser Ala Asn Gly Val Thr Thr His Tyr Val
225 230 235 240

Ser Gln Ile Gly Asp Phe Pro Asp Gln Thr Glu Asp Gly Gly Leu Pro
245 250 255

Gln Ser Gly Arg Ile Val Val Asp Tyr Met Val Gln Lys Pro Gly Lys
260 265 270

Thr Gly Thr Ile Val Tyr Gln Arg Gly Val Leu Leu Pro Gln Lys Val
275 280 285

Trp Cys Ala Ser Gly Arg Ser Lys Val Ile Lys Gly Ser Leu Pro Leu
290 295 300

Ile Gly Glu Ala Asp Cys Leu His Glu Glu Tyr Gly Gly Leu Asn Lys
305 310 315 320

Ser Lys Pro Tyr Tyr Thr Gly Lys His Ala Lys Ala Ile Gly Asn Cys
325 330 335

Pro Ile Trp Val Lys Thr Pro Leu Lys Leu Ala Asn Gly Thr Lys Tyr
340 345 350

Arg Pro Pro Ala Lys Leu Leu Lys Glu Arg Gly Phe Phe Gly Ala Ile
355 360 365

Ala Gly Phe Leu Glu Gly Gly Trp Glu Gly Met Ile Ala Gly Trp His
370 375 380

Gly Tyr Thr Ser His Gly Ala His Gly Val Ala Val Ala Ala Asp Leu
385 390 395 400

Lys Ser Thr Gln Glu Ala Ile Asn Lys Ile Thr Lys Asn Leu Asn Ser
405 410 415

Leu Ser Glu Leu Glu Val Lys Asn Leu Gln Arg Leu Ser Gly Ala Met
420 425 430

Asp Glu Leu His Asn Glu Ile Leu Glu Leu Asp Glu Lys Val Asp Asp
435 440 445

Leu Arg Ala Asp Thr Ile Ser Ser Gln Ile Glu Leu Ala Val Leu Leu
450 455 460

Ser Asn Glu Gly Ile Ile Asn Ser Glu Asp Glu His Leu Leu Ala Leu
465 470 475 480

Glu Arg Lys Leu Lys Lys Met Leu Gly Pro Ser Ala Val Asp Ile Gly
485 490 495

Asn Gly Cys Phe Glu Thr Lys His Lys Cys Asn Gln Thr Cys Leu Asp
500 505 510

Arg Ile Ala Ala Gly Thr Phe Asn Ala Gly Glu Phe Ser Leu Pro Thr
515 520 525

Phe Asp Ser Leu Asn Ile Thr Ala Ala Ser Leu Asn Asp Asp Gly Leu
530 535 540

Asp Asn His Thr Ile Leu Leu Tyr Tyr Ser Thr Ala Ala Ser Ser Leu
545 550 555 560

Ala Val Thr Leu Met Leu Ala Ile Phe Ile Val Tyr Met Val Ser Arg
565 570 575

Asp Asn Val Ser Cys Ser Ile Cys Leu
580 585

<210> 29

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 29

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

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

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Thr Tyr Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser Ser Leu Tyr
65 70 75 80

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

Ala Arg Asp Arg Gly Thr Thr Met Val Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 30

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 30

Gly Phe Thr Phe Ser Asp Tyr Tyr
1 5

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

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

<400> 31
Ile Thr Tyr Ser Gly Ser Thr Ile
1 5

<210> 32
<211> 13
<212> PRT
<213> Artificial Sequence

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

<400> 32
Ala Arg Asp Arg Gly Thr Thr Met Val Pro Phe Asp Tyr
1 5 10

<210> 33
<211> 107
<212> PRT
<213> Artificial Sequence

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

<400> 33
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

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

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Gly Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 34
<211> 6
<212> PRT
<213> Artificial Sequence

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

<400> 34
Gln Asp Ile Thr Asn Tyr
1 5

<210> 35
<211> 3
<212> PRT
<213> Artificial Sequence

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

<400> 35
Ala Ala Ser
1

<210> 36
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 36
Gln Gln Tyr Asp Asn Leu Pro Leu Thr
1 5

<210> 37
<211> 450
<212> PRT
<213> Artificial Sequence

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

<400> 37
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

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

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Thr Tyr Ser Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser Ser Leu Tyr
65 70 75 80

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

Ala Arg Asp Arg Gly Thr Thr Met Val Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

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

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

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

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

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

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

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg

290

295

300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

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

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 38

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 38

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

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

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

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

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Gly Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 39
<211> 360
<212> DNA
<213> Artificial Sequence

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

<400> 39
caggtgcagc tgggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgccaggct 120
ccagggaagg ggctggagtg ggtttcatac attacttata gtggtagtac catatactac 180
gcagactctg tgaagggccg attcaccatc tccagggaca acgccaagag ctactgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagatcgc 300
ggtacaacta tgggtcccctt tgactactgg ggccaggga ccttggtcac cgtctcctca 360

<210> 40
<211> 24
<212> DNA
<213> Artificial Sequence

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

<400> 40
ggattcacct tcagtgacta ctac 24

<210> 41
<211> 24

<212> DNA
 <213> Artificial Sequence

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

 <400> 41
 attacttata gtggtagtag cata 24

 <210> 42
 <211> 39
 <212> DNA
 <213> Artificial Sequence

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

 <400> 42
 gcgagagatc gcggtacaac tatgggtcccc ttgactac 39

 <210> 43
 <211> 321
 <212> DNA
 <213> Artificial Sequence

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

 <400> 43
 gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc aggcgagtca ggacattacc aactatttaa attggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctacgct gcatccaatt tggaaacagg ggtcccatca 180
 aggttcagtg gaagtggatc tgggacagat ttactttca ccatcagcgg cctgcagcct 240
 gaagatattg caacatatta ctgtcaacag tatgataatc tccctctcac tttcggcgga 300
 gggaccaagg tggagatcaa a 321

<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

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

<400> 44
caggacatta ccaactat

18

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

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

<400> 45
gctgcatcc

9

<210> 46
<211> 27
<212> DNA
<213> Artificial Sequence

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

<400> 46
caacagtatg ataatctccc tctcact

27

<210> 47
<211> 1353
<212> DNA
<213> Artificial Sequence

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

polynucleotide"

<400> 47

cagggtgcagc tgggtggagtc tggggggaggc ttgggtcaagc ctggagggtc cctgagactc	60
tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgccaggct	120
ccagggaagg ggctggagtg ggtttcatatc attacttata gtggtagtag catatactac	180
gcagactctg tgaagggccg attcaccatc tccaggggaca acgccaagag ctactgtat	240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagatcgc	300
ggtacaacta tgggtccccctt tgactactgg ggccaggga ccctgggtcac cgtctcctca	360
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg	420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg	480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc	600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	660
aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctggggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct	780
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg	840
tacgtggacg gcgtggagggt gcataatgcc aagacaaaagc gcggggagga gcagtacaac	900
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaagggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1020
aaagccaaaag ggagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag	1080
ctgaccaaga accagggtcag cctgacctgc ctgggtcaaaag gcttctatcc cagcgacatc	1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1200
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcagggtg	1260
cagcaggggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	1320
cagaagtccc tctccctgtc tccgggtaaa tga	1353

<210> 48
<211> 645
<212> DNA
<213> Artificial Sequence

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

<400> 48
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc aggcgagtca ggacattacc aactatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctacgct gcatccaatt tggaaacagg ggtcccatca 180
aggttcagtg gaagtggatc tgggacagat ttacttttca ccatcagcgg cctgcagcct 240
gaagatattg caacatatta ctgtcaacag tatgataatc tccctctcac tttcggcgga 300
gggaccaagg tggagatcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttag 645

<210> 49
<211> 120
<212> PRT
<213> Artificial Sequence

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

<400> 49
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Thr Phe Ser Asn Ala

20

25

30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Arg Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala
50 55 60

Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Thr Ala Arg Trp Asp Trp Tyr Phe Asp Leu Trp Gly Arg
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 50

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 50

Gly Ile Thr Phe Ser Asn Ala Trp
1 5

<210> 51

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

peptide"

<400> 51

Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr
1 5 10

<210> 52

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 52

Thr Thr Ala Arg Trp Asp Trp Tyr Phe Asp Leu
1 5 10

<210> 53

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 53

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

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

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

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

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro

65

70

75

80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln His Asp Asp Leu Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 54

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 54

Gln Asp Ile Trp Asn Tyr
1 5

<210> 55

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 55

Asp Ala Ser
1

<210> 56

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 56

Gln Gln His Asp Asp Leu Pro Pro Thr
1 5

<210> 57

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 57

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Thr Phe Ser Asn Ala
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Arg Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala
50 55 60

Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Thr Ala Arg Trp Asp Trp Tyr Phe Asp Leu Trp Gly Arg
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala

130

135

140

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

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

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

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220

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

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335

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

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 58

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 58

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

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

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

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

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln His Asp Asp Leu Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 59
<211> 360
<212> DNA
<213> Artificial Sequence

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

<400> 59
gaggtgcagc tgggtggagtc tggggggaggc ttggtaaagc ctgggggggtc ccttagactc 60
tcctgtgcag cctctggaat cactttcagt aacgcctgga tgagttgggt ccgccaggct 120
ccagggaagg ggctggagtg ggttggccgt attaaaagca aaactgatgg tgggacaaca 180
gactacgccg caccctgtaa aggagattc accatctcaa gagatgattc aaaaaacacg 240
ctgtatctac aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtaccaca 300
gcgaggtggg actggtactt cgatctctgg ggccgtggca ccctgggtcac tgtctcctca 360

<210> 60
<211> 24
<212> DNA
<213> Artificial Sequence

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

<400> 60
ggaatcactt tcagtaacgc ctgg 24

<210> 61
<211> 30
<212> DNA
<213> Artificial Sequence

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

<400> 61
attaaaagca aaactgatgg tgggacaaca 30

<210> 62
<211> 33
<212> DNA
<213> Artificial Sequence

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

<400> 62
accacagcga ggtgggactg gtacttcgat ctc 33

<210> 63
<211> 321
<212> DNA
<213> Artificial Sequence

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

<400> 63
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc aggcgagtca ggacatttgg aattatataa attggtatca gcagaaacca 120
gggaaggccc ctaagctcct gatctacgat gcatccaatt tgaaaacagg ggtcccatca 180
aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240
gaagatattg caacatatta ctgtcaacag catgatgatc tccctccgac cttcggccaa 300
gggaccaagg tggaaatcaa a 321

<210> 64
<211> 18
<212> DNA
<213> Artificial Sequence

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

<400> 64
caggacattt ggaattat 18

<210> 65
<211> 9
<212> DNA
<213> Artificial Sequence

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

<400> 65
gatgcatcc 9

<210> 66
<211> 27
<212> DNA
<213> Artificial Sequence

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

<400> 66
caacagcatg atgatctccc tccgacc 27

<210> 67
<211> 1353
<212> DNA
<213> Artificial Sequence

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

<400> 67
gaggtgcagc tgggtggagtc tggggggaggc ttggtaaagc ctgggggggtc ccttagactc 60

tcctgtgcag cctctggaat cactttcagt aacgcctgga tgagttgggt ccgccaggct 120

ccagggaagg ggctggagtg ggttggccgt attaaaagca aaactgatgg tgggacaaca 180

gactacgccg caccctgaa aggcagattc accatctcaa gagatgattc aaaaaacacg 240

ctgtatctac aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtaccaca	300
gcgagggtggg actgggtactt cgatctcttg ggccgtggca ccctgggtcac tgtctcctca	360
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg	420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg	480
tggaaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc	600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	660
aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct	780
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac	900
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaagggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1020
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag	1080
ctgaccaaga accagggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc	1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1200
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcagggtg	1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	1320
cagaagtccc tctccctgtc tccgggtaaa tga	1353

<210> 68

<211> 645

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 68
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc aggcgagtca ggacatttgg aattatataa attggtatca gcagaaacca 120
gggaaggccc ctaagctcct gatctacgat gcatccaatt tgaaaacagg ggtcccatca 180
aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240
gaagatattg caacatatta ctgtcaacag catgatgatc tccctccgac cttcggccaa 300
gggaccaagg tggaaatcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttag 645

<210> 69
<211> 120
<212> PRT
<213> Artificial Sequence

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

<400> 69
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Ala Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Ser Gly Ser Asp Tyr Gly Asp Tyr Leu Leu Val Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 70

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 70

Gly Phe Thr Phe Ser Asn Tyr Ala
1 5

<210> 71

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 71

Ile Ser Tyr Asp Gly Ser Asn Lys
1 5

<210> 72

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 72

Ala Ser Gly Ser Asp Tyr Gly Asp Tyr Leu Leu Val Tyr
1 5 10

<210> 73

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 73

Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

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

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

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Leu Thr Ser Ile
85 90 95

Ser Thr Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 74
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 74
Ser Ser Asp Val Gly Gly Tyr Asn Tyr
1 5

<210> 75
<211> 3
<212> PRT
<213> Artificial Sequence

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

<400> 75
Asp Val Ser
1

<210> 76
<211> 10
<212> PRT
<213> Artificial Sequence

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

<400> 76
Asn Ser Leu Thr Ser Ile Ser Thr Trp Val
1 5 10

<210> 77
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<221> source

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

<400> 77

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Ala Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Ser Gly Ser Asp Tyr Gly Asp Tyr Leu Leu Val Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

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

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

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

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

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

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

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

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

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp

370

375

380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Lys
 450

<210> 78

<211> 216

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 78

Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30

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

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

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Leu Thr Ser Ile
85 90 95

Ser Thr Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
115 120 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

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

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

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

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 79

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 79
 caggtgcagc tgggtggagtc tgggggaggc gtgggtccagc ctgggaggtc cctgagactc 60
 tcctgtgcag cctctggatt caccttcagt aactatgcta tgtactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgag aactgaggac acggctgtgt attactgtgc gagtggctcc 300
 gactacggtg actacttatt ggtttactgg ggccagggaa ccctgggtcac cgtctcctca 360

<210> 80
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 oligonucleotide"

<400> 80
 ggattcacct tcagtaacta tgct 24

<210> 81
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 oligonucleotide"

<400> 81
 atatcatatg atggaagtaa taaa 24

<210> 82
 <211> 39
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

oligonucleotide"

<400> 82

gcgagtggct ccgactacgg tgactactta ttggtttac

39

<210> 83

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 83

cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggg ggttataact atgtctcctg gtaccaacaa 120

caccaggca aagcccccaa actcatgatt tatgatgtca gtaagcggcc ctcaggggtt 180

tctaatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

cagtctgagg acgaggctga ttattactgc aactctttga caagcatcag cacttgggtg 300

ttcggcggag ggaccaagct gaccgtccta 330

<210> 84

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 84

agcagtgacg ttggtggtta taactat

27

<210> 85

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

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

<400> 85
gatgtcagt

9

<210> 86
<211> 30
<212> DNA
<213> Artificial Sequence

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

<400> 86
aactctttga caagcatcag cacttgggtg

30

<210> 87
<211> 1353
<212> DNA
<213> Artificial Sequence

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

<400> 87
cagggtgcagc tgggtggagtc tggggggaggc gtgggtccagc ctgggagggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt aactatgcta tgtactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag aactgaggac acggctgtgt attactgtgc gagtggctcc 300
gactacggtg actacttatt ggtttactgg ggccaggga ccctgggtcac cgtctcctca 360
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg caccagacc	600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	660
aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct	780
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac	900
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaaggcttc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1020
aaagccaaaag ggagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag	1080
ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc	1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1200
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg	1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	1320
cagaagtccc tctccctgtc tccgggtaaa tga	1353

<210> 88

<211> 651

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 88

cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc	60
tcctgcactg gaaccagcag tgacgttggg ggttataact atgtctcctg gtaccaacaa	120
cacccaggca aagcccccaa actcatgatt tatgatgtca gtaagcggcc ctgaggggtt	180
tctaatacgt tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc	240
cagtctgagg acgaggctga ttattactgc aactctttga caagcatcag cacttgggtg	300

ttcggcggag	ggaccaagct	gaccgtccta	ggccagccca	aggccgcccc	ctccgtgacc	360
ctgttcccc	cctcctccga	ggagctgcag	gccaacaagg	ccaccctggt	gtgcctgata	420
tccgacttct	accccggcgc	cgtgaccgtg	gcctggaagg	ccgactcctc	ccccgtgaag	480
gccggcgtgg	agaccaccac	cccctccaag	cagtccaaca	acaagtacgc	cgctctctcc	540
tacctgtccc	tgacccccga	gcagtggaag	tcccaccggt	cctactcctg	ccaggtgacc	600
cacgagggct	ccaccgtgga	gaagaccgtg	gccccaccg	agtgctcctg	a	651

<210> 89

$\langle 211 \rangle$ 123

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<221> source

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"
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<400> 89

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Gly Tyr

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

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

Ala Arg Gly Ser Arg Tyr Asp Trp Asn Gln Asn Asn Trp Phe Asp Pro

100

105

110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 90

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 90

Gly Tyr Ile Phe Thr Gly Tyr Tyr
1 5

<210> 91

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 91

Ile Asn Pro Asn Ser Gly Gly Ala
1 5

<210> 92

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 92

Ala Arg Gly Ser Arg Tyr Asp Trp Asn Gln Asn Asn Trp Phe Asp Pro
1 5 10 15

<210> 93
<211> 110
<212> PRT
<213> Artificial Sequence

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

<400> 93
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Thr Tyr
20 25 30

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

Met Ile Phe Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Phe Thr Thr Ser
85 90 95

Ser Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 94
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 94

Ser Ser Asp Val Gly Thr Tyr Asn Tyr
1 5

<210> 95

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 95

Ser Ser Phe Thr Thr Ser Ser Thr Val Val
1 5 10

<210> 96

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 96

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

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

Ala Arg Gly Ser Arg Tyr Asp Trp Asn Gln Asn Asn Trp Phe Asp Pro
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

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

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

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

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

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

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

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

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
245 250 255

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

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

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

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

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

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

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

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
370 375 380

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

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

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

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

Leu Ser Pro Gly Lys
450

<210> 97

<211> 216

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 97

Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Thr Tyr
20 25 30

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

Met Ile Phe Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Phe Thr Thr Ser
85 90 95

Ser Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
115 120 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr

165

170

175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
 180 185 190

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

Thr Val Ala Pro Thr Glu Cys Ser
 210 215

<210> 98

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 98

cagggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata catcttcacc ggctactata tgcactgggt gcgacaggcc 120

cctggacagg ggcttgagtg gatgggatgg atcaacccta acagtgggtg cgcaaactat 180

gcacagaagt ttcagggcag ggtcaccctg accagggaca cgtccatcac cacagtctac 240

atggaactga gcaggctgag atttgacgac acggccgtgt attactgtgc gagaggatcc 300

cggtatgact ggaaccagaa caactgggtc gacccctggg gccagggaac cctggtcacc 360

gtctcctca 369

<210> 99

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 99
ggatacatct tcaccggcta ctat 24

<210> 100
<211> 24
<212> DNA
<213> Artificial Sequence

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

<400> 100
atcaacccta acagtgggtg cgca 24

<210> 101
<211> 48
<212> DNA
<213> Artificial Sequence

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

<400> 101
gcgagaggat cccggtatga ctggaaccag aacaactggt tcgacccc 48

<210> 102
<211> 330
<212> DNA
<213> Artificial Sequence

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

<400> 102
cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt acttataact atgtctcctg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatt tttgatgtca gtaatcggcc ctcagggggtt 180

tctgatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc	240
caggctgagg acgaggctga ttattactgc agctcattta caaccagcag cactgtgggtt	300
ttcggcggag ggaccaagct gaccgtccta	330

<210> 103
 <211> 27
 <212> DNA
 <213> Artificial Sequence

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

<400> 103	
agcagtgcacg ttggtactta taactat	27

<210> 104
 <211> 9
 <212> DNA
 <213> Artificial Sequence

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

<400> 104	
gatgtcagt	9

<210> 105
 <211> 30
 <212> DNA
 <213> Artificial Sequence

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

<400> 105	
agctcattta caaccagcag cactgtgggtt	30

<210> 106

<211> 1362
<212> DNA
<213> Artificial Sequence

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

<400> 106
caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggata catcttcacc ggctactata tgcactgggt gcgacaggcc 120
cctggacagg ggcttgagt gatgggatgg atcaacccta acagtgggtg cgcaaactat 180
gcacagaagt ttcagggcag ggtcaccctg accaggggaca cgtccatcac cacagtctac 240
atggaactga gcaggctgag atttgacgac acggccgtgt attactgtgc gagaggatcc 300
cggtatgact ggaaccagaa caactggttc gaccctggg gccagggaac cctggtcacc 360
gtctcctcag cctccaccaa gggcccatcg gtcttcccc tggcacctc ctccaagagc 420
acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480
acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540
cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 600
accagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 660
gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720
ctgggggggac cgtcagtcct cctcttcccc caaaaacca aggacaccct catgatctcc 780
cggacccctg aggtcacatg cgtgggtggg gacgtgagcc acgaagacc tgaggtcaag 840
ttcaactggg acgtggacgg cgtggagggt cataatgcca agacaaaagcc gcgggaggag 900
cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 960
aatggcaagg agtacaagtg caaggtctcc aacaaagccc tccagcccc catcgagaaa 1020
accatctcca aagccaaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 1080
cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtaaaagg cttctatccc 1140
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200

cttcccgtgc	tggactccga	cggctccttc	ttcctctaca	gcaagctcac	cgtggacaag	1260
agcaggtggc	agcaggggaa	cgtcttctca	tgctccgtga	tgcatgaggc	tctgcacaac	1320
cactacacgc	agaagtcctt	ctccctgtct	ccgggtaaat	ga		1362

<210> 107

<211> 651

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<221> source

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<223> /note="Description of Artificial Sequence: Synthetic  
polynucleotide"
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<400> 107

cagtctgccc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60

tcctgcactg gaaccagcag tgacgttggt acttataact atgtctcctg gtaccaacaa 120

cacccaggca aagcccccaa actcatgatt tttgatgtca gtaatcggcc ctcagggggtt 180

tctgatcgct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

caggctgagg acgaggctga ttattactgc agctcattta caaccagcag cactgtgggtt 300

ttcggcgagg ggaccaagct gaccgtccta ggccagccca aggccgcccc ctccgtgacc 360

ctgttcccc cctcctccga ggagctgcag gccacaagg ccaccctggg gtgcctgatc 420

tccgacttct accccggcgc cgtgaccgtg gcctggaagg ccgactcctc ccccggtgaag 480

gccggcggtgg agaccaccac cccctccaag cagtccaaca acaagtacgc cgcctcctcc 540

tacctgtccc tgacccccga gcagtggaag tcccaccggt cctactcctg ccaggtgacc 600

cacgaggggct ccaccgtgga gaagaccgtg gccccaccg agtgctcctg a 651

$\langle 210 \rangle$ 108

$\langle 211 \rangle$ 1273

<212> PRT

<213> Severe acute respiratory syndrome coronavirus 2

<400> 108

Met Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser Ser Gln Cys Val

1

5

10

15

Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
20 25 30

Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
35 40 45

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
50 55 60

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

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

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
100 105 110

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
115 120 125

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
130 135 140

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
145 150 155 160

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
165 170 175

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
180 185 190

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
195 200 205

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu

210

215

220

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 225 230 235 240

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 245 250 255

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 260 265 270

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 275 280 285

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 290 295 300

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 305 310 315 320

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 325 330 335

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 340 345 350

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 355 360 365

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 370 375 380

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

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 405 410 415

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
420 425 430

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
435 440 445

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
450 455 460

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
465 470 475 480

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
485 490 495

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
500 505 510

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
515 520 525

Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
530 535 540

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
545 550 555 560

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
565 570 575

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
580 585 590

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
595 600 605

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile

610

615

620

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 625 630 635 640

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 645 650 655

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 660 665 670

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
 675 680 685

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 690 695 700

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 705 710 715 720

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 725 730 735

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 740 745 750

Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 755 760 765

Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln
 770 775 780

Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe
 785 790 795 800

Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser
 805 810 815

Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly
820 825 830

Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
835 840 845

Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
850 855 860

Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
865 870 875 880

Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
885 890 895

Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
900 905 910

Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
915 920 925

Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
930 935 940

Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
945 950 955 960

Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
965 970 975

Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
980 985 990

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
995 1000 1005

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn

1010

1015

1020

Leu Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys
 1025 1030 1035

Arg Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro
 1040 1045 1050

Gln Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr Val
 1055 1060 1065

Pro Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His
 1070 1075 1080

Asp Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser Asn
 1085 1090 1095

Gly Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro Gln
 1100 1105 1110

Ile Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val
 1115 1120 1125

Val Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro
 1130 1135 1140

Glu Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn
 1145 1150 1155

His Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn
 1160 1165 1170

Ala Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu
 1175 1180 1185

Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu
 1190 1195 1200

Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Ile Trp Leu
1205 1210 1215

Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile Met
1220 1225 1230

Leu Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Cys Cys
1235 1240 1245

Ser Cys Gly Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro
1250 1255 1260

Val Leu Lys Gly Val Lys Leu His Tyr Thr
1265 1270