

F072070001W000-SEQLIST-YJC
SEQUENCE LISTING

<110> Fountain Biopharma Inc.
<120> METHOD OF PRODUCING RECOMBINANT PROTEINS WITH CONTROLLED GLYCAN
FORM
<130> F0720.70001W000
<150> US 61/954,337
<151> 2014-03-17
<160> 12
<170> PatentIn version 3.5
<210> 1
<211> 461
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic Polypeptide
<400> 1

Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Gly Ala Arg Cys Gln Pro Pro Arg Arg Tyr Thr Pro Asp Trp Pro Ser
20 25 30

Leu Asp Ser Arg Pro Leu Pro Ala Trp Phe Asp Glu Ala Lys Phe Gly
35 40 45

Val Phe Ile His Trp Gly Val Phe Ser Val Pro Ala Trp Gly Ser Glu
50 55 60

Trp Phe Trp Trp His Trp Gln Gly Glu Gly Arg Pro Gln Tyr Gln Arg
65 70 75 80

Phe Met Arg Asp Asn Tyr Pro Pro Gly Phe Ser Tyr Ala Asp Phe Gly
85 90 95

F072070001W000-SEQLIST-YJC

Pro Gln Phe Thr Ala Arg Phe Phe His Pro Glu Glu Trp Ala Asp Leu
100 105 110

Phe Gln Ala Ala Gly Ala Lys Tyr Val Val Leu Thr Thr Lys His His
115 120 125

Glu Gly Phe Thr Asn Trp Pro Ser Pro Val Ser Trp Asn Trp Asn Ser
130 135 140

Lys Asp Val Gly Pro His Arg Asp Leu Val Gly Glu Leu Gly Thr Ala
145 150 155 160

Leu Arg Lys Arg Asn Ile Arg Tyr Gly Leu Tyr His Ser Leu Leu Glu
165 170 175

Trp Phe His Pro Leu Tyr Leu Leu Asp Lys Lys Asn Gly Phe Lys Thr
180 185 190

Gln His Phe Val Ser Ala Lys Thr Met Pro Glu Leu Tyr Asp Leu Val
195 200 205

Asn Ser Tyr Lys Pro Asp Leu Ile Trp Ser Asp Gly Glu Trp Glu Cys
210 215 220

Pro Asp Thr Tyr Trp Asn Ser Thr Asn Phe Leu Ser Trp Leu Tyr Asn
225 230 235 240

Asp Ser Pro Val Lys Asp Glu Val Val Val Asn Asp Arg Trp Gly Gln
245 250 255

Asn Cys Ser Cys His His Gly Gly Tyr Tyr Asn Cys Glu Asp Lys Phe
260 265 270

Lys Pro Gln Ser Leu Pro Asp His Lys Trp Glu Met Cys Thr Ser Ile
275 280 285

F072070001W000-SEQLIST-YJC

Asp Lys Phe Ser Trp Gly Tyr Arg Arg Asp Met Ala Leu Ser Asp Val
 290 295 300

Thr Glu Glu Ser Glu Ile Ile Ser Glu Leu Val Gln Thr Val Ser Leu
 305 310 315 320

Gly Gly Asn Tyr Leu Leu Asn Ile Gly Pro Thr Lys Asp Gly Leu Ile
 325 330 335

Val Pro Ile Phe Gln Glu Arg Leu Leu Ala Val Gly Lys Trp Leu Ser
 340 345 350

Ile Asn Gly Glu Ala Ile Tyr Ala Ser Lys Pro Trp Arg Val Gln Trp
 355 360 365

Glu Lys Asn Thr Thr Ser Val Trp Tyr Thr Ser Lys Gly Ser Ala Val
 370 375 380

Tyr Ala Ile Phe Leu His Trp Pro Glu Asn Gly Val Leu Asn Leu Glu
 385 390 395 400

Ser Pro Ile Thr Thr Ser Thr Thr Lys Ile Thr Met Leu Gly Ile Gln
 405 410 415

Gly Asp Leu Lys Trp Ser Thr Asp Pro Asp Lys Gly Leu Phe Ile Ser
 420 425 430

Leu Pro Gln Leu Pro Pro Ser Ala Val Pro Ala Glu Phe Ala Trp Thr
 435 440 445

Ile Lys Leu Thr Gly Val Lys His His His His His His
 450 455 460

<210> 2

<211> 1386

F072070001W000-SEQLIST-YJC

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

<400> 2

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tggtttgacg aggccaagtt cggcgtgttc atccactggg gcgtgttctc cgtgcctgcc	180
tggggctctg agtggttctg gtggcattgg cagggcgagg gcagacctca gtaccagcgg	240
ttcatgcggg acaactaccc ccctggcttc tcctacgccg acttcggccc tcagttcacc	300
gcccggttct tccaccctga ggaatgggcc gatctgttcc aggccgtgg cgccaaatac	360
gtggtgctga ccaccaagca ccacgagggc ttcaccaact ggccctcccc cgtgtcctgg	420
aactggaact ctaaggacgt gggccccac cgggatctcg tgggagaact gggaaccgcc	480
ctgcggaagc ggaacatcag atacggcctg taccactccc tgctggaatg gttccacccc	540
ctgtacctgc tggacaagaa gaacggcttc aagaccagc acttcgtgtc cgccaagacc	600
atgcccgagc tgtacgacct cgtgaactcc tacaagcccg acctgatttg gagcgacggc	660
gagtgggagt gccccgacac ctattggaac tccaccaact ttctgtcctg gctgtacaac	720
gactccccctg tgaaggacga ggtggtcgtg aacgacagat ggggccagaa ctgctcctgt	780
caccacggcg gctactacaa ctgcgaggac aagttcaagc cccagtcctt gcccgaccac	840
aagtgggaga tgtgcacctc tatcgacaag ttctcctggg gctaccggcg ggacatggcc	900
ctgtctgatg tgaccgagga atccgagatc atctccgagc tggcgcagac cgtgtccctg	960
ggcggcaact acctgctgaa catcggccct accaaggacg gcctgatcgt gcccattctc	1020
caggaacggc tgctggccgt gggcaagtgg ctgtctatca acggcgaggc catctacgcc	1080
tccaagcctt ggcgagtga gtgggagaag aacaccacct ccgtgtggta cacctccaag	1140
ggctctgccg tgtacgcat cttcctgcac tggcccgaga acggcgtgct gaacctggaa	1200
tcccccatca ccacctctac caccaagatc accatgctgg gcatccaggg cgacctgaag	1260

F072070001W000-SEQLIST-YJC

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gtgcctgctg agttcgctg gaccatcaag ctgaccggcg tgaagcacca ccaccatcac 1380
cattga 1386

<210> 3
<211> 465
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 3

Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Gly Ala Arg Cys His Ser Ala Thr Arg Phe Asp Pro Thr Trp Glu Ser
20 25 30

Leu Asp Ala Arg Gln Leu Pro Ala Trp Phe Asp Gln Ala Lys Phe Gly
35 40 45

Ile Phe Ile His Trp Gly Val Phe Ser Val Pro Ser Phe Gly Ser Glu
50 55 60

Trp Phe Trp Trp Tyr Trp Gln Lys Glu Lys Ile Pro Lys Tyr Val Glu
65 70 75 80

Phe Met Lys Asp Asn Tyr Pro Pro Ser Phe Lys Tyr Glu Asp Phe Gly
85 90 95

Pro Leu Phe Thr Ala Lys Phe Phe Asn Ala Asn Gln Trp Ala Asp Ile
100 105 110

Phe Gln Ala Ser Gly Ala Lys Tyr Ile Val Leu Thr Ser Lys His His
115 120 125

F072070001W000-SEQLIST-YJC

Glu Gly Phe Thr Leu Trp Gly Ser Glu Tyr Ser Trp Asn Trp Asn Ala
 130 135 140

Ile Asp Glu Gly Pro Lys Arg Asp Ile Val Lys Glu Leu Glu Val Ala
 145 150 155 160

Ile Arg Asn Arg Thr Asp Leu Arg Phe Gly Leu Tyr Tyr Ser Leu Phe
 165 170 175

Glu Trp Phe His Pro Leu Phe Leu Glu Asp Glu Ser Ser Ser Phe His
 180 185 190

Lys Arg Gln Phe Pro Val Ser Lys Thr Leu Pro Glu Leu Tyr Glu Leu
 195 200 205

Val Asn Asn Tyr Gln Pro Glu Val Leu Trp Ser Asp Gly Asp Gly Gly
 210 215 220

Ala Pro Asp Gln Tyr Trp Asn Ser Thr Gly Phe Leu Ala Trp Leu Tyr
 225 230 235 240

Asn Glu Ser Pro Val Arg Gly Thr Val Val Thr Asn Asp Arg Trp Gly
 245 250 255

Ala Gly Ser Ile Cys Lys His Gly Gly Phe Tyr Thr Cys Ser Asp Arg
 260 265 270

Tyr Asn Pro Gly His Leu Leu Pro His Lys Trp Glu Asn Cys Met Thr
 275 280 285

Ile Asp Lys Leu Ser Trp Gly Tyr Arg Arg Glu Ala Gly Ile Ser Asp
 290 295 300

Tyr Leu Thr Ile Glu Glu Leu Val Lys Gln Leu Val Glu Thr Val Ser
 305 310 315 320

F072070001W000-SEQLIST-YJC

Cys Gly Gly Asn Leu Leu Met Asn Ile Gly Pro Thr Leu Asp Gly Thr
 325 330 335

Ile Ser Val Val Phe Glu Glu Arg Leu Arg Gln Met Gly Ser Trp Leu
 340 345 350

Lys Val Asn Gly Glu Ala Ile Tyr Glu Thr His Thr Trp Arg Ser Gln
 355 360 365

Asn Asp Thr Val Thr Pro Asp Val Trp Tyr Thr Ser Lys Pro Lys Glu
 370 375 380

Lys Leu Val Tyr Ala Ile Phe Leu Lys Trp Pro Thr Ser Gly Gln Leu
 385 390 395 400

Phe Leu Gly His Pro Lys Ala Ile Leu Gly Ala Thr Glu Val Lys Leu
 405 410 415

Leu Gly His Gly Gln Pro Leu Asn Trp Ile Ser Leu Glu Gln Asn Gly
 420 425 430

Ile Met Val Glu Leu Pro Gln Leu Thr Ile His Gln Met Pro Cys Lys
 435 440 445

Trp Gly Trp Ala Leu Ala Leu Thr Asn Val Ile His His His His His
 450 455 460

His
 465

<210> 4
 <211> 1398
 <212> DNA
 <213> Artificial Sequence
 <220>

<223> Synthetic Polynucleotide

<400> 4

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cactccgcca ccagattcga cccacactgg gagtctctgg acgccagaca gctgcccgt	120
tggtttgacc aggccaagtt cggcatcttc atccactggg gcgtgttctc cgtgcccagc	180
ttcggctctg agtggttctg gtggtactgg cagaaagaga agatcccca atactgtggag	240
ttcatgaagg acaactaccc cccagcttt aagtacgagg acttcggccc cctgttcacc	300
gccaagttct tcaacgcca ccagtgggccc gacatcttcc aggcctctgg cgccaagtac	360
atcgtgctga cctccaagca ccacgagggc ttcaccctgt ggggctccga gtactcctgg	420
aactggaacg ccatcgacga gggccccaag cgggacatcg tgaaagaact ggaagtggcc	480
atccggaacc ggaccgacct gagattcggc ctgtactact ccctgttcga gtggttccac	540
cccctgtttc tggaagatga gtcctccagc ttccacaagc ggcagttccc cgtgtccaag	600
accctgcccc agctgtacga gtcgtgaac aactaccagc ccgaggtgct gtggagtgaac	660
ggggatggtg gtgccccga tcagtactgg aactctaccg gcttcctggc ctggctgtac	720
aacgagtctc ctgtgcgggg caccgtcgtg accaacgata gatggggcgc tggctccatc	780
tgcaagcacg gcggcttcta cacctgttcc gaccgtaca accccggcca tctgctgcct	840
cacaagtggg agaactgcat gaccatcgac aagctgtcct ggggctacag aagagaggcc	900
ggcatctccg actacctgac aatcgaggaa ctcgtgaagc agctgggtgga aaccgtgtcc	960
tgcggcggca acctgctgat gaacatcggc cctaccctgg acggcaccat ctccgtggtg	1020
ttcgaggaac ggctgcggca gatgggctcc tggctgaaag tgaacggcga ggccatctac	1080
gagacacaca cctggcggtc ccagaacgac accgtgacct ctgacgtgtg gtacaccagc	1140
aagcccaaag aaaagctggt gtatgccatc ttcctgaagt ggcctacctc cggccagctg	1200
ttcctgggcc accctaaggc tatcctgggc gccaccgaag tgaaactgct gggccatgga	1260
cagccccctga actggatctc cctggaacag aacggcatca tgggtggaact gccccagctg	1320
accatccatc agatgccctg caaatggggc tgggccctgg ccctgaccaa cgtgatccac	1380

catcaccacc accactga

1398

<210> 5

<211> 465

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 5

Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro
 1 5 10 15

Gly Ala Arg Cys Lys Ser Ser Arg Arg Tyr Asp Pro Thr Trp Glu Ser
 20 25 30

Leu Asp Arg Arg Pro Leu Pro Ser Trp Phe Asp Gln Ala Lys Phe Gly
 35 40 45

Ile Phe Ile His Trp Gly Val Phe Ser Val Pro Ser Phe Gly Ser Glu
 50 55 60

Trp Phe Trp Trp Tyr Trp Gln Lys Glu Lys Arg Pro Lys Phe Val Asp
 65 70 75 80

Phe Met Asn Asn Asn Tyr Pro Pro Gly Phe Lys Tyr Glu Asp Phe Gly
 85 90 95

Val Leu Phe Thr Ala Lys Phe Phe Asn Ala Ser Gln Trp Ala Asp Ile
 100 105 110

Leu Gln Ala Ser Gly Ala Lys Tyr Leu Val Leu Thr Ser Lys His His
 115 120 125

Glu Gly Phe Thr Leu Trp Gly Ser Glu Tyr Ser Trp Asn Trp Asn Ala
 130 135 140

F072070001W000-SEQLIST-YJC

Val Asp Glu Gly Pro Lys Arg Asp Ile Val Lys Glu Leu Lys Val Ala
145 150 155 160

Ile Thr Lys Asn Thr Asp Leu Arg Phe Gly Leu Tyr Tyr Ser Leu Phe
165 170 175

Glu Trp Phe His Pro Leu Phe Leu Glu Asp Lys Leu Ser Ser Phe Gln
180 185 190

Lys Arg Gln Phe Pro Ile Ser Lys Met Leu Pro Glu Leu Tyr Glu Leu
195 200 205

Val Asn Lys Tyr Gln Pro Asp Ile Leu Trp Thr Asp Gly Asp Gly Gly
210 215 220

Ala Pro Asp Arg Tyr Trp Asn Ser Thr Gly Phe Leu Ala Trp Leu Tyr
225 230 235 240

Asn Glu Ser Pro Val Arg Asn Thr Val Val Thr Asn Asp Arg Trp Gly
245 250 255

Ala Gly Ser Ile Cys Lys His Gly Gly Tyr Tyr Thr Cys Ser Asp Arg
260 265 270

Tyr Asn Pro Gly His Leu Leu Pro His Lys Trp Glu Asn Cys Met Thr
275 280 285

Ile Asp Gln Phe Ser Trp Gly Tyr Arg Arg Glu Ala Val Ile Ser Asp
290 295 300

Tyr Leu Thr Ile Glu Glu Leu Val Lys Gln Leu Val Glu Thr Val Ala
305 310 315 320

Cys Gly Gly Asn Leu Leu Met Asn Ile Gly Pro Thr Leu Asp Gly Ile
325 330 335

F072070001W000-SEQLIST-YJC

Ile Pro Val Ile Phe Glu Glu Arg Leu Arg Gln Met Gly Met Trp Leu
 340 345 350

Lys Val Asn Gly Glu Ala Ile Tyr Glu Thr Gln Pro Trp Arg Ser Gln
 355 360 365

Asn Asp Thr Ala Thr Pro Asp Val Trp Tyr Thr Tyr Lys Pro Glu Glu
 370 375 380

Lys Ile Val Tyr Ala Ile Phe Leu Lys Trp Pro Val Ser Arg Glu Leu
 385 390 395 400

Phe Leu Glu Gln Pro Ile Gly Ser Leu Gly Glu Thr Glu Val Ala Leu
 405 410 415

Leu Gly Glu Gly Lys Pro Leu Thr Trp Thr Ser Leu Lys Pro Asn Gly
 420 425 430

Ile Ile Val Glu Leu Pro Gln Leu Thr Leu His Gln Met Pro Cys Lys
 435 440 445

Trp Gly Trp Thr Leu Ala Leu Thr Asn Val Thr His His His His His
 450 455 460

His
 465

<210> 6
 <211> 1398
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

<400> 6
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60

F072070001W000-SEQLIST-YJC

aagtcctctc ggagatacga ccccacctgg gagtccctgg acagaaggcc tctgcccagt	120
tggttcgacc aggccaagtt cggcatcttc atccactggg gcgtgttctc cgtgcccagc	180
ttcggctctg agtggttctg gtggtactgg cagaaagaga agcggcccaa gttcgtggac	240
ttcatgaaca acaactaccc ccctggcttt aagtacgagg acttcggcgt gctgttcacc	300
gccaagttct tcaacgcctc ccagtgggcc gacatcctgc aggcttccgg cgctaagtac	360
ctggtgctga cctccaagca ccacgagggc tttaccctgt ggggctccga gtactcctgg	420
aactggaacg ccgtggacga gggccctaag cgggacatcg tgaaagaact gaagggtggcc	480
atcaccaaga acaccgacct gagattcggc ctgtactact ccctgttcga gtggttccac	540
cccctgtttc tggaagataa gctgtccagc ttccagaagc ggcagttccc catctccaag	600
atgctgcccc agctgtacga gctcgtgaac aagtaccagc ctgacatcct gtggaccgac	660
ggggatgggtg gcgcccctga cagatactgg aactctaccg gcttcctggc ctggctgtac	720
aacgagtccc ctgtgcggaa caccgtcgtg accaacgaca gatggggcgc tggctccatc	780
tgcaagcacg gcggctacta cacctgttcc gaccgggtaca accccggcca tctgctgcct	840
cacaagtggg agaactgcat gacaatcgac cagttctcct ggggctaccg gcgcgaggcc	900
gtgatctctg actacctgac catcgaggaa ctcgtgaagc agctgggtgga aaccgtggcc	960
tgtggcggca acctgctgat gaacatcggc cctaccctgg acggcatcat ccccgtgatc	1020
ttcgaggaac ggctgcggca gatgggcatg tggctgaaag tgaacggcga ggccatctac	1080
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aagcccgaag agaagatcgt gtacgccatc ttcctgaagt ggcccgtgtc cagagagctg	1200
tttctggaac agcccatcgg ctccctgggc gagacagaag tggctctgct gggcgagggc	1260
aagcctctga cctggacctc cctgaagccc aatggcatca tcgtggaact gcccagctg	1320
accctgcacc agatgccctg taaatggggc tggaccctgg ccctgaccaa cgtgaccac	1380
caccaccatc accactga	1398

F072070001W000-SEQLIST-YJC

<210> 7
 <211> 481
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 7

Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro
 1 5 10 15

Gly Ala Arg Cys His Asn Val Ser Glu Gly Tyr Glu Lys Pro Ala Asp
 20 25 30

Pro Leu Val Val Gln Asn Leu Glu Gln Trp Gln Asp Leu Lys Phe Gly
 35 40 45

Leu Phe Met His Trp Gly Thr Tyr Ser Gln Trp Gly Ile Val Glu Ser
 50 55 60

Trp Ser Leu Cys Pro Glu Asp Glu Ser Trp Thr Gln Arg Lys Pro Glu
 65 70 75 80

His Gly Lys Ser Tyr Asn Glu Tyr Val Lys Asn Tyr Glu Asn Leu Gln
 85 90 95

Thr Thr Phe Asn Pro Val Gln Phe Asn Pro Gln Lys Trp Ala Asp Ala
 100 105 110

Thr Lys Lys Ala Gly Met Lys Tyr Val Val Phe Thr Thr Lys His His
 115 120 125

Asp Gly Phe Ala Met Phe Asp Thr Lys Gln Ser Asp Tyr Lys Ile Thr
 130 135 140

Ser Ser Lys Thr Pro Phe Ser Lys Asn Pro Lys Ala Asp Val Ala Lys
 145 150 155 160

F072070001W000-SEQLIST-YJC

Glu Ile Phe Asn Thr Phe Arg Asp Asn Gly Phe Arg Ile Gly Ala Tyr
165 170 175

Phe Ser Lys Pro Asp Trp His Ser Asp Asp Tyr Trp Trp Ser Tyr Phe
180 185 190

Pro Pro Lys Asp Arg Asn Val Asn Tyr Asp Pro Gln Lys Tyr Pro Ala
195 200 205

Arg Trp Glu Asn Phe Lys Lys Phe Thr Phe Asn Gln Leu Asn Glu Ile
210 215 220

Thr Ser Asn Tyr Gly Lys Ile Asp Ile Leu Trp Leu Asp Gly Gly Trp
225 230 235 240

Val Arg Pro Phe His Thr Ile Asp Pro Asn Ile Glu Trp Gln Arg Thr
245 250 255

Ile Lys Val Glu Gln Asp Ile Asp Met Asp Lys Ile Gly Thr Met Ala
260 265 270

Arg Lys Asn Gln Pro Gly Ile Ile Ile Val Asp Arg Thr Val Pro Gly
275 280 285

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

Leu Ser Ile Pro Trp Glu Ser Cys Ile Thr Met Gly Asp Ser Phe Ser
305 310 315 320

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

Leu Ile Arg Ile Ile Ser Arg Gly Gly Asn Tyr Leu Met Asn Ile Ala
340 345 350

F072070001W000-SEQLIST-YJC

Pro Gly Pro Asn Gly Asp Tyr Asp Ala Val Val Tyr Glu Arg Leu Lys
355 360 365

Glu Ile Ser Gly Trp Met Asp Lys Asn Gln Ser Ala Val Phe Thr Thr
370 375 380

Arg Ala Leu Ala Pro Tyr His Glu Ser Asp Phe Tyr Tyr Thr Gln Ser
385 390 395 400

Lys Asp Gly Lys Ile Val Asn Val Phe His Ile Ser Glu Lys Ser Asn
405 410 415

Tyr Gln Ala Pro Ser Glu Leu Ser Phe Ser Ile Pro Glu Asn Ile Asn
420 425 430

Pro Lys Thr Val Lys Val Leu Gly Ile Ser Ser Gln Ile Lys Trp Lys
435 440 445

Lys Lys Gly Asn Lys Ile His Val Gln Leu Pro Glu Glu Arg Thr Lys
450 455 460

Leu Asn Tyr Ser Thr Val Ile Gln Ile Thr Gln His His His His His
465 470 475 480

His

<210> 8
<211> 1446
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 8
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60

F072070001W000-SEQLIST-YJC

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cagtggcagg acctgaagtt cggcctgttc atgcactggg gcacctactc ccagtggggc	180
atcgtggaat cctggtccct gtgccctgag gacgagtctt ggacccagcg gaagcctgag	240
cacggcaagt cctacaacga gtacgtgaag aactacgaga acctgcagac caccttcaac	300
cccgtgcagt tcaacccccca gaagtgggcc gacgccacca agaaagccgg catgaaatac	360
gtggtgttca ccaccaagca ccacgacggc ttcgccatgt tcgacaccaa gcagtccgac	420
tacaagatca cctcctcaa gacccccctt agcaagaacc ccaaggccga cgtggccaaa	480
gagattttca acaccttccg ggacaacggc ttccggatcg gcgcctactt ctccaagcct	540
gactggcact ccgacgacta ctggtggtcc tacttcccac ccaaggaccg gaacgtgaac	600
tacgaccctc agaaataccc cgccagatgg gagaacttca agaagtccac cttcaatcag	660
ctgaacgaga tcaccagcaa ctacggcaag atcgacatcc tgtggctgga cggcggatgg	720
gtgcgaccct tccacaccat cgaccccaac atcgagtggc agcggaccat caaggtggaa	780
caggacatcg acatggacaa gatcggcacc atggcccga agaaccagcc cggcatcatc	840
atcgtggacc ggaccgtgcc tggcaagtgg gagaattacg tgacccccga gcaggccgtg	900
cctgagcatg ccctgtctat cccttgggag tcctgtatca caatgggcga cagcttctcc	960
tacgtgcccc acgacaacta caagtcctcc cagaagatca tcgagacact gatcaggatc	1020
atctccagag gcggcaacta cctgatgaat atcgcccctg gcccacacgg cgactacgac	1080
gctgtggtgt acgagcggct gaaagaaatc tccggctgga tggataagaa ccagtccgcc	1140
gtgtttacca cccgggctct ggcccccttac cacgagtccg acttctacta caccagtc	1200
aaggacggaa agatcgtgaa cgtgttccac atctccgaga agtccaacta ccaggcccc	1260
tccgagctgt ccttcagcat ccccgagaac atcaaccca agaccgtgaa ggtgctgggc	1320
atctccagcc agatcaagtg gaagaagaag ggcaacaaga tccacgtgca gctgcccag	1380
gaacggacca agctgaacta ctccaccgtg atccagatca ccagcacca ccaccatcac	1440
cactga	1446

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<210> 9
 <211> 440
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 9

Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro
 1 5 10 15

Gly Ala Arg Cys Gln Gln Lys Tyr Gln Pro Thr Glu Ala Asn Leu Lys
 20 25 30

Ala Arg Ser Glu Phe Gln Asp Asn Lys Phe Gly Ile Phe Leu His Trp
 35 40 45

Gly Leu Tyr Ala Met Leu Ala Thr Gly Glu Trp Thr Met Thr Asn Asn
 50 55 60

Asn Leu Asn Tyr Lys Glu Tyr Ala Lys Leu Ala Gly Gly Phe Tyr Pro
 65 70 75 80

Ser Lys Phe Asp Ala Asp Lys Trp Val Ala Ala Ile Lys Ala Ser Gly
 85 90 95

Ala Lys Tyr Ile Cys Phe Thr Thr Arg His His Glu Gly Phe Ser Met
 100 105 110

Phe Asp Thr Lys Tyr Ser Asp Tyr Asn Ile Val Lys Ala Thr Pro Phe
 115 120 125

Lys Arg Asp Val Val Lys Glu Leu Ala Asp Ala Cys Ala Lys His Gly
 130 135 140

F072070001W000-SEQLIST-YJC

Ile Lys Leu His Phe Tyr Tyr Ser His Ile Asp Trp Tyr Arg Glu Asp
145 150 155 160

Ala Pro Gln Gly Arg Thr Gly Arg Arg Thr Gly Arg Pro Asn Pro Lys
165 170 175

Gly Asp Trp Lys Ser Tyr Tyr Gln Phe Met Asn Asn Gln Leu Thr Glu
180 185 190

Leu Leu Thr Asn Tyr Gly Pro Ile Gly Ala Ile Trp Phe Asp Gly Trp
195 200 205

Trp Asp Gln Asp Ile Asn Pro Asp Phe Asp Trp Glu Leu Pro Glu Gln
210 215 220

Tyr Ala Leu Ile His Arg Leu Gln Pro Ala Cys Leu Val Gly Asn Asn
225 230 235 240

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

Asp Leu Pro Gly Glu Asn Thr Ala Gly Leu Ser Gly Gln Ser Val Ser
260 265 270

His Leu Pro Leu Glu Thr Cys Glu Thr Met Asn Gly Met Trp Gly Tyr
275 280 285

Lys Ile Thr Asp Gln Asn Tyr Lys Ser Thr Lys Thr Leu Ile His Tyr
290 295 300

Leu Val Lys Ala Ala Gly Lys Asp Ala Asn Leu Leu Met Asn Ile Gly
305 310 315 320

Pro Gln Pro Asp Gly Glu Leu Pro Glu Val Ala Val Gln Arg Leu Lys
325 330 335

F072070001W000-SEQLIST-YJC

Glu Val Gly Glu Trp Met Ser Lys Tyr Gly Glu Thr Ile Tyr Gly Thr
340 345 350

Arg Gly Gly Leu Val Ala Pro His Asp Trp Gly Val Thr Thr Gln Lys
355 360 365

Gly Asn Lys Leu Tyr Val His Ile Leu Asn Leu Gln Asp Lys Ala Leu
370 375 380

Phe Leu Pro Ile Val Asp Lys Lys Val Lys Lys Ala Val Val Phe Ala
385 390 395 400

Asp Lys Thr Pro Val Arg Phe Thr Lys Asn Lys Glu Gly Ile Val Leu
405 410 415

Glu Leu Ala Lys Val Pro Thr Asp Val Asp Tyr Val Val Glu Leu Thr
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aagttcggca tcttcctgca ctggggcctg tacgccatgc tggctactgg cgagtggacc 180
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tccaagttcg acgccgacaa atgggtggcc gccatcaagg cctctggcgc caagtacatc 300
tgcttcacca cccggcacca cgagggttc tccatgttcg acaccaagta ctccgactac 360

F072070001W000-SEQLIST-YJC

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ggcgccattt ggttcgacgg gtggtgggac caggacatca accccgactt cgactgggag	660
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F072070001W000-SEQLIST-YJC

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

F072070001W000-SEQLIST-YJC

Ala Lys Ala Ile Val Asp Glu Tyr Val Tyr Lys Tyr Asn Leu Asp Gly
210 215 220

Leu Asp Val Asp Ile Glu Arg Asp Ser Ile Pro Lys Val Asn Gly Lys
225 230 235 240

Glu Ser Asn Glu Asn Ile Gln Arg Ser Ile Ala Val Phe Glu Glu Ile
245 250 255

Gly Lys Leu Ile Gly Pro Lys Gly Ala Asp Lys Ser Arg Leu Phe Ile
260 265 270

Met Asp Ser Thr Tyr Met Ala Asp Lys Asn Pro Leu Ile Glu Arg Gly
275 280 285

Ala Pro Tyr Ile Asp Leu Leu Leu Val Gln Val Tyr Gly Ile Gln Gly
290 295 300

Glu Lys Gly Asp Trp Asp Pro Val Ala Arg Lys Pro Glu Lys Thr Met
305 310 315 320

Glu Glu Arg Trp Glu Ser Tyr Ser Lys Tyr Ile Arg Pro Glu Gln Tyr
325 330 335

Met Val Gly Phe Ser Phe Tyr Glu Glu Asn Ala Gly Ser Gly Asn Leu
340 345 350

Trp Tyr Asp Ile Asn Glu Arg Lys Asp Asp His Asn Pro Leu Asn Ser
355 360 365

Glu Ile Ala Gly Thr Arg Ala Glu Arg Tyr Ala Lys Trp Gln Pro Lys
370 375 380

Thr Gly Gly Val Lys Gly Gly Ile Phe Ser Tyr Ala Ile Asp Arg Asp
385 390 395 400

F072070001W000-SEQLIST-YJC

Gly Val Ala His Gln Pro Lys Lys Val Ser Asp Asp Glu Lys Arg Thr
405 410 415

Asn Lys Ala Ile Lys Asp Ile Thr Asp Gly Ile Val Lys Ser Asp Tyr
420 425 430

Lys Val Ser Lys Ala Leu Lys Lys Val Met Glu Asn Asp Lys Ser Tyr
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Glu Leu Ile Asp Gln Lys Asp Phe Pro Asp Lys Ala Leu Arg Glu Ala
450 455 460

Val Ile Ala Gln Val Gly Ser Arg Arg Gly Asp Leu Glu Arg Phe Asn
465 470 475 480

Gly Thr Leu Arg Leu Asp Asn Pro Asp Ile Lys Ser Leu Glu Gly Leu
485 490 495

Asn Lys Leu Lys Lys Leu Ala Lys Leu Glu Leu Ile Gly Leu Ser Gln
500 505 510

Ile Thr Lys Leu Asp Ser Ser Val Leu Pro Glu Asn Ile Lys Pro Thr
515 520 525

Lys Asp Thr Leu Val Ser Val Leu Glu Thr Tyr Lys Asn Asp Asp Arg
530 535 540

Lys Glu Glu Ala Lys Ala Ile Pro Gln Val Ala Leu Thr Ile Ser Gly
545 550 555 560

Leu Thr Gly Leu Lys Glu Leu Asn Leu Ala Gly Phe Asp Arg Asp Ser
565 570 575

Leu Ala Gly Ile Asp Ala Ala Ser Leu Thr Ser Leu Glu Lys Val Asp
580 585 590

F072070001W000-SEQLIST-YJC

Leu Ser Lys Asn Lys Leu Asp Leu Ala Ala Gly Thr Glu Asn Arg Gln
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Ile Phe Asp Val Met Leu Ser Thr Val Ser Asn Arg Val Gly Ser Asn
610 615 620

Glu Gln Thr Val Thr Phe Asp His Gln Lys Pro Thr Gly His Tyr Pro
625 630 635 640

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

Ile Asp Leu Gln Ser Gln Leu Leu Phe Gly Thr Val Thr Asn Gln Gly
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Thr Leu Ile Asn Ser Glu Ala Asp Tyr Lys Ala Tyr Gln Glu Gln Leu
675 680 685

Ile Ala Gly Arg Arg Phe Val Asp Pro Gly Tyr Ala Tyr Lys Asn Phe
690 695 700

Ala Val Thr Tyr Asp Ala Tyr Lys Val Arg Val Thr Asp Ser Thr Leu
705 710 715 720

Gly Val Thr Asp Glu Lys Lys Leu Ser Thr Ser Lys Glu Glu Thr Tyr
725 730 735

Lys Val Glu Phe Phe Ser Pro Thr Asn Gly Thr Lys Pro Val His Glu
740 745 750

Ala Lys Val Val Val Gly Ala Glu Lys Thr Met Met Val Asn Leu Ala
755 760 765

Ala Gly Ala Thr Val Ile Lys Ser Asp Ser His Glu Asn Ala Lys Lys
770 775 780

F072070001W000-SEQLIST-YJC

Val Phe Asp Gly Ala Ile Glu Tyr Asn Pro Leu Ser Phe Ser Ser Lys
785 790 795 800

Thr Ser Ile Thr Phe Glu Phe Lys Glu Pro Gly Leu Val Lys Tyr Trp
805 810 815

Arg Phe Phe Asn Asp Ile Thr Arg Lys Asp Asp Tyr Ile Lys Glu Ala
820 825 830

Lys Leu Glu Ala Phe Val Gly His Leu Glu Asp Asp Ser Lys Val Lys
835 840 845

Asp Ser Leu Glu Lys Ser Thr Glu Trp Val Thr Val Ser Asp Tyr Ser
850 855 860

Gly Glu Ala Gln Glu Phe Ser Gln Pro Leu Asp Asn Ile Ser Ala Lys
865 870 875 880

Tyr Trp Arg Val Thr Val Asp Thr Lys Gly Gly Arg Tyr Ser Ser Pro
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Asp Tyr Lys Asp Asp Asp Asp Lys
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