

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
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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

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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

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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

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<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 aggccgttgg 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
atgcccagc tgtacgacct cgtgaactcc tacaagccg acctgatttg gagcgacggc	660
gagtgggagt gccccgacac ctattggaac tccaccaact ttctgtcctg gctgtacaac	720
gactcccctg tgaaggacga ggtggctgtg aacgacagat ggggccagaa ctgctcctgt	780
caccacggcg gctactacaa ctgcgaggac aagttcaagc cccagtccct gcccgaccac	840
aagtgggaga tgtgcacctc tatcgacaag ttctcctggg gctaccggcg ggacatggcc	900
ctgtctgatg tgaccgagga atccgagatc atctccgagc tggcgcagac cgtgtccctg	960
ggcggcaact acctgctgaa catcggccct accaaggacg gcctgatcgt gcccatcttc	1020
caggaacggc tgctggccgt gggcaagtgg ctgtctatca acggcgaggc catctacgcc	1080
tccaagcctt ggcgagtgc gtgggagaag aacaccacct ccgtgtggta cacctccaag	1140
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tccccatca ccacctctac caccaagatc accatgctgg gcatccaggg cgacctgaag	1260

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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

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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

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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>

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<223> Synthetic Polynucleotide

<400> 4

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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 gctcgtgaac aactaccagc ccgaggtgct gtggagtgaac	660
ggggatggtg gtgccccga tcagtactgg aactctaccg gcttcctggc ctggctgtac	720
aacgagtctc ctgtgcgggg caccgtcgtg accaacgata gatggggcgc tggctccatc	780
tgcaagcacg gcggcttcta cacctgttcc gaccgttaca accccggcca tctgctgcct	840
cacaagtggg agaactgcat gaccatcgac aagctgtcct ggggctacag aagagaggcc	900
ggcatctccg actacctgac aatcgaggaa ctctgaagc agctgggtgga aaccgtgtcc	960
tcgggcggca acctgctgat gaacatcggc cctaccctgg acggcaccat ctccgtgggtg	1020
ttcgaggaac ggctgcggca gatgggctcc tggctgaaag tgaacggcga ggccatctac	1080
gagacacaca cctggcggtc ccagaacgac accgtgaccc ctgacgtgtg gtacaccagc	1140
aagcccaaag aaaagctggt gtatgccatc ttctgaagt ggcctacctc cggccagctg	1200
ttcctgggccc accctaaggc tatcctgggc gccaccgaag tgaaactgct gggccatgga	1260
cagcccctga actggatctc cctggaacag aacggcatca tgggtggaact gcccagctg	1320
accatccatc agatgccctg caaatggggc tgggcccctgg ccctgaccaa cgtgatccac	1380

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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

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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

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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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tggttcgacc aggccaaagt cggcactctc atccactggg gcgtgttctc cgtgcccagc	180
ttcggctctg agtggttctg gtgggtactgg cagaaagaga agcggcccaa gttcgtggac	240
ttcatgaaca acaactaccc ccctggcttt aagtacgagg acttcggcgt gctgttcacc	300
gccaagttct tcaacgcctc ccagtgggccc gacatcctgc aggcttccgg cgctaagtac	360
ctgggtgctga cctccaagca ccacgagggc ttaccctgt 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 ctctgtgaagc agctgggtgga aaccgtggcc	960
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gagacacagc cttggcggtc ccagaacgac accgccacac ctgacgtgtg gtacacctac	1140
aagcccgaag agaagatcgt gtacgccatc ttctgaagt gggcgtgtc 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

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<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

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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

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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

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atcgtggaat cctgggtccct gtgccctgag gacgagtctt ggacccagcg gaagcctgag	240
cacggcaagt cctacaacga gtacgtgaag aactacgaga acctgcagac caccttcaac	300
cccgtgcagt tcaacccccca gaagtgggccc gacgccacca agaaagccgg catgaaatac	360
gtggtgttca ccaccaagca ccacgacggc ttccgcatgt tcgacaccaa gcagtccgac	420
tacaagatca cctcctccaa gacccccctc 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
tacgtgcca acgacaacta caagtcctcc cagaagatca tcgagacact gatcaggatc	1020
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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 cccagcacca 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

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 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

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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

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Arg Gly Gly Leu Val Ala Pro His Asp Trp Gly Val Thr Thr Gln Lys
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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
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Asp Lys Val Val Gln Thr Ser Pro Ser Val Ser Ala Ile Asp Asp Leu
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His Tyr Leu Ser Glu Asn Ser Lys Lys Glu Phe Lys Glu Gly Leu Ser
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Lys Ala Gly Glu Val Pro Glu Lys Leu Lys Asp Ile Leu Ser Lys Ala
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Gln Gln Ala Asp Lys Gln Ala Lys Val Leu Ala Glu Met Lys Val Pro
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Glu Lys Ile Ala Met Lys Pro Leu Lys Gly Pro Leu Tyr Gly Gly Tyr
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Phe Arg Thr Trp His Asp Lys Thr Ser Asp Pro Ala Glu Lys Asp Lys
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Val Asn Ser Met Gly Glu Leu Pro Lys Glu Val Asp Leu Ala Phe Val
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Phe His Asp Trp Thr Lys Asp Tyr Ser Leu Phe Trp Gln Glu Leu Ala
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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
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Ala Lys Ala Ile Val Asp Glu Tyr Val Tyr Lys Tyr Asn Leu Asp Gly
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Leu Asp Val Asp Ile Glu Arg Asp Ser Ile Pro Lys Val Asn Gly Lys
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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
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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
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Gly Val Ala His Gln Pro Lys Lys Val Ser Asp Asp Glu Lys Arg Thr
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Asn Lys Ala Ile Lys Asp Ile Thr Asp Gly Ile Val Lys Ser Asp Tyr
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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
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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
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Asn Lys Leu Lys Lys Leu Ala Lys Leu Glu Leu Ile Gly Leu Ser Gln
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Ile Thr Lys Leu Asp Ser Ser Val Leu Pro Glu Asn Ile Lys Pro Thr
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Lys Asp Thr Leu Val Ser Val Leu Glu Thr Tyr Lys Asn Asp Asp Arg
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Lys Glu Glu Ala Lys Ala Ile Pro Gln Val Ala Leu Thr Ile Ser Gly
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Leu Thr Gly Leu Lys Glu Leu Asn Leu Ala Gly Phe Asp Arg Asp Ser
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Asn Thr Tyr Gly Thr Thr Ser Leu Arg Leu Pro Val Gly Glu Gly Lys
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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
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Ala Val Thr Tyr Asp Ala Tyr Lys Val Arg Val Thr Asp Ser Thr Leu
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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
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Thr Ser Ile Thr Phe Glu Phe Lys Glu Pro Gly Leu Val Lys Tyr Trp
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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
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Asp Ser Leu Glu Lys Ser Thr Glu Trp Val Thr Val Ser Asp Tyr Ser
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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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