

eolf-othd-000002
SEQUENCE LISTING

<110> GlaxoSmithKline Biologicals S.A.
ID Biomedical Corporation of Quebec
BAUDOUX, Guy J-M
BLAIS, Normand
Rheault, Patrick
RUELLE, Jean-Louis
CYR, Sonya

<120> Recombinant RSV Antigens

<130> VU62788-1 PCT

<150> 61/219,964

<151> 2009-06-24

<150> 61/334,568

<151> 2010-05-13

<160> 22

<170> PatentIn version 3.5

<210> 1

<211> 1697

<212> DNA

<213> respiratory syncytial virus

<400> 1	
atggagttgc taatcctcaa agcaaatgca attaccacaa tcctcactgc agtcacattt	60
gttttgcttc tgggtcaaac atcactgaag aattttatca atcaacatgc agtgcagtag	120
caaaggctat cttagtgtc tgagaactgg ttggtatacc agtggtataa ctatagatta	180
agtaatatca aggaaaataa gtgtaatgga acagatgcta aggtaaaatt gataaacaag	240
aattagataa atataaaaaat gctgtaacag aattgcagtt gctcatgcaa agcaccacagc	300
aacaaacaat cgagccagaa gagaactacc aagggtttatg aattatacac tcaaaatgcc	360
aaaaaaacca atgtaacatt aagcaagaaa aggaaaagaa gatttcttgg tttttgtag	420
gtgttggtatc tgcaatcgcc agtggcgttg ctgtatctaa ggtcctgcac ctgaagggga	480
agtgaacaag atcaaaagtg ctctactatc cacaaacaag gctgtagtca gttatcaa	540
ggagttagtg tcttaaccag caaagtgtta gacctcaaaa actatataga aaacaattgt	600
tacctattgt gaacaagcaa agctgcagca tatcaaatat agcaactgta tagagttcca	660
acaaaagaac aacagactac tagagattac cagggaattt agtgtaagc aggtgtaact	720
acacctgtaa gcacttacat gttaactaat agtgaattat tgtcattatc aatgatatgc	780
ctataacaaa tgatcagaaa aagttaattgt ccaacaattgt tcaaatgtta gacagcaaag	840
ttactctatc atgtccataa taaaagagga agtcttagca tatgtgtaca attaccacta	900
tatggtgtta tagatacacc ctgttggaac ctacacacat ccccttatgt acaaccaaca	960
caaaagaagg gtccaacatc tgtttaacaa gaactgacag aggtgggtact gtgacaatgc	1020

eo1f-othd-000002

```

aggatcagta tctttcttcc cacaagctga aacatgtaaa gtcaatcaaa tcgagtattt 1080
tgtgacacaa tgaacagttt aacattacca agtgaagtaa actctgcaat gttgacatat 1140
tcaaccccaa atatgattgt aaaattatga cttcaaaaac gatgtaagca gctccgttat 1200
cacatctcta ggagccattg tgtcatgcta tggcaaaaca aatgtacagc atccaataaa 1260
aatcgtggaa tcataaagac attttctaac ggggtgcgata tgtatcaaata aaaggggtgg 1320
acactgtgtc tgtaggtaac acattatatt atgtaaaaag caagaaggta aaagtctcta 1380
tgtaaaagggt gaaccaataa taaatttcta tgacccttag tattcccctc tgatgaattt 1440
gatgcatcaa tatctcaagt caacgagaag attaacagag cctagcattt attcgtaaata 1500
ccgatgaatt attacataat gtaaatgctg gtaatccacc ataaatatca tgataactac 1560
tataattata gtgattatag taatattgtt atcttaattg ctgttggact gctcttatac 1620
tgtaaggcca gaagcacacc agtcacacta agaaagatca actgagtggg ataaataata 1680
ttgcatttag taactaa 1697

```

<210> 2
 <211> 574
 <212> PRT
 <213> respiratory syncytial virus

<400> 2

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
 1 5 10 15

Ala Val Thr Phe Cys Phe Ala Ser Gly Gln Asn Ile Thr Glu Glu Phe
 20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
 35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
 50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
 65 70 75 80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
 100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
 115 120 125

eo1f-othd-000002

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
 130 135 140
 Gly Ser Ala Ile Ala Ser Gly Val Ala Val Ser Lys Val Leu His Leu
 145 150 155 160
 Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
 165 170 175
 Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val
 180 185 190
 Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Val Asn
 195 200 205
 Lys Gln Ser Cys Ser Ile Ser Asn Ile Ala Thr Val Ile Glu Phe Gln
 210 215 220
 Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
 225 230 235 240
 Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
 245 250 255
 Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
 260 265 270
 Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
 275 280 285
 Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
 290 295 300
 Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
 305 310 315 320
 Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
 325 330 335
 Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
 340 345 350
 Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
 355 360 365
 Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val

eo1f-othd-000002

370

375

380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385 390 395 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
405 410 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
420 425 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
435 440 445

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

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465 470 475 480

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

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
500 505 510

Leu His Asn Val Asn Ala Gly Lys Ser Thr Ile Asn Ile Met Ile Thr
515 520 525

Thr Ile Ile Ile Val Ile Ile Val Ile Leu Leu Ser Leu Ile Ala Val
530 535 540

Gly Leu Leu Leu Tyr Cys Lys Ala Arg Ser Thr Pro Val Thr Leu Ser
545 550 555 560

Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe Ser Asn
565 570

<210> 3
<211> 897
<212> DNA
<213> respiratory syncytial virus

<400> 3
atgtccaaaa acaaggacca acgcaccgct aagacactag aaaagacctg ggacactctc 60
aatcatttat tattcatatc atcgggctta tataagttaa atcttaaadc tatagcacia 120
atcacattat ccattctggc aatgataatc tcaacttcac ttataattac agccatcata 180

eolf-othd-000002

ttcatagcct	cggcaaacca	caaagtcaca	ctaacaactg	caatcataca	agatgcaaca	240
agccagatca	agaacacaac	cccaacatac	ctcactcagg	atcctcagct	tggaatcagc	300
ttctccaatc	tgtctgaaat	tacatcacaa	accaccacca	tactagcttc	aacaacacca	360
ggagtcaagt	caaacctgca	acccacaaca	gtcaagacta	aaaacacaac	aacaacccaa	420
acacaaccca	gcaagcccac	tacaaaacaa	cgccaaaaca	aaccaccaaa	caaacccaat	480
aatgattttc	acttcgaagt	gtttaacttt	gtacctgca	gcatatgcag	caacaatcca	540
acctgctggg	ctatctgcaa	aagaatacca	aacaaaaaac	caggaaagaa	aaccaccacc	600
aagcctacaa	aaaaaccaac	cttcaagaca	accaaaaaag	atctcaaacc	tcaaaccact	660
aaaccaaagg	aagtaccac	caccaagccc	acagaagagc	caaccatcaa	caccaccaaa	720
acaaacatca	caactacact	gctcaccaac	aacaccacag	gaaatccaaa	actcacaagt	780
caaatggaaa	ccttccactc	aacctcctcc	gaaggcaatc	taagcccttc	tcaagtctcc	840
acaacatccg	agcaccatc	acaacctca	tctccacca	acacaacacg	ccagtag	897

<210> 4
 <211> 298
 <212> PRT
 <213> respiratory syncytial virus

<400> 4

Met Ser Lys Asn Lys Asp Gln Arg Thr Ala Lys Thr Leu Glu Lys Thr
 1 5 10 15

Trp Asp Thr Leu Asn His Leu Leu Phe Ile Ser Ser Gly Leu Tyr Lys
 20 25 30

Leu Asn Leu Lys Ser Ile Ala Gln Ile Thr Leu Ser Ile Leu Ala Met
 35 40 45

Ile Ile Ser Thr Ser Leu Ile Ile Thr Ala Ile Ile Phe Ile Ala Ser
 50 55 60

Ala Asn His Lys Val Thr Leu Thr Thr Ala Ile Ile Gln Asp Ala Thr
 65 70 75 80

Ser Gln Ile Lys Asn Thr Thr Pro Thr Tyr Leu Thr Gln Asp Pro Gln
 85 90 95

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

Thr Ile Leu Ala Ser Thr Thr Pro Gly Val Lys Ser Asn Leu Gln Pro
 115 120 125

eo1f-othd-000002

Thr Thr Val Lys Thr Lys Asn Thr Thr Thr Thr Gln Thr Gln Pro Ser
130 135 140

Lys Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro Pro Asn Lys Pro Asn
145 150 155 160

Asn Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Cys Ser Ile Cys
165 170 175

Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys Arg Ile Pro Asn Lys
180 185 190

Lys Pro Gly Lys Lys Thr Thr Thr Lys Pro Thr Lys Lys Pro Thr Phe
195 200 205

Lys Thr Thr Lys Lys Asp Leu Lys Pro Gln Thr Thr Lys Pro Lys Glu
210 215 220

Val Pro Thr Thr Lys Pro Thr Glu Glu Pro Thr Ile Asn Thr Thr Lys
225 230 235 240

Thr Asn Ile Thr Thr Thr Leu Leu Thr Asn Asn Thr Thr Gly Asn Pro
245 250 255

Lys Leu Thr Ser Gln Met Glu Thr Phe His Ser Thr Ser Ser Glu Gly
260 265 270

Asn Leu Ser Pro Ser Gln Val Ser Thr Thr Ser Glu His Pro Ser Gln
275 280 285

Pro Ser Ser Pro Pro Asn Thr Thr Arg Gln
290 295

<210> 5
<211> 1566
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant PreF polynucleotide

<400> 5
aagcttgcca ccatggagct gctgatcctg aaaaccaacg ccatcaccgc catcctggcc 60
gccgtgaccc tgtgcttcgc ctctcccag aacatcaccg aggagttcta ccagtccacc 120
tgctccgccg tgtccaaggg ctacctgtcc gccctgcgga ccggctggta cacctccgtg 180
atcaccatcg agctgtccaa catcaaggaa aacaagtgca acggcaccga cgccaagggtg 240
aagctgatca agcaggagct ggacaagtac aagagcgccg tgaccgaact ccagctgctg 300

eo1f-othd-000002

atgcagtcca	cccctgccac	caacaacaag	tttctgggct	tcctgctggg	cgtgggctcc	360
gccatcgct	ccggcatcgc	cgtgagcaag	gtgctgcacc	tggagggcga	ggtgaacaag	420
atcaagagcg	ccctgctgtc	caccaacaag	gccgtggtgt	ccctgtccaa	cggcgtgtcc	480
gtgctgacct	ccaaggtgct	ggatctgaag	aactacatcg	acaagcagct	gctgcctatc	540
gtgaacaagc	agtcctgtct	catctccaac	atcgagaccg	tgatcgagtt	ccagcagaag	600
aacaaccggc	tgctggagat	cacccgcgag	ttctccgtga	acgccggcgt	gaccacccct	660
gtgtccacct	acatgctgac	caactccgag	ctgctgtccc	tgatcaacga	catgcctatc	720
accaacgacc	agaaaaaact	gatgtccaac	aacgtgcaga	tcgtgcggca	gcagtcctac	780
agcatcatga	gcatcatcaa	ggaagagggtg	ctggcctacg	tggcgcagct	gcctctgtac	840
ggcgtgatcg	acaccccttg	ctggaagctg	cacacctccc	ccctgtgcac	caccaacacc	900
aaggaggggct	ccaacatctg	cctgacccgg	accgaccggg	gctggtactg	cgacaacgcc	960
ggctccgtgt	ccttcttccc	tctggccgag	acctgcaagg	tgacgtccaa	ccgggtgttc	1020
tgcgacacca	tgaactccct	gaccctgcct	tccgagggtga	acctgtgcaa	catcgacatc	1080
ttcaacccca	agtacgactg	caagatcatg	accagcaaga	ccgacgtgtc	ctccagcgtg	1140
atcacctccc	tgggcgccat	cgtgtcctgc	tacggcaaga	ccaagtgcac	cgctccaac	1200
aagaaccggg	gaatcatcaa	gaccttctcc	aacggctgcg	actacgtgtc	caataagggc	1260
gtggacaccg	tgtccgtggg	caacacactg	tactacgtga	ataagcagga	gggcaagagc	1320
ctgtacgtga	agggcgagcc	tatcatcaac	ttctacgacc	ctctggtgtt	cccttccgac	1380
gagttcgacg	cctccatcag	ccagggtgaac	gagaagatca	accagtcctt	ggccttcac	1440
cggaagtccg	acgagaagct	gcataacgtg	gaggacaaga	tcgaggagat	cctgtccaaa	1500
atctaccaca	tcgagaacga	gatcgcccgg	atcaagaagc	tgatcggcga	ggcctgataa	1560
tctaga						1566

<210> 6
 <211> 514
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant PreF Antigen

<400> 6

Met	Glu	Leu	Leu	Ile	Leu	Lys	Thr	Asn	Ala	Ile	Thr	Ala	Ile	Leu	Ala
1				5					10					15	

Ala	Val	Thr	Leu	Cys	Phe	Ala	Ser	Ser	Gln	Asn	Ile	Thr	Glu	Glu	Phe
			20					25					30		

eo1f-othd-000002

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
 35 40 45
 Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
 50 55 60
 Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
 65 70 75 80
 Gln Glu Leu Asp Lys Tyr Lys Ser Ala Val Thr Glu Leu Gln Leu Leu
 85 90 95
 Met Gln Ser Thr Pro Ala Thr Asn Asn Lys Phe Leu Gly Phe Leu Leu
 100 105 110
 Gly Val Gly Ser Ala Ile Ala Ser Gly Ile Ala Val Ser Lys Val Leu
 115 120 125
 His Leu Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr
 130 135 140
 Asn Lys Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser
 145 150 155 160
 Lys Val Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile
 165 170 175
 Val Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu
 180 185 190
 Phe Gln Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser
 195 200 205
 Val Asn Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn
 210 215 220
 Ser Glu Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln
 225 230 235 240
 Lys Lys Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr
 245 250 255
 Ser Ile Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln
 260 265 270
 Leu Pro Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr
 275 280 285

eo1f-othd-000002

Ser Pro Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu
290 295 300

Thr Arg Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser
305 310 315 320

Phe Phe Pro Leu Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe
325 330 335

Cys Asp Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys
340 345 350

Asn Ile Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser
355 360 365

Lys Thr Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val
370 375 380

Ser Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly
385 390 395 400

Ile Ile Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly
405 410 415

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

Glu Gly Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr
435 440 445

Asp Pro Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln
450 455 460

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

Glu Lys Leu His Asn Val Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys
485 490 495

Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly
500 505 510

Glu Ala

<210> 7

eo1f-othd-000002

<211> 1855
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric PreF-G Antigen polynucleotide sequence

<400> 7
aagcttgcca ccatggagct gctgatcctc aagaccaacg ccatcaccgc catcctggcc 60
gccgtgaccc tgtgcttcgc ctctcccag aacatcaccg aagagttcta ccagtcacc 120
tgctccgccg tgtccaaggg ctacctgtcc gccctgcgga ccggctggta cacctccgtg 180
atcaccatcg agctgtccaa catcaaagaa aacaagtgca acggcaccga cgccaaggtc 240
aagctgatca agcaggaact ggacaagtac aagagcgccg tgaccgaact ccagctgctg 300
atgcagtcca cccctgccac caacaacaag aagtttctgg gcttcctgct gggcgtgggc 360
tccgccatcg cctccggcat cgccgtgagc aagggtgctgc acctggaggg cgagggtgaac 420
aagatcaaga gcgccctgct gtccaccaac aaggccgtgg tgtccctgtc caacggcgtg 480
tccgtgctga cctccaaggt gctggatctg aagaactaca tcgacaagca gctgctgcct 540
atcgtgaaca agcagtcctg ctccatctcc aacatcgaga ccgtgatcga gttccagcag 600
aagaacaacc ggctgctgga gatcaccgc gagttctccg tgaacgccgg cgtgaccacc 660
cctgtgtcca cctacatgct gacaaaactcc gagctgctct ccctgatcaa cgacatgcct 720
atcaccaacg accaaaaaaaa gctgatgtcc aacaacgtgc agatcgtgcg gcagcagtcc 780
tacagcatca tgagcatcat caaggaagaa gtcctggcct acgtcgtgca gctgcctctg 840
tacggcgtga tcgacacccc ttgctggaag ctgcacacct cccccctgtg caccaccaac 900
accaaagagg gctccaacat ctgcctgacc cggaccgacc ggggctggta ctgcgacaac 960
gccggctccg tgtccttctt ccctctggcc gagacctgca aggtgcagtc caaccgggtg 1020
ttctgcgaca ccatgaactc cctgaccctg ccttccgagg tgaacctgtg caacatcgac 1080
atcttcaacc ccaagtacga ctgcaagatc atgaccagca agaccgacgt gtcctccagc 1140
gtgatcacct ccctgggcgc catcgtgtcc tgctacggca agaccaagtg caccgcctcc 1200
aacaagaacc ggggaatcat caagacctc tccaacggct gcgactacgt gtccaataag 1260
ggcgtggaca ccgtgtccgt gggcaacaca ctgtactacg tgaataagca ggaaggcaag 1320
agcctgtacg tgaagggcga gcctatcatc aacttctacg accctctggt gttcccttcc 1380
gacgagttcg acgcctccat cagccaggtc aacgagaaga tcaaccagtc cctggccttc 1440
atccggaagt ccgacgagaa gctgcataac gtggaggaca agatcgaaga gatcctgtcc 1500
aaaatctacc acatcgagaa cgagatcgcc cggatcaaga agctgatcgg cgaggctggc 1560
ggctctggcg gcagcggcgg ctccaagcag cggcagaaca agcctcctaa caagcccaac 1620
aacgacttcc acttcgaggt gttcaacttc gtgccttgct ccactctgctc caacaaccct 1680

eo1f-othd-000002

acctgctggg ccattctgcaa gagaatcccc aacaagaagc ctggcaagaa aaccaccacc 1740
aagcctacca agaagcctac cttcaagacc accaagaagg accacaagcc tcagaccaca 1800
aagcctaagg aagtgccaac caccaagcac caccaccatc accactgata atcta 1855

<210> 8
<211> 605
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric PreF-G polypeptide

<400> 8

Met Glu Leu Leu Ile Leu Lys Thr Asn Ala Ile Thr Ala Ile Leu Ala
1 5 10 15

Ala Val Thr Leu Cys Phe Ala Ser Ser Gln Asn Ile Thr Glu Glu Phe
20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Lys Lys Phe Leu Gly Phe Leu
100 105 110

Leu Gly Val Gly Ser Ala Ile Ala Ser Gly Ile Ala Val Ser Lys Val
115 120 125

Leu His Leu Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser
130 135 140

Thr Asn Lys Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr
145 150 155 160

Ser Lys Val Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro
165 170 175

Ile Val Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile

180

185

190

Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe
 195 200 205
 Ser Val Asn Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr
 210 215 220
 Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp
 225 230 235 240
 Gln Lys Lys Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser
 245 250 255
 Tyr Ser Ile Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val
 260 265 270
 Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His
 275 280 285
 Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys
 290 295 300
 Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val
 305 310 315 320
 Ser Phe Phe Pro Leu Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val
 325 330 335
 Phe Cys Asp Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu
 340 345 350
 Cys Asn Ile Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr
 355 360 365
 Ser Lys Thr Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile
 370 375 380
 Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg
 385 390 395 400
 Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys
 405 410 415
 Gly Val Asp Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys
 420 425 430

eo1f-othd-000002

Gln Glu Gly Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe
435 440 445

Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser
450 455 460

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

Asp Glu Lys Leu His Asn Val Glu Asp Lys Ile Glu Glu Ile Leu Ser
485 490 495

Lys Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile
500 505 510

Gly Glu Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser Lys Gln Arg Gln
515 520 525

Asn Lys Pro Pro Asn Lys Pro Asn Asn Asp Phe His Phe Glu Val Phe
530 535 540

Asn Phe Val Pro Cys Ser Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala
545 550 555 560

Ile Cys Lys Arg Ile Pro Asn Lys Lys Pro Gly Lys Lys Thr Thr Thr
565 570 575

Lys Pro Thr Lys Lys Pro Thr Phe Lys Thr Thr Lys Lys Asp His Lys
580 585 590

Pro Gln Thr Thr Lys Pro Lys Glu Val Pro Thr Thr Lys
595 600 605

<210> 9
<211> 1834
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric PreF-G polynucleotide

<400> 9
aagcttgcca ccatggagct gctgacctc aagaccaacg ccatcaccgc catcctggcc 60
gccgtgaccc tgtgcttcgc ctctcccag aacatcaccg aagagttcta ccagtcacc 120
tgctccgccg tgtccaaggg ctacctgtcc gccctgcgga ccggctggta cacctccgtg 180
atcaccatcg agctgtccaa catcaaagaa aacaagtgca acggcaccga cgccaaggctc 240
aagctgatca agcaggaact ggacaagtac aagagcgccg tgaccgaact ccagctgctg 300

eolf-othd-000002

atgcagtcca	cccctgccac	caacaacaag	aagtttctgg	gcttcctgct	gggcgtgggc	360
tccgccatcg	cctccggcat	cgccgtgagc	aagggtgctgc	acctggaggg	cgagggtgaac	420
aagatcaaga	gcgccctgct	gtccaccaac	aaggccgtgg	tgtccctgtc	caacggcgtg	480
tccgtgctga	cctccaaggt	gctggatctg	aagaactaca	tcgacaagca	gctgctgcct	540
atcgtgaaca	agcagtccctg	ctccatctcc	aacatcgaga	ccgtgatcga	gttccagcag	600
aagaacaacc	ggctgctgga	gatcacccgc	gagttctccg	tgaacgccgg	cgtgaccacc	660
cctgtgtcca	cctacatgct	gacaaaactcc	gagctgctct	ccctgatcaa	cgacatgcct	720
atcaccaacg	accaaaaaaa	gctgatgtcc	aacaacgtgc	agatcgtgcg	gcagcagtcc	780
tacagcatca	tgagcatcat	caaggaagaa	gtcctggcct	acgtcgtgca	gctgcctctg	840
tacggcgtga	tcgacacccc	ttgctggaag	ctgcacacct	ccccctgtg	caccaccaac	900
accaaagagg	gtccaacat	ctgcctgacc	cggaccgacc	ggggctggta	ctgcgacaac	960
gccggctccg	tgtccttctt	ccctctggcc	gagacctgca	agggtgcagtc	caaccgggtg	1020
ttctgcgaca	ccatgaactc	cctgaccctg	ccttccgagg	tgaacctgtg	caacatcgac	1080
atcttcaacc	ccaagtacga	ctgcaagatc	atgaccagca	agaccgacgt	gtcctccagc	1140
gtgatcacct	ccctgggcgc	catcgtgtcc	tgctacggca	agaccaagtg	caccgcctcc	1200
aacaagaacc	ggggaatcat	caagaccttc	tccaacggct	gcgactacgt	gtccaataag	1260
ggcgtggaca	ccgtgtccgt	gggcaacaca	ctgtactacg	tgaataagca	ggaaggcaag	1320
agcctgtacg	tgaagggcga	gcctatcatc	aacttctacg	accctctggt	gttcccttcc	1380
gacgagttcg	acgcctccat	cagccaggtc	aacgagaaga	tcaaccagtc	cctggccttc	1440
atccggaagt	ccgacgagaa	gctgcataac	gtggaggaca	agatcgaaga	gatcctgtcc	1500
aaaatctacc	acatcgagaa	cgagatcgcc	cggatcaaga	agctgatcgg	cgaggctggc	1560
ggcaagcagc	ggcagaacaa	gcctcctaac	aagcccaaca	acgacttcca	cttcgagggtg	1620
ttcaacttcg	tgcttgctc	catctgtctc	aacaacccta	cctgctgggc	catctgcaag	1680
agaatcccca	acaagaagcc	tggcaagaaa	accaccacca	agcctaccaa	gaagcctacc	1740
ttcaagacca	ccaagaagga	ccacaagcct	cagaccacaa	agcctaagga	agtgccaacc	1800
accaagcacc	accaccatca	ccactgataa	tcta			1834

<210> 10
 <211> 598
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Chimeric PreF-G polypeptide

 <400> 10

eo1f-othd-000002

Met Glu Leu Leu Ile Leu Lys Thr Asn Ala Ile Thr Ala Ile Leu Ala
1 5 10 15

Ala Val Thr Leu Cys Phe Ala Ser Ser Gln Asn Ile Thr Glu Glu Phe
20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Lys Lys Phe Leu Gly Phe Leu
100 105 110

Leu Gly Val Gly Ser Ala Ile Ala Ser Gly Ile Ala Val Ser Lys Val
115 120 125

Leu His Leu Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser
130 135 140

Thr Asn Lys Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr
145 150 155 160

Ser Lys Val Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro
165 170 175

Ile Val Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile
180 185 190

Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe
195 200 205

Ser Val Asn Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr
210 215 220

Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp
225 230 235 240

Gln Lys Lys Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser
245 250 255

eo1f-othd-000002

Tyr Ser Ile Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val
 260 265 270
 Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His
 275 280 285
 Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys
 290 295 300
 Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val
 305 310 315 320
 Ser Phe Phe Pro Leu Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val
 325 330 335
 Phe Cys Asp Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu
 340 345 350
 Cys Asn Ile Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr
 355 360 365
 Ser Lys Thr Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile
 370 375 380
 Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg
 385 390 395 400
 Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys
 405 410 415
 Gly Val Asp Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys
 420 425 430
 Gln Glu Gly Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe
 435 440 445
 Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser
 450 455 460
 Gln Val Asn Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser
 465 470 475 480
 Asp Glu Lys Leu His Asn Val Glu Asp Lys Ile Glu Glu Ile Leu Ser
 485 490 495
 Lys Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile
 500 505 510

eo1f-othd-000002

Gly Glu Ala Gly Gly Lys Gln Arg Gln Asn Lys Pro Pro Asn Lys Pro
515 520 525

Asn Asn Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Cys Ser Ile
530 535 540

Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys Arg Ile Pro Asn
545 550 555 560

Lys Lys Pro Gly Lys Lys Thr Thr Thr Lys Pro Thr Lys Lys Pro Thr
565 570 575

Phe Lys Thr Thr Lys Lys Asp His Lys Pro Gln Thr Thr Lys Pro Lys
580 585 590

Glu Val Pro Thr Thr Lys
595

<210> 11
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Isoleucine substituted GCN4 leucine zipper
<400> 11

Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu Asn
1 5 10 15

Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Ala
20 25

<210> 12
<211> 1563
<212> DNA
<213> Artificial sequence

<220>
<223> Codon optimized PreF nucleotide sequence

<400> 12
atggagctgc ccattcctgaa gaccaacgcc atcaccacca tcctcgccgc cgtgaccctg 60
tgcttcgcca gcagccagaa catcacggag gagttctacc agagcacgtg cagcgccgtg 120
agcaagggct acctgagcgc gctgcgacg ggctggtaca cgagcgtgat cacgatcgag 180
ctgagcaaca tcaaggagaa caagtgaac ggcacggacg cgaaggtgaa gctgatcaag 240
caggagctgg acaagtacaa gagcgcggtg acggagctgc agctgctgat gcagagcacg 300

eolF-othd-000002

ccggcgacga	acaacaagtt	cctcggcttc	ctgctgggcg	tgggcagcgc	gatcgcgagc	360
ggcatcgccg	tgagcaaggt	gctgcacctg	gagggcgagg	tgaacaagat	caagtccgcg	420
ctgctgagca	cgaacaaggc	ggtcgtgagc	ctgagcaacg	gcgtgagcgt	gctgacgagc	480
aaggtgctcg	acctgaagaa	ctacatcgac	aagcagctgc	tgccgatcgt	gaacaagcag	540
agctgcagca	tcagcaacat	cgagaccgtg	atcgagttcc	agcagaagaa	caaccgcctg	600
ctggagatca	cgcgggagtt	ctccgtgaac	gcaggcgtga	cgacgcccgt	gtctacgtac	660
atgctgacga	acagcgagct	gctcagcctg	atcaacgaca	tgccgatcac	gaacgaccag	720
aagaagctga	tgagcaacaa	cgtgcagatc	gtgcgccagc	agagctacag	catcatgagc	780
atcatcaagg	aggagggtgct	ggcatacgtg	gtgcagctgc	cgctgtacgg	cgatcatcgac	840
acgccctgct	ggaagctgca	cacgagccccg	ctgtgcacga	ccaacacgaa	ggagggcagc	900
aacatctgcc	tgacgcggac	ggaccggggc	tggtactgcy	acaacgcggg	cagcgtgagc	960
ttcttcccgc	tcgcggagac	gtgcaagggtg	cagagcaacc	gcgtcttctg	cgacacgatg	1020
aacagcctga	cgctgccgag	cgagggtgaac	ctgtgcaaca	tcgacatctt	caacccgaag	1080
tacgactgca	agatcatgac	gagcaagacc	gatgtcagca	gcagcgtgat	cacgagcctc	1140
ggcgcgatcg	tgagctgcta	cggcaagacg	aagtgcacgg	cgagcaacaa	gaaccgcggc	1200
atcatcaaga	cgttcagcaa	cggctgcgac	tatgtgagca	acaagggcgt	ggacactgtg	1260
agcgtcggca	acacgctgta	ctacgtgaac	aagcaggagg	gcaagagcct	gtacgtgaag	1320
ggcgagccga	tcatcaactt	ctacgacccg	ctcgtgttcc	cgagcgacga	gttcgacgcg	1380
agcatcagcc	aagtgaacga	gaagatcaac	cagagcctgg	cgttcatccg	caagagcgac	1440
gagaagctgc	acaacgtgga	ggacaagatc	gaggagatcc	tgagcaagat	ctaccacatc	1500
gagaacgaga	tcgcgcgcat	caagaagctg	atcggcgagg	cgcatcatca	ccatcaccat	1560
tga						1563

<210> 13
 <211> 1685
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PreF polynucleotide sequence with intron

<400> 13	
atggagctgc	tgatcctgaa aaccaacgcc atcaccgcca tcctggccgc cgtgaccctg 60
tgcttcgcct	cctcccagaa catcaccgag gagttctacc agtccacctg ctccgccgtg 120
tccaagggct	acctgtccgc cctgcggacc ggctggtaca cctccgtgat caccatcgag 180
ctgtccaaca	tcaaggaaaa caagtgaac ggaccgacg ccaagggtgaa gctgatcaag 240
caggagctgg	acaagtacaa gagcgccgtg accgaactcc agctgctgat gcagtccacc 300

eo1f-othd-000002

cctgccacca acaacaagtt tctgggcttc ctgctgggcg tgggctccgc catcgcctcc	360
ggcatcgccg tgagcaaggt acgtgtcggg acttgtgttc cccttttttt aataaaaaagt	420
tatatcttta atgttatata catatttcct gtatgtgatc catgtgctta tgactttggt	480
tatcatgtgt ttaggtgctg cacctggagg gcgaggtgaa caagatcaag agcgccctgc	540
tgtccaccaa caaggccgtg gtgtcccctgt ccaacggcgt gtccgtgctg acctccaagg	600
tgctggatct gaagaactac atcgacaagc agctgtgcc tatcgtgaac aagcagtcct	660
gctccatctc caacatcgag accgtgatcg agttccagca gaagaacaac cggctgctgg	720
agatcacccg cgagttctcc gtgaacgccg gctgaccac ccctgtgtcc acctacatgc	780
tgaccaactc cgagctgctg tccctgatca acgacatgcc tatcaccaac gaccagaaaa	840
aactgatgtc caacaacgtg cagatcgtgc ggcagcagtc ctacagcatc atgagcatca	900
tcaaggaaga ggtgctggcc tacgtggtgc agctgcctct gtacggcgtg atcgacaccc	960
cttgctggaa gctgcacacc tccccctgt gcaccaccaa caccaaggag ggctccaaca	1020
tctgcctgac ccggaccgac cggggctggt actgcgacaa cgccggctcc gtgtccttct	1080
tccctctggc cgagacctgc aaggtgcagt ccaaccgggt gttctgagac accatgaact	1140
ccctgaccct gccttccgag gtgaacctgt gcaacatcga catcttcaac cccaagtacg	1200
actgcaagat catgaccagc aagaccgacg tgtcctccag cgtgatcacc tccctgggcg	1260
ccatcgtgtc ctgctacggc aagaccaagt gcaccgcctc caacaagaac cggggaatca	1320
tcaagacctt ctccaacggc tgcgactacg tgtccaataa gggcgtggac accgtgtccg	1380
tgggcaacac actgtactac gtgaataagc aggagggcaa gagcctgtac gtgaagggcg	1440
agcctatcat caacttctac gaccctctgg tgttcccttc cgacgagttc gacgcctcca	1500
tcagccaggt gaacgagaag atcaaccagt ccctggcctt catccggaag tccgacgaga	1560
agctgcataa cgtggaggac aagatcgagg agatcctgtc caaaatctac cacatcgaga	1620
acgagatcgc ccgatcaag aagctgatcg gcgaggccgg aggtcaccac caccatcacc	1680
actga	1685

<210> 14
 <211> 9
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> Synthetic linker peptide
 <400> 14

Gly Gly Ser Gly Gly Ser Gly Gly Ser
 1 5

eo1f-othd-000002

<210> 15
 <211> 4
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Furin cleavage consensus motif

<400> 15

Arg Ala Arg Arg
 1

<210> 16
 <211> 4
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Furin cleavage consensus motif

<400> 16

Arg Lys Arg Arg
 1

<210> 17
 <211> 1542
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic PreF Polynucleotide

<400> 17
 atggagctgc tgatcctgaa aaccaacgcc atcaccgccca tcctggccgc cgtgaccctg 60
 tgcttcgcct cctcccagaa catcaccgag gagttctacc agtccacctg ctccgccgtg 120
 tccaagggct acctgtccgc cctgcggaacc ggctggtaca cctccgtgat caccatcgag 180
 ctgtccaaca tcaaggaaaa caagtgaac ggcaccgacg ccaaggtgaa gctgatcaag 240
 caggagctgg acaagtacaa gagcgccgtg accgaactcc agctgctgat gcagtccacc 300
 cctgccacca acaacaagtt tctgggcttc ctgctgggcg tgggctccgc catcgctcc 360
 ggcatcgccg tgagcaaggt gctgcacctg gagggcgagg tgaacaagat caagagcgcc 420
 ctgctgtcca ccaacaaggc cgtggtgtcc ctgtccaacg gcgtgtccgt gctgacctcc 480
 aagggtgctg atctgaagaa ctacatcgac aagcagctgc tgcctatcgt gaacaagcag 540
 tcctgctcca tctccaacat cgagaccgtg atcgagttcc agcagaagaa caaccggctg 600
 ctggagatca cccgcgagtt ctccgtgaac gccggcgatga ccaccctgt gtccacctac 660
 atgctgacca actccgagct gctgtccctg atcaacgaca tgcctatcac caacgaccag 720
 aaaaaactga tgtccaacaa cgtgcagatc gtgcggcagc agtcctacag catcatgagc 780

eo1f-othd-000002

atcatcaagg aagaggtgct ggcctacgtg gtgcagctgc ctctgtacgg cgtgatcgac 840
 accccttgct ggaagctgca cacctcccc ctgtgcacca ccaacaccaa ggagggctcc 900
 aacatctgcc tgacccggac cgaccggggc tggactgctg acaacgccgg ctccgtgtcc 960
 ttcttccctc tggccgagac ctgcaaggtg cagtccaacc ggggtgttctg cgacaccatg 1020
 aactccctga ccctgccttc cgaggtgaac ctgtgcaaca tcgacatctt caaccccaag 1080
 tacgactgca agatcatgac cagcaagacc gacgtgtcct ccagcgtgat cacctccctg 1140
 ggcgccatcg tgcctgcta cggcaagacc aagtgcaccg cctccaacaa gaaccgggga 1200
 atcatcaaga ccttctccaa cggctgcgac tacgtgtcca ataagggcgt ggacaccgtg 1260
 tccgtgggca acacactgta ctacgtgaat aagcaggagg gcaagagcct gtacgtgaag 1320
 ggcgagccta tcatcaactt ctacgaccct ctgggtgtcc cttccgacga gttcgacgcc 1380
 tccatcagcc aggtgaacga gaagatcaac gggaccctgg ccttcatccg gaagtccgac 1440
 gagaagctgc ataacgtgga ggacaagatc gaggagatcc tgtccaaaat ctaccacatc 1500
 gagaacgaga tcgcccggat caagaagctg atcggcgagg cc 1542

<210> 18
 <211> 514
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic PreF Polypeptide

<400> 18

Met Glu Leu Leu Ile Leu Lys Thr Asn Ala Ile Thr Ala Ile Leu Ala
 1 5 10 15

Ala Val Thr Leu Cys Phe Ala Ser Ser Gln Asn Ile Thr Glu Glu Phe
 20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
 35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
 50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
 65 70 75 80

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

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

100

105

110

Gly Val Gly Ser Ala Ile Ala Ser Gly Ile Ala Val Ser Lys Val Leu
 115 120 125
 His Leu Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr
 130 135 140
 Asn Lys Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser
 145 150 155 160
 Lys Val Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile
 165 170 175
 Val Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu
 180 185 190
 Phe Gln Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser
 195 200 205
 Val Asn Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn
 210 215 220
 Ser Glu Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln
 225 230 235 240
 Lys Lys Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr
 245 250 255
 Ser Ile Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln
 260 265 270
 Leu Pro Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr
 275 280 285
 Ser Pro Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu
 290 295 300
 Thr Arg Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser
 305 310 315 320
 Phe Phe Pro Leu Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe
 325 330 335
 Cys Asp Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys
 340 345 350

eo1f-othd-000002

Asn Ile Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser
355 360 365

Lys Thr Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val
370 375 380

Ser Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly
385 390 395 400

Ile Ile Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly
405 410 415

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

Glu Gly Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr
435 440 445

Asp Pro Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln
450 455 460

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

Glu Lys Leu His Asn Val Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys
485 490 495

Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly
500 505 510

Glu Ala

<210> 19

<211> 1542

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic PreF Polynucleotide

<400> 19

atggagctgc tgatcctgaa aaccaacgcc atcaccgcca tcctggccgc cgtgaccctg 60

tgcttcgcct cctcccagaa catcaccgag gagttctacc agtccacctg ctccgccgtg 120

tccaagggct acctgtccgc cctgcggacc ggctggtaca cctccgtgat caccatcgag 180

ctgtccaaca tcaaggaaaa caagtgaac ggcaccgacg ccaaggtgaa gctgatcaag 240

caggagctgg acaagtacaa gagcgccgtg accgaactcc agctgctgat gcagtcacc 300

eol-f-othd-000002

cctgccacca	acaacaagtt	tctgggcttc	ctgcagggcg	tgggctccgc	catcgctcc	360
ggcatcgccg	tgagcaaggt	gctgcacctg	gagggcgagg	tgaacaagat	caagagcgcc	420
ctgctgtcca	ccaacaaggc	cgtggtgtcc	ctgtccaacg	gcgtgtccgt	gctgacctcc	480
aaggtgctgg	atctgaagaa	ctacatcgac	aagcagctgc	tgcctatcgt	gaacaagcag	540
tcctgctcca	tctccaacat	cgagaccgtg	atcgagttcc	agcagaagaa	caaccggctg	600
ctggagatca	cccgcgagtt	ctccgtgaac	gccggcgatg	ccacccctgt	gtccacctac	660
atgctgacca	actccgagct	gctgtccctg	atcaacgaca	tgcctatcac	caacgaccag	720
aaaaaactga	tgtccaacaa	cgtgcagatc	gtgcggcagc	agtccctacag	catcatgagc	780
atcatcaagg	aagagggtgct	ggcctacgtg	gtgcagctgc	ctctgtacgg	cgtgatcgac	840
accccttgct	ggaagctgca	cacctcccc	ctgtgcacca	ccaacaccaa	ggagggctcc	900
aacatctgcc	tgacccggac	cgaccggggc	tgggtactgcg	acaacgccgg	ctccgtgtcc	960
ttcttccctc	tggccgagac	ctgcaagggtg	cagtccaacc	gggtgttctg	cgacaccatg	1020
aactccctga	ccctgccttc	cgagggtgaac	ctgtgcaaca	tcgacatctt	caaccccaag	1080
tacgactgca	agatcatgac	cagcaagacc	gacgtgtcct	ccagcgtgat	cacctccctg	1140
ggcgccatcg	tgtcctgcta	cggcaagacc	aagtgcaccg	cctccaacaa	gaaccgggga	1200
atcatcaaga	ccttctccaa	cggctgcgac	tacgtgtcca	ataagggcgt	ggacaccgtg	1260
tccgtgggca	acacactgta	ctacgtgaat	aagcaggagg	gcaagagcct	gtacgtgaag	1320
ggcgagccta	tcatcaactt	ctacgaccct	ctggtgttcc	cttccgacga	gttcgacgcc	1380
tccatcagcc	aggtgaacga	gaagatcaac	cagtccctgg	ccttcatccg	gaagtccgac	1440
gagaagctgc	ataacgtgga	ggacaagatc	gaggagatcc	tgtccaaaat	ctaccacatc	1500
gagaacgaga	tcgcccggat	caagaagctg	atcggcgagg	cc		1542

<210> 20
 <211> 514
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic PreF Polypeptide
 <400> 20

Met	Glu	Leu	Leu	Ile	Leu	Lys	Thr	Asn	Ala	Ile	Thr	Ala	Ile	Leu	Ala
1				5					10					15	

Ala	Val	Thr	Leu	Cys	Phe	Ala	Ser	Ser	Gln	Asn	Ile	Thr	Glu	Glu	Phe
			20					25					30		

Tyr	Gln	Ser	Thr	Cys	Ser	Ala	Val	Ser	Lys	Gly	Tyr	Leu	Ser	Ala	Leu
		35					40					45			

eo1f-othd-000002

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Lys Phe Leu Gly Phe Leu Gln
100 105 110

Gly Val Gly Ser Ala Ile Ala Ser Gly Ile Ala Val Ser Lys Val Leu
115 120 125

His Leu Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr
130 135 140

Asn Lys Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser
145 150 155 160

Lys Val Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile
165 170 175

Val Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu
180 185 190

Phe Gln Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser
195 200 205

Val Asn Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn
210 215 220

Ser Glu Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln
225 230 235 240

Lys Lys Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr
245 250 255

Ser Ile Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln
260 265 270

Leu Pro Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr
275 280 285

Ser Pro Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu

eo1f-othd-000002

290

295

300

Thr Arg Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser
305 310 315 320

Phe Phe Pro Leu Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe
325 330 335

Cys Asp Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys
340 345 350

Asn Ile Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser
355 360 365

Lys Thr Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val
370 375 380

Ser Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly
385 390 395 400

Ile Ile Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly
405 410 415

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

Glu Gly Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr
435 440 445

Asp Pro Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln
450 455 460

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

Glu Lys Leu His Asn Val Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys
485 490 495

Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly
500 505 510

Glu Ala

<210> 21
<211> 1542
<212> DNA
<213> Artificial Sequence

eo1f-othd-000002

<220>

<223> Synthetic PreF Polynucleotide

<400> 21

atggagctgc tgatcctgaa aaccaacgcc atcaccgccca tcctggccgc cgtgaccctg	60
tgcttcgcct cctcccagaa catcaccgag gagttctacc agtccacctg ctccgccgtg	120
tccaagggct acctgtccgc cctgcggacc ggctggtaca cctccgtgat caccatcgag	180
ctgtccaaca tcaaggaaaa caagtgaac ggcaccgacg ccaaggtgaa gctgatcaag	240
caggagctgg acaagtacaa gagcgccgtg accgaactcc agctgctgat gcagtccacc	300
cctgccacca acaacaagtt tctgggcttc ctgcagggcg tgggctccgc catcgctcc	360
ggcatcgccg tgagcaaggt gctgcacctg gagggcgagg tgaacaagat caagagcgcc	420
ctgctgtcca ccaacaaggc cgtggtgtcc ctgtccaacg gcgtgtccgt gctgacctcc	480
aagggtgctgg atctgaagaa ctacatcgac aagcagctgc tgcctatcgt gaacaagcag	540
tcctgctcca tctccaacat cgagaccgtg atcgagttcc agcagaagaa caaccggctg	600
ctggagatca cccgcgagtt ctccgtgaac gccggcgtga ccacccctgt gtccacctac	660
atgctgacca actccgagct gctgtccctg atcaacgaca tgcctatcac caacgaccag	720
aaaaaactga tgtccaacaa cgtgcagatc gtgcggcagc agtcctacag catcatgagc	780
atcatcaagg aagaggtgct ggcctacgtg gtgcagctgc ctctgtacgg cgtgatcgac	840
accccttgct ggaagctgca cacctcccc ctgtgcacca ccaacaccaa ggagggctcc	900
aacatctgcc tgacccggac cgaccggggc tggctactgcg acaacgccgg ctccgtgtcc	960
ttcttcctc tggccgagac ctgcaagggt cagtccaacc ggggtgttctg cgacaccatg	1020
aactccctga ccctgccttc cgagggtgaac ctgtgcaaca tcgacatctt caacccaag	1080
tacgactgca agatcatgac cagcaagacc gacgtgtcct ccagcgtgat cacctccctg	1140
ggcgccatcg tgcctgcta cggcaagacc aagtgcaccg cctccaacaa gaaccgggga	1200
atcatcaaga ctttctcaa cggctgcgac tacgtgtcca ataagggcgt ggacaccgtg	1260
tccgtgggca acacactgta ctacgtgaat aagcaggagg gcaagagcct gtacgtgaag	1320
ggcgagccta tcatcaactt ctacgacctt ctggtgttcc cttccgacga gttcgacgcc	1380
tccatcagcc aggtgaacga gaagatcaac gggaccctgg cttcatccg gaagtccgac	1440
gagaagctgc ataacgtgga ggacaagatc gaggagatcc tgtccaaaat ctaccacatc	1500
gagaacgaga tcgcccggat caagaagctg atcggcgagg cc	1542

<210> 22

<211> 514

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic PreF Polypeptide

<400> 22

Met Glu Leu Leu Ile Leu Lys Thr Asn Ala Ile Thr Ala Ile Leu Ala
 1 5 10 15

Ala Val Thr Leu Cys Phe Ala Ser Ser Gln Asn Ile Thr Glu Glu Phe
 20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
 35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
 50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
 65 70 75 80

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

Met Gln Ser Thr Pro Ala Thr Asn Asn Lys Phe Leu Gly Phe Leu Gln
 100 105 110

Gly Val Gly Ser Ala Ile Ala Ser Gly Ile Ala Val Ser Lys Val Leu
 115 120 125

His Leu Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr
 130 135 140

Asn Lys Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser
 145 150 155 160

Lys Val Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile
 165 170 175

Val Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu
 180 185 190

Phe Gln Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser
 195 200 205

Val Asn Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn
 210 215 220

Ser Glu Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln
 225 230 235 240

eo1f-othd-000002

Lys Lys Leu Met Ser₂₄₅ Asn Asn Val Gln Ile₂₅₀ Val Arg Gln Gln Ser₂₅₅ Tyr
 Ser Ile Met Ser₂₆₀ Ile Ile Lys Glu Glu₂₆₅ Val Leu Ala Tyr Val₂₇₀ Val Gln
 Leu Pro Leu₂₇₅ Tyr Gly Val Ile Asp₂₈₀ Thr Pro Cys Trp Lys₂₈₅ Leu His Thr
 Ser Pro₂₉₀ Leu Cys Thr Thr Asn₂₉₅ Thr Lys Glu Gly Ser₃₀₀ Asn Ile Cys Leu
 Thr₃₀₅ Arg Thr Asp Arg Gly₃₁₀ Trp Tyr Cys Asp Asn₃₁₅ Ala Gly Ser Val Ser₃₂₀
 Phe Phe Pro Leu Ala₃₂₅ Glu Thr Cys Lys Val₃₃₀ Gln Ser Asn Arg Val₃₃₅ Phe
 Cys Asp Thr Met₃₄₀ Asn Ser Leu Thr Leu₃₄₅ Pro Ser Glu Val Asn₃₅₀ Leu Cys
 Asn Ile Asp₃₅₅ Ile Phe Asn Pro Lys₃₆₀ Tyr Asp Cys Lys Ile₃₆₅ Met Thr Ser
 Lys Thr₃₇₀ Asp Val Ser Ser Ser₃₇₅ Val Ile Thr Ser Leu₃₈₀ Gly Ala Ile Val
 Ser₃₈₅ Cys Tyr Gly Lys Thr₃₉₀ Lys Cys Thr Ala Ser₃₉₅ Asn Lys Asn Arg Gly₄₀₀
 Ile Ile Lys Thr Phe₄₀₅ Ser Asn Gly Cys Asp₄₁₀ Tyr Val Ser Asn Lys₄₁₅ Gly
 Val Asp Thr Val₄₂₀ Ser Val Gly Asn Thr₄₂₅ Leu Tyr Tyr Val Asn₄₃₀ Lys Gln
 Glu Gly Lys₄₃₅ Ser Leu Tyr Val Lys₄₄₀ Gly Glu Pro Ile Ile₄₄₅ Asn Phe Tyr
 Asp Pro₄₅₀ Leu Val Phe Pro Ser₄₅₅ Asp Glu Phe Asp Ala₄₆₀ Ser Ile Ser Gln
 Val₄₆₅ Asn Glu Lys Ile Asn₄₇₀ Gly Thr Leu Ala Phe Ile Arg Lys Ser Asp₄₈₀
 Glu Lys Leu His Asn Val Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys

eo1f-othd-000002
490

485

495

Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly
500 505 510

Glu Ala