

eolf-othd-000002
SEQUENCE LISTING

<110> GlaxoSmithKline Biologicals S.A.
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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

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 <212> PRT
 <213> respiratory syncytial virus

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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

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Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
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 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
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 Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
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 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

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370

375

380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
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Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
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Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
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Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
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Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
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Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
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Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
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Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
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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
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Gly Leu Leu Leu Tyr Cys Lys Ala Arg Ser Thr Pro Val Thr Leu Ser
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Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe Ser Asn
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<211> 897
<212> DNA
<213> respiratory syncytial virus

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atcacattat ccattctggc aatgataatc tcaacttcac ttataattac agccatcata 180

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agccagatca	agaacacaac	cccaacatac	ctcactcagg	atcctcagct	tggaatcagc	300
ttctccaatc	tgtctgaaat	tacatcacaa	accaccacca	tactagcttc	aacaacacca	360
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acacaaccca	gcaagcccac	tacaaaacaa	cgccaaaaca	aaccaccaaa	caaacccaat	480
aatgattttc	acttcgaagt	gtttaacttt	gtacctgca	gcatatgcag	caacaatcca	540
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aagcctacaa	aaaaaccaac	cttcaagaca	accaaaaaag	atctcaaacc	tcaaaccact	660
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<210> 4
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 <212> PRT
 <213> respiratory syncytial virus

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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

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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
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Pro Ser Ser Pro Pro Asn Thr Thr Arg Gln
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<211> 1566
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant PreF polynucleotide

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tgctccgccg tgtccaaggg ctacctgtcc gccctgcgga ccggctggta cacctccgtg 180
atcaccatcg agctgtccaa catcaaggaa aacaagtgca acggcaccga cgccaagggtg 240
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aagaaccggg	gaatcatcaa	gaccttctcc	aacggctgcy	actacgtgtc	caataagggc	1260
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 <213> Artificial Sequence

<220>
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 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

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Ser Pro Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu
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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
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Asn Ile Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser
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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
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Glu Ala

<210> 7

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

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

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aagcctacca agaagcctac cttcaagacc accaagaagg accacaagcc tcagaccaca 1800
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<210> 8
<211> 605
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric PreF-G polypeptide

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35 40 45
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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

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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

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Pro Gln Thr Thr Lys Pro Lys Glu Val Pro Thr Thr Lys
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<210> 9

<211> 1834

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric PreF-G polynucleotide

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aagctgatca agcaggaact ggacaagtac aagagcgccg tgaccgaact ccagctgctg 300

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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	tgctcttctt	ccctctggcc	gagacctgca	agggtgcagtc	caaccgggtg	1020
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gtgatcacct	ccctgggcgc	catcgtgtcc	tgctacggca	agaccaagtg	caccgcctcc	1200
aacaagaacc	ggggaatcat	caagaccttc	tccaacggct	gcgactacgt	gtccaataag	1260
ggcgtggaca	ccgtgtccgt	gggcaacaca	ctgtactacg	tgaataagca	ggaaggcaag	1320
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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
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<210> 10
 <211> 598
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Chimeric PreF-G polypeptide

 <400> 10

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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

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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

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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 gctgcgcacg ggctggtaca cgagcgtgat cacgatcgag 180
ctgagcaaca tcaaggagaa caagtgaac ggcacggacg cgaaggtgaa gctgatcaag 240
caggagctgg acaagtacaa gagcgcggtg acggagctgc agctgctgat gcagagcacg 300

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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 cgtcatcgac	840
acgccctgct ggaagctgca cacgagccccg ctgtgcacga ccaacacgaa ggagggcagc	900
aacatctgcc tgacgcggac ggaccggggc tgggtactgcy 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 ggcaccgacg ccaagggtgaa gctgatcaag	240
caggagctgg acaagtacaa gagcgccgtg accgaactcc agctgctgat gcagtccacc	300

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cctgccacca acaacaagtt tctgggcttc ctgctgggcg tgggctccgc catcgcctcc	360
ggcatcgccg tgagcaaggt acgtgtcggg acttgtgttc cccttttttt aataaaaaagt	420
tatatcttta atgttatata catatttcct gtatgtgata catgtgctta tgactttggt	480
tatcatgtgt ttaggtgctg cacctggagg gcgaggtgaa caagatcaag agcgccctgc	540
tgtccacca caaggccgtg gtgtccctgt 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
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aactgatgtc caacaacgtg cagatcgtgc ggcagcagtc ctacagcatc atgagcatca	900
tcaaggaaga ggtgctggcc tacgtggtgc agctgcctct gtacggcgtg atcgacaccc	960
cttgctggaa gctgcacacc tccccctgt gcaccacca caaccaaggag 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 tgcctccag cgtgatcacc tccctgggcg	1260
ccatcgtgtc ctgctacggc aagaccaagt gcaccgcctc caacaagaac cggggaatca	1320
tcaagacctt ctccaacggc tgcgactacg tgtccaataa gggcgtggac accgtgtccg	1380
tgggcaacac actgtactac gtgaataagc aggagggcaa gagcctgtac gtgaaggcg	1440
agcctatcat caacttctac gacctctggt 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

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

<220>
 <223> Furin cleavage consensus motif

<400> 15

Arg Ala Arg Arg
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<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
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 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

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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
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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

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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

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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

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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	gccggcgatga	ccacccctgt	gtccacctac	660
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aaaaaactga	tgtccaacaa	cgtgcagatc	gtgcggcagc	agtccctacag	catcatgagc	780
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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	tcacaaactt	ctacgaccct	ctggtgttcc	cttccgacga	gttcgacgcc	1380
tccatcagcc	aggtgaacga	gaagatcaac	cagtccctgg	ccttcacccg	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			

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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

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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
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Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly
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Glu Ala

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<220>

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<213> Artificial Sequence

<220>

<223> Synthetic PreF Polypeptide

<400> 22

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Ala Val Thr Leu Cys Phe Ala Ser Ser Gln Asn Ile Thr Glu Glu Phe
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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

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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 Phe₄₇₅ Ile Arg Lys Ser Asp₄₈₀
 Glu Lys Leu His Asn Val Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys

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485

495

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

Glu Ala