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SEQUENCE LISTING

<110> GreenLight Biosciences, Inc.
Blake, William J
Cunningham, Drew S

<120> ENGINEERED PROTEINS WITH A PROTEASE CLEAVAGE SITE

<130> G0830.70013W000

<140> Not Yet Assigned

<141> 2014-08-05

<150> US 61/987,518

<151> 2014-05-02

<150> US 61/862,363

<151> 2013-08-05

<160> 87

<170> PatentIn version 3.5

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<223> Synthetic Oligonucleotide

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<223> Synthetic Oligonucleotide

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<223> Synthetic Oligonucleotide

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<213> Artificial Sequence

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<223> Synthetic Oligonucleotide

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<213> Artificial Sequence

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<223> Synthetic Oligonucleotide

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<212> DNA

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<223> Synthetic Oligonucleotide

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ttcgagttct gggactgggt tggcgccgt tactctttgt ggtcagcgat tggcctgtcg	840
attgttctct ccatcggctt tgataacttc gttgaactgc tttccggcgc acacgcgatg	900
gacaagcatt tctccaccac gcctgccgag aaaaacctgc ctgtactgct ggcgctgatt	960
ggcatctggt acaacaatth ctttgggtgcg gaaactgaag cgattctgcc gtatgaccag	1020
tatatgcacc gtttcgcggc gtacttccag cagggaataa tggagtccaa cggtaaagtat	1080
gttgaccgta acggtaacgt tgtggattac cagactggcc cgattatctg ggggtgaacca	1140
ggcactaacg gtcagcacgc gttctaccag ctgatccacc agggaaacaa aatggtaccg	1200
tgcgatttca tcgctccggc tatcaccat aaccgctct ctgatcatca ccagaaactg	1260
ctgtctaact tcttcgcca gaccgaagcg ctggcgtttg gtaaatcccg cgaagtgggt	1320
gagcaggaat atcgtgatca gggtaaagat ccggcaacgc ttgactacgt ggtgccgttc	1380
aaagtattcg aaggtaaccg cccgaccaac tccatcctgc tgcgtgaaat cactccgttc	1440
agcctgggtg cgttgattgc gctgtatgag cacaaaatct ttactcaggg cgtgatcctg	1500
aacatcttca ccttcgacca gtggggcgtg gaactgggta aacagctggc gaaccgtatt	1560

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ctgccagagc tgaaagatga taaagaaatc agcagcctgg aagtgtgtt tcagggtccg 1620
cacgatagct cgaccaatgg tctgattaac cgctataaag cgtggcgcgg ttaa 1674

<210> 16
<211> 1674
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 16
atgaaaaaca tcaatccaac gcagaccgct gcctggcagg cactacagaa acacttcgat 60
gaaatgaaaag acgttacgat cgccgatctt tttgctaaag atggtgatcg tttttctaag 120
ttctccgcaa ccttcgacga tcagatgctg gtggattact caaaaaacg catcactgaa 180
gagacgctgg cgaaattaca ggatctggcg aaagagtgcg atctggcggg cgcgattaag 240
tcgatgttct ctggcgagaa gatcaaccgc actgaaaacc gcgccgtgct gcacgtagcg 300
ctgcgtaacc gtagcaatac cccgattttg gttgatggca aagacgtaat gccggaagtc 360
aacgcggtgc tggagaagat gaaaaccttc tcagaagcga ttatttccgg tgagtggaaa 420
ggttataacc gcaaagcaat cactgacgta gtgaacatcg ggatcggcgg ttctgacctc 480
ggcccataca tggtagaccga agctctgcgt ccgtacaaaa accacctgaa catgcacttt 540
gtttctaacg tcgatgggac tcacatcgcg gaagtgtga aaaaagtaaa cccggaaacc 600
acgctgttct tggtagcatc taaaaccttc accactcagg aaactatgac caacgccccat 660
agcgcgcgtg actggttcct gaaagcggca ggtgatgaga agcacgttgc aaaacacttt 720
gcggcgcttt ccaccaatgc caaagccgtt ggcgagtttg gtattgatac tgccaacatg 780
ttcgagttct gggactgggt tggcggccgt tactctttgt ggtcagcgat tggcctgtcg 840
attgttctct ccatcggtt tgataacttc gttgaactgc tttccggcgc acacgcgatg 900
gacaagcatt tctccaccac gcctgccgag aaaaacctgc ctgtactgct ggcgctgatt 960
ggcatctggt acaacaatth ctttgggtgcg gaaactgaag cgattctgcc gtatgaccag 1020

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tatatgcacc gtttcgcggc gtacttccag cagggaata tggagtccaa cggtaagtat	1080
gttgaccgta acggtaacgt tgtggattac cagactggcc cgattatctg gggatgaacca	1140
ggcactaacg gtcagcacgc gttctaccag ctgatccacc agggaaacaa aatgggtaccg	1200
tgcgatttca tcgctccggc tatcacccat aaccgctct ctgatcatca ccagaaactg	1260
ctgtctaact tcttcgcca gaccgaagcg ctggcgtttg gtaaattccc cgaagtgggt	1320
gagcaggaat atcgtgatca gggtaaagat ccggcaacgc ttgactacgt ggtgccgttc	1380
aaagtattcg aaggtaaccg cccgaccaac tccatcctgc tgcgtgaaat cactccgttc	1440
agcctgggtg cgttgattgc gctgtatgag cacaaaatct ttactcaggc cgtgatcctg	1500
aacatcttca ccttcgacca gtggggcggtg gaactgggta aacagctggc gaaccgtatt	1560
ctgccagagc tgaaagatga taaagaaatc agcagccacg atagctcgac caatggtctg	1620
attaaccgct ataaactgga agtgctgttt cagggtccgg cgtggcgcg ttaa	1674

<210> 17
 <211> 549
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 17

Met	Lys	Asn	Ile	Asn	Pro	Thr	Gln	Thr	Ala	Ala	Trp	Gln	Ala	Leu	Gln
1				5					10					15	

Lys	His	Phe	Asp	Glu	Met	Lys	Asp	Val	Thr	Ile	Ala	Asp	Leu	Phe	Ala
			20					25					30		

Lys	Asp	Gly	Asp	Arg	Phe	Ser	Lys	Phe	Ser	Ala	Thr	Phe	Asp	Asp	Gln
		35					40					45			

Met	Leu	Val	Asp	Tyr	Ser	Lys	Asn	Arg	Ile	Thr	Glu	Glu	Thr	Leu	Ala
	50					55					60				

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Lys Leu Gln Asp Leu Ala Lys Glu Cys Asp Leu Ala Gly Ala Ile Lys
65 70 75 80

Ser Met Phe Ser Gly Glu Lys Ile Asn Arg Thr Glu Asn Arg Ala Val
85 90 95

Leu His Val Ala Leu Arg Asn Arg Ser Asn Thr Pro Ile Leu Val Asp
100 105 110

Gly Lys Asp Val Met Pro Glu Val Asn Ala Val Leu Glu Lys Met Lys
115 120 125

Thr Phe Ser Glu Ala Ile Ile Ser Gly Glu Trp Lys Gly Tyr Thr Gly
130 135 140

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

Gly Pro Tyr Met Val Thr Glu Ala Leu Arg Pro Tyr Lys Asn His Leu
165 170 175

Asn Met His Phe Val Ser Asn Val Asp Gly Thr His Ile Ala Glu Val
180 185 190

Leu Lys Lys Val Asn Pro Glu Thr Thr Leu Phe Leu Val Ala Ser Lys
195 200 205

Thr Phe Thr Thr Gln Glu Thr Met Thr Asn Ala His Ser Ala Arg Asp
210 215 220

Trp Phe Leu Lys Ala Ala Gly Asp Glu Lys His Val Ala Lys His Phe
225 230 235 240

Ala Ala Leu Ser Thr Asn Ala Lys Ala Val Gly Glu Phe Gly Ile Asp
245 250 255

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Thr Ala Asn Met Phe Glu Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser
 260 265 270

Leu Trp Ser Ala Ile Gly Leu Ser Ile Val Leu Ser Ile Gly Phe Asp
 275 280 285

Asn Phe Val Glu Leu Leu Ser Gly Ala His Ala Met Asp Lys His Phe
 290 295 300

Ser Thr Thr Pro Ala Glu Lys Asn Leu Pro Val Leu Leu Ala Leu Ile
 305 310 315 320

Gly Ile Trp Tyr Asn Asn Phe Phe Gly Ala Glu Thr Glu Ala Ile Leu
 325 330 335

Pro Tyr Asp Gln Tyr Met His Arg Phe Ala Ala Tyr Phe Gln Gln Gly
 340 345 350

Asn Met Glu Ser Asn Gly Lys Tyr Val Asp Arg Asn Gly Asn Val Val
 355 360 365

Asp Tyr Gln Thr Gly Pro Ile Ile Trp Gly Glu Pro Gly Thr Asn Gly
 370 375 380

Gln His Ala Phe Tyr Gln Leu Ile His Gln Gly Thr Lys Met Val Pro
 385 390 395 400

Cys Asp Phe Ile Ala Pro Ala Ile Thr His Asn Pro Leu Ser Asp His
 405 410 415

His Gln Lys Leu Leu Ser Asn Phe Phe Ala Gln Thr Glu Ala Leu Ala
 420 425 430

Phe Gly Lys Ser Arg Glu Val Val Glu Gln Glu Tyr Arg Asp Gln Gly
 435 440 445

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Lys Asp Pro Ala Thr Leu Asp Tyr Val Val Pro Phe Lys Val Phe Glu
450 455 460

Gly Asn Arg Pro Thr Asn Ser Ile Leu Leu Arg Glu Ile Thr Pro Phe
465 470 475 480

Ser Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Lys Ile Phe Thr Gln
485 490 495

Gly Val Ile Leu Asn Ile Phe Thr Phe Asp Gln Trp Gly Val Glu Leu
500 505 510

Gly Lys Gln Leu Ala Asn Arg Ile Leu Pro Glu Leu Lys Asp Asp Lys
515 520 525

Glu Ile Ser Ser His Asp Ser Ser Thr Asn Gly Leu Ile Asn Arg Tyr
530 535 540

Lys Ala Trp Arg Gly
545

<210> 18
<211> 557
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 18

Met Lys Asn Ile Asn Pro Thr Gln Thr Ala Ala Trp Gln Ala Leu Gln
1 5 10 15

Lys His Phe Asp Glu Met Lys Asp Val Thr Ile Ala Asp Leu Phe Ala
20 25 30

Lys Asp Gly Asp Arg Phe Ser Lys Phe Ser Ala Thr Phe Asp Asp Gln

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35

40

45

Met Leu Val Asp Tyr Ser Lys Asn Arg Ile Thr Glu Glu Thr Leu Ala
 50 55 60

Lys Leu Gln Asp Leu Ala Lys Glu Cys Asp Leu Ala Gly Ala Ile Lys
 65 70 75 80

Ser Met Phe Ser Gly Glu Lys Ile Asn Arg Thr Glu Asn Arg Ala Val
 85 90 95

Leu His Val Ala Leu Arg Asn Arg Ser Asn Thr Pro Leu Glu Val Leu
 100 105 110

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

Asn Ala Val Leu Glu Lys Met Lys Thr Phe Ser Glu Ala Ile Ile Ser
 130 135 140

Gly Glu Trp Lys Gly Tyr Thr Gly Lys Ala Ile Thr Asp Val Val Asn
 145 150 155 160

Ile Gly Ile Gly Gly Ser Asp Leu Gly Pro Tyr Met Val Thr Glu Ala
 165 170 175

Leu Arg Pro Tyr Lys Asn His Leu Asn Met His Phe Val Ser Asn Val
 180 185 190

Asp Gly Thr His Ile Ala Glu Val Leu Lys Lys Val Asn Pro Glu Thr
 195 200 205

Thr Leu Phe Leu Val Ala Ser Lys Thr Phe Thr Thr Gln Glu Thr Met
 210 215 220

Thr Asn Ala His Ser Ala Arg Asp Trp Phe Leu Lys Ala Ala Gly Asp

225 230 235 240

Ala Val Gly Glu Phe Gly Ile Asp Thr Ala Asn Met Phe Glu Phe Trp
260 265 270

Asp Trp Val Gly Gly Arg Tyr Ser Leu Trp Ser Ala Ile Gly Leu Ser
275 280 285

Ile Val Leu Ser Ile Gly Phe Asp Asn Phe Val Glu Leu Leu Ser Gly
290 295 300

Ala His Ala Met Asp Lys His Phe Ser Thr Thr Pro Ala Glu Lys Asn
305 310 315 320

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

Gly Ala Glu Thr Glu Ala Ile Leu Pro Tyr Asp Gln Tyr Met His Arg
340 345 350

Phe Ala Ala Tyr Phe Gln Gln Gly Asn Met Glu Ser Asn Gly Lys Tyr
355 360 365

Val	Asp	Arg	Asn	Gly	Asn	Val	Val	Asp	Tyr	Gln	Thr	Gly	Pro	Ile	Ile
	370					375					380				

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

His Gln Gly Thr Lys Met Val Pro Cys Asp Phe Ile Ala Pro Ala Ile
405 410 415

Thr His Asn Pro Leu Ser Asp His His Gln Lys Leu Leu Ser Asn Phe

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420

425

430

Phe Ala Gln Thr Glu Ala Leu Ala Phe Gly Lys Ser Arg Glu Val Val
435 440 445

Glu Gln Glu Tyr Arg Asp Gln Gly Lys Asp Pro Ala Thr Leu Asp Tyr
450 455 460

Val Val Pro Phe Lys Val Phe Glu Gly Asn Arg Pro Thr Asn Ser Ile
465 470 475 480

Leu Leu Arg Glu Ile Thr Pro Phe Ser Leu Gly Ala Leu Ile Ala Leu
485 490 495

Tyr Glu His Lys Ile Phe Thr Gln Gly Val Ile Leu Asn Ile Phe Thr
500 505 510

Phe Asp Gln Trp Gly Val Glu Leu Gly Lys Gln Leu Ala Asn Arg Ile
515 520 525

Leu Pro Glu Leu Lys Asp Asp Lys Glu Ile Ser Ser His Asp Ser Ser
530 535 540

Thr Asn Gly Leu Ile Asn Arg Tyr Lys Ala Trp Arg Gly
545 550 555

<210> 19

<211> 557

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 19

Met Lys Asn Ile Asn Pro Thr Gln Thr Ala Ala Trp Gln Ala Leu Gln
1 5 10 15

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Lys His Phe Asp Glu Met Lys Asp Val Thr Ile Ala Asp Leu Phe Ala
20 25 30

Lys Asp Gly Asp Arg Phe Ser Lys Phe Ser Ala Thr Phe Asp Asp Gln
35 40 45

Met Leu Val Asp Tyr Ser Lys Asn Arg Ile Thr Glu Glu Thr Leu Ala
50 55 60

Lys Leu Gln Asp Leu Ala Lys Glu Cys Asp Leu Ala Gly Ala Ile Lys
65 70 75 80

Ser Met Phe Ser Gly Glu Lys Ile Asn Arg Thr Glu Asn Arg Ala Val
85 90 95

Leu His Val Ala Leu Arg Asn Arg Ser Asn Thr Pro Ile Leu Glu Val
100 105 110

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

Asn Ala Val Leu Glu Lys Met Lys Thr Phe Ser Glu Ala Ile Ile Ser
130 135 140

Gly Glu Trp Lys Gly Tyr Thr Gly Lys Ala Ile Thr Asp Val Val Asn
145 150 155 160

Ile Gly Ile Gly Gly Ser Asp Leu Gly Pro Tyr Met Val Thr Glu Ala
165 170 175

Leu Arg Pro Tyr Lys Asn His Leu Asn Met His Phe Val Ser Asn Val
180 185 190

Asp Gly Thr His Ile Ala Glu Val Leu Lys Lys Val Asn Pro Glu Thr
195 200 205

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Thr Leu Phe Leu Val Ala Ser Lys Thr Phe Thr Thr Gln Glu Thr Met
 210 215 220

Thr Asn Ala His Ser Ala Arg Asp Trp Phe Leu Lys Ala Ala Gly Asp
 225 230 235 240

Glu Lys His Val Ala Lys His Phe Ala Ala Leu Ser Thr Asn Ala Lys
 245 250 255

Ala Val Gly Glu Phe Gly Ile Asp Thr Ala Asn Met Phe Glu Phe Trp
 260 265 270

Asp Trp Val Gly Gly Arg Tyr Ser Leu Trp Ser Ala Ile Gly Leu Ser
 275 280 285

Ile Val Leu Ser Ile Gly Phe Asp Asn Phe Val Glu Leu Leu Ser Gly
 290 295 300

Ala His Ala Met Asp Lys His Phe Ser Thr Thr Pro Ala Glu Lys Asn
 305 310 315 320

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

Gly Ala Glu Thr Glu Ala Ile Leu Pro Tyr Asp Gln Tyr Met His Arg
 340 345 350

Phe Ala Ala Tyr Phe Gln Gln Gly Asn Met Glu Ser Asn Gly Lys Tyr
 355 360 365

Val Asp Arg Asn Gly Asn Val Val Asp Tyr Gln Thr Gly Pro Ile Ile
 370 375 380

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

G083070013W000-SEQLISTING-CHB

His Gln Gly Thr Lys Met Val Pro Cys Asp Phe Ile Ala Pro Ala Ile
405 410 415

Thr His Asn Pro Leu Ser Asp His His Gln Lys Leu Leu Ser Asn Phe
420 425 430

Phe Ala Gln Thr Glu Ala Leu Ala Phe Gly Lys Ser Arg Glu Val Val
435 440 445

Glu Gln Glu Tyr Arg Asp Gln Gly Lys Asp Pro Ala Thr Leu Asp Tyr
450 455 460

Val Val Pro Phe Lys Val Phe Glu Gly Asn Arg Pro Thr Asn Ser Ile
465 470 475 480

Leu Leu Arg Glu Ile Thr Pro Phe Ser Leu Gly Ala Leu Ile Ala Leu
485 490 495

Tyr Glu His Lys Ile Phe Thr Gln Gly Val Ile Leu Asn Ile Phe Thr
500 505 510

Phe Asp Gln Trp Gly Val Glu Leu Gly Lys Gln Leu Ala Asn Arg Ile
515 520 525

Leu Pro Glu Leu Lys Asp Asp Lys Glu Ile Ser Ser His Asp Ser Ser
530 535 540

Thr Asn Gly Leu Ile Asn Arg Tyr Lys Ala Trp Arg Gly
545 550 555

<210> 20

<211> 556

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

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<400> 20

Met Lys Asn Ile Asn Pro Thr Gln Thr Ala Ala Trp Gln Ala Leu Gln
 1 5 10 15

Lys His Phe Asp Glu Met Lys Asp Val Thr Ile Ala Asp Leu Phe Ala
 20 25 30

Lys Asp Gly Asp Arg Phe Ser Lys Phe Ser Ala Thr Phe Asp Asp Gln
 35 40 45

Met Leu Val Asp Tyr Ser Lys Asn Arg Ile Thr Glu Glu Thr Leu Ala
 50 55 60

Lys Leu Gln Asp Leu Ala Lys Glu Cys Asp Leu Ala Gly Ala Ile Lys
 65 70 75 80

Ser Met Phe Ser Gly Glu Lys Ile Asn Arg Thr Glu Asn Arg Ala Val
 85 90 95

Leu His Val Ala Leu Arg Asn Arg Ser Asn Thr Pro Ile Leu Glu Val
 100 105 110

Leu Phe Gln Gly Pro Val Asp Gly Lys Asp Val Met Pro Glu Val Asn
 115 120 125

Ala Val Leu Glu Lys Met Lys Thr Phe Ser Glu Ala Ile Ile Ser Gly
 130 135 140

Glu Trp Lys Gly Tyr Thr Gly Lys Ala Ile Thr Asp Val Val Asn Ile
 145 150 155 160

Gly Ile Gly Gly Ser Asp Leu Gly Pro Tyr Met Val Thr Glu Ala Leu
 165 170 175

Arg Pro Tyr Lys Asn His Leu Asn Met His Phe Val Ser Asn Val Asp

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180

185

190

Gly Thr His Ile Ala Glu Val Leu Lys Lys Val Asn Pro Glu Thr Thr
 195 200 205

Leu Phe Leu Val Ala Ser Lys Thr Phe Thr Thr Gln Glu Thr Met Thr
 210 215 220

Asn Ala His Ser Ala Arg Asp Trp Phe Leu Lys Ala Ala Gly Asp Glu
 225 230 235 240

Lys His Val Ala Lys His Phe Ala Ala Leu Ser Thr Asn Ala Lys Ala
 245 250 255

Val Gly Glu Phe Gly Ile Asp Thr Ala Asn Met Phe Glu Phe Trp Asp
 260 265 270

Trp Val Gly Gly Arg Tyr Ser Leu Trp Ser Ala Ile Gly Leu Ser Ile
 275 280 285

Val Leu Ser Ile Gly Phe Asp Asn Phe Val Glu Leu Leu Ser Gly Ala
 290 295 300

His Ala Met Asp Lys His Phe Ser Thr Thr Pro Ala Glu Lys Asn Leu
 305 310 315 320

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

Ala Glu Thr Glu Ala Ile Leu Pro Tyr Asp Gln Tyr Met His Arg Phe
 340 345 350

Ala Ala Tyr Phe Gln Gln Gly Asn Met Glu Ser Asn Gly Lys Tyr Val
 355 360 365

Asp Arg Asn Gly Asn Val Val Asp Tyr Gln Thr Gly Pro Ile Ile Trp

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370

375

380

Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe Tyr Gln Leu Ile His
 385 390 395 400

Gln Gly Thr Lys Met Val Pro Cys Asp Phe Ile Ala Pro Ala Ile Thr
 405 410 415

His Asn Pro Leu Ser Asp His His Gln Lys Leu Leu Ser Asn Phe Phe
 420 425 430

Ala Gln Thr Glu Ala Leu Ala Phe Gly Lys Ser Arg Glu Val Val Glu
 435 440 445

Gln Glu Tyr Arg Asp Gln Gly Lys Asp Pro Ala Thr Leu Asp Tyr Val
 450 455 460

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

Leu Arg Glu Ile Thr Pro Phe Ser Leu Gly Ala Leu Ile Ala Leu Tyr
 485 490 495

Glu His Lys Ile Phe Thr Gln Gly Val Ile Leu Asn Ile Phe Thr Phe
 500 505 510

Asp Gln Trp Gly Val Glu Leu Gly Lys Gln Leu Ala Asn Arg Ile Leu
 515 520 525

Pro Glu Leu Lys Asp Asp Lys Glu Ile Ser Ser His Asp Ser Ser Thr
 530 535 540

Asn Gly Leu Ile Asn Arg Tyr Lys Ala Trp Arg Gly
 545 550 555

<210> 21

G083070013W000-SEQLISTING-CHB

<211> 557
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 21

Met Lys Asn Ile Asn Pro Thr Gln Thr Ala Ala Trp Gln Ala Leu Gln
 1 5 10 15

Lys His Phe Asp Glu Met Lys Asp Val Thr Ile Ala Asp Leu Phe Ala
 20 25 30

Lys Asp Gly Asp Arg Phe Ser Lys Phe Ser Ala Thr Phe Asp Asp Gln
 35 40 45

Met Leu Val Asp Tyr Ser Lys Asn Arg Ile Thr Glu Glu Thr Leu Ala
 50 55 60

Lys Leu Gln Asp Leu Ala Lys Glu Cys Asp Leu Ala Gly Ala Ile Lys
 65 70 75 80

Ser Met Phe Ser Gly Glu Lys Ile Asn Arg Thr Glu Asn Arg Ala Val
 85 90 95

Leu His Val Ala Leu Arg Asn Arg Ser Asn Thr Pro Ile Leu Val Asp
 100 105 110

Gly Lys Asp Val Met Pro Glu Val Asn Ala Val Leu Glu Lys Met Lys
 115 120 125

Thr Phe Ser Glu Ala Ile Ile Ser Gly Glu Leu Glu Val Leu Phe Gln
 130 135 140

Gly Pro Trp Lys Gly Tyr Thr Gly Lys Ala Ile Thr Asp Val Val Asn
 145 150 155 160

G083070013W000-SEQLISTING-CHB

Ile Gly Ile Gly Gly Ser Asp Leu Gly Pro Tyr Met Val Thr Glu Ala
165 170 175

Leu Arg Pro Tyr Lys Asn His Leu Asn Met His Phe Val Ser Asn Val
180 185 190

Asp Gly Thr His Ile Ala Glu Val Leu Lys Lys Val Asn Pro Glu Thr
195 200 205

Thr Leu Phe Leu Val Ala Ser Lys Thr Phe Thr Thr Gln Glu Thr Met
210 215 220

Thr Asn Ala His Ser Ala Arg Asp Trp Phe Leu Lys Ala Ala Gly Asp
225 230 235 240

Glu Lys His Val Ala Lys His Phe Ala Ala Leu Ser Thr Asn Ala Lys
245 250 255

Ala Val Gly Glu Phe Gly Ile Asp Thr Ala Asn Met Phe Glu Phe Trp
260 265 270

Asp Trp Val Gly Gly Arg Tyr Ser Leu Trp Ser Ala Ile Gly Leu Ser
275 280 285

Ile Val Leu Ser Ile Gly Phe Asp Asn Phe Val Glu Leu Leu Ser Gly
290 295 300

Ala His Ala Met Asp Lys His Phe Ser Thr Thr Pro Ala Glu Lys Asn
305 310 315 320

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

Gly Ala Glu Thr Glu Ala Ile Leu Pro Tyr Asp Gln Tyr Met His Arg
340 345 350

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Phe Ala Ala Tyr Phe Gln Gln Gly Asn Met Glu Ser Asn Gly Lys Tyr
 355 360 365

Val Asp Arg Asn Gly Asn Val Val Asp Tyr Gln Thr Gly Pro Ile Ile
 370 375 380

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

His Gln Gly Thr Lys Met Val Pro Cys Asp Phe Ile Ala Pro Ala Ile
 405 410 415

Thr His Asn Pro Leu Ser Asp His His Gln Lys Leu Leu Ser Asn Phe
 420 425 430

Phe Ala Gln Thr Glu Ala Leu Ala Phe Gly Lys Ser Arg Glu Val Val
 435 440 445

Glu Gln Glu Tyr Arg Asp Gln Gly Lys Asp Pro Ala Thr Leu Asp Tyr
 450 455 460

Val Val Pro Phe Lys Val Phe Glu Gly Asn Arg Pro Thr Asn Ser Ile
 465 470 475 480

Leu Leu Arg Glu Ile Thr Pro Phe Ser Leu Gly Ala Leu Ile Ala Leu
 485 490 495

Tyr Glu His Lys Ile Phe Thr Gln Gly Val Ile Leu Asn Ile Phe Thr
 500 505 510

Phe Asp Gln Trp Gly Val Glu Leu Gly Lys Gln Leu Ala Asn Arg Ile
 515 520 525

Leu Pro Glu Leu Lys Asp Asp Lys Glu Ile Ser Ser His Asp Ser Ser
 530 535 540

G083070013W000-SEQLISTING-CHB

Thr Asn Gly Leu Ile Asn Arg Tyr Lys Ala Trp Arg Gly
545 550 555

<210> 22
<211> 557
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 22

Met Lys Asn Ile Asn Pro Thr Gln Thr Ala Ala Trp Gln Ala Leu Gln
1 5 10 15

Lys His Phe Asp Glu Met Lys Asp Val Thr Ile Ala Asp Leu Phe Ala
20 25 30

Lys Asp Gly Asp Arg Phe Ser Lys Phe Ser Ala Thr Phe Asp Asp Gln
35 40 45

Met Leu Val Asp Tyr Ser Lys Asn Arg Ile Thr Glu Glu Thr Leu Ala
50 55 60

Lys Leu Gln Asp Leu Ala Lys Glu Cys Asp Leu Ala Gly Ala Ile Lys
65 70 75 80

Ser Met Phe Ser Gly Glu Lys Ile Asn Arg Thr Glu Asn Arg Ala Val
85 90 95

Leu His Val Ala Leu Arg Asn Arg Ser Asn Thr Pro Ile Leu Val Asp
100 105 110

Gly Lys Asp Val Met Pro Glu Val Asn Ala Val Leu Glu Lys Met Lys
115 120 125

Thr Phe Ser Glu Ala Ile Ile Ser Gly Glu Trp Lys Gly Tyr Thr Gly

G083070013W000-SEQLISTING-CHB

130

135

140

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

Gly Pro Tyr Met Val Thr Glu Ala Leu Arg Pro Tyr Lys Asn His Leu
 165 170 175

Asn Met His Phe Val Ser Asn Val Asp Gly Thr His Ile Ala Glu Val
 180 185 190

Leu Lys Lys Val Asn Pro Glu Thr Thr Leu Phe Leu Val Ala Ser Lys
 195 200 205

Thr Phe Thr Thr Gln Glu Thr Met Thr Asn Ala His Ser Ala Arg Asp
 210 215 220

Trp Phe Leu Lys Ala Ala Gly Asp Glu Lys His Val Ala Lys His Phe
 225 230 235 240

Ala Ala Leu Ser Thr Asn Ala Lys Ala Val Gly Glu Phe Gly Ile Asp
 245 250 255

Thr Ala Asn Met Phe Glu Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser
 260 265 270

Leu Trp Ser Ala Ile Gly Leu Ser Ile Val Leu Ser Ile Gly Phe Asp
 275 280 285

Asn Phe Val Glu Leu Leu Ser Gly Ala His Ala Met Asp Lys His Phe
 290 295 300

Ser Thr Thr Pro Ala Glu Lys Asn Leu Pro Val Leu Leu Ala Leu Ile
 305 310 315 320

Gly Ile Trp Tyr Asn Asn Phe Phe Gly Ala Glu Thr Glu Ala Ile Leu

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325

330

335

Pro Tyr Asp Gln Tyr Met His Arg Phe Ala Ala Tyr Phe Gln Gln Gly
 340 345 350

Asn Met Glu Ser Asn Gly Lys Tyr Val Asp Arg Asn Gly Asn Val Val
 355 360 365

Asp Tyr Gln Thr Gly Pro Ile Ile Trp Gly Glu Pro Gly Thr Asn Gly
 370 375 380

Gln His Ala Phe Tyr Gln Leu Ile His Gln Gly Thr Lys Met Val Pro
 385 390 395 400

Cys Asp Phe Ile Ala Pro Ala Ile Thr His Leu Glu Val Leu Phe Gln
 405 410 415

Gly Pro Asn Pro Leu Ser Asp His His Gln Lys Leu Leu Ser Asn Phe
 420 425 430

Phe Ala Gln Thr Glu Ala Leu Ala Phe Gly Lys Ser Arg Glu Val Val
 435 440 445

Glu Gln Glu Tyr Arg Asp Gln Gly Lys Asp Pro Ala Thr Leu Asp Tyr
 450 455 460

Val Val Pro Phe Lys Val Phe Glu Gly Asn Arg Pro Thr Asn Ser Ile
 465 470 475 480

Leu Leu Arg Glu Ile Thr Pro Phe Ser Leu Gly Ala Leu Ile Ala Leu
 485 490 495

Tyr Glu His Lys Ile Phe Thr Gln Gly Val Ile Leu Asn Ile Phe Thr
 500 505 510

Phe Asp Gln Trp Gly Val Glu Leu Gly Lys Gln Leu Ala Asn Arg Ile

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515

520

525

Leu Pro Glu Leu Lys Asp Asp Lys Glu Ile Ser Ser His Asp Ser Ser
 530 535 540

Thr Asn Gly Leu Ile Asn Arg Tyr Lys Ala Trp Arg Gly
 545 550 555

<210> 23

<211> 556

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 23

Met Lys Asn Ile Asn Pro Thr Gln Thr Ala Ala Trp Gln Ala Leu Gln
 1 5 10 15

Lys His Phe Asp Glu Met Lys Asp Val Thr Ile Ala Asp Leu Phe Ala
 20 25 30

Lys Asp Gly Asp Arg Phe Ser Lys Phe Ser Ala Thr Phe Asp Asp Gln
 35 40 45

Met Leu Val Asp Tyr Ser Lys Asn Arg Ile Thr Glu Glu Thr Leu Ala
 50 55 60

Lys Leu Gln Asp Leu Ala Lys Glu Cys Asp Leu Ala Gly Ala Ile Lys
 65 70 75 80

Ser Met Phe Ser Gly Glu Lys Ile Asn Arg Thr Glu Asn Arg Ala Val
 85 90 95

Leu His Val Ala Leu Arg Asn Arg Ser Asn Thr Pro Ile Leu Val Asp
 100 105 110

G083070013W000-SEQLISTING-CHB

Gly Lys Asp Val Met Pro Glu Val Asn Ala Val Leu Glu Lys Met Lys
115 120 125

Thr Phe Ser Glu Ala Ile Ile Ser Gly Glu Trp Lys Gly Tyr Thr Gly
130 135 140

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

Gly Pro Tyr Met Val Thr Glu Ala Leu Arg Pro Tyr Lys Asn His Leu
165 170 175

Asn Met His Phe Val Ser Asn Val Asp Gly Thr His Ile Ala Glu Val
180 185 190

Leu Lys Lys Val Asn Pro Glu Thr Thr Leu Phe Leu Val Ala Ser Lys
195 200 205

Thr Phe Thr Thr Gln Glu Thr Met Thr Asn Ala His Ser Ala Arg Asp
210 215 220

Trp Phe Leu Lys Ala Ala Gly Asp Glu Lys His Val Ala Lys His Phe
225 230 235 240

Ala Ala Leu Ser Thr Asn Ala Lys Ala Val Gly Glu Phe Gly Ile Asp
245 250 255

Thr Ala Asn Met Phe Glu Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser
260 265 270

Leu Trp Ser Ala Ile Gly Leu Ser Ile Val Leu Ser Ile Gly Phe Asp
275 280 285

Asn Phe Val Glu Leu Leu Ser Gly Ala His Ala Met Asp Lys His Phe
290 295 300

G083070013W000-SEQLISTING-CHB

Ser Thr Thr Pro Ala Glu Lys Asn Leu Pro Val Leu Leu Ala Leu Ile
305 310 315 320

Gly Ile Trp Tyr Asn Asn Phe Phe Gly Ala Glu Thr Glu Ala Ile Leu
325 330 335

Pro Tyr Asp Gln Tyr Met His Arg Phe Ala Ala Tyr Phe Gln Gln Gly
340 345 350

Asn Met Glu Ser Asn Gly Lys Tyr Val Asp Arg Asn Gly Asn Val Val
355 360 365

Asp Tyr Gln Thr Gly Pro Ile Ile Trp Gly Glu Pro Gly Thr Asn Gly
370 375 380

Gln His Ala Phe Tyr Gln Leu Ile His Gln Gly Thr Lys Met Val Pro
385 390 395 400

Cys Asp Phe Ile Ala Pro Ala Ile Thr His Asn Pro Leu Ser Asp His
405 410 415

His Gln Lys Leu Leu Ser Asn Phe Phe Ala Gln Thr Glu Ala Leu Ala
420 425 430

Phe Gly Lys Ser Arg Glu Val Val Glu Gln Glu Tyr Arg Asp Gln Gly
435 440 445

Lys Asp Pro Ala Thr Leu Asp Tyr Val Val Pro Phe Lys Val Phe Glu
450 455 460

Gly Asn Arg Pro Thr Asn Ser Ile Leu Leu Arg Glu Ile Thr Pro Phe
465 470 475 480

Ser Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Lys Ile Phe Thr Gln
485 490 495

G083070013W000-SEQLISTING-CHB

Gly Val Ile Leu Asn Ile Phe Thr Phe Asp Gln Trp Gly Val Glu Leu
500 505 510

Gly Lys Gln Leu Ala Asn Arg Ile Leu Pro Glu Leu Glu Val Leu Phe
515 520 525

Gln Gly Pro Lys Asp Asp Lys Glu Ile Ser Ser His Asp Ser Ser Thr
530 535 540

Asn Gly Leu Ile Asn Arg Tyr Lys Ala Trp Arg Gly
545 550 555

<210> 24
<211> 557
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 24

Met Lys Asn Ile Asn Pro Thr Gln Thr Ala Ala Trp Gln Ala Leu Gln
1 5 10 15

Lys His Phe Asp Glu Met Lys Asp Val Thr Ile Ala Asp Leu Phe Ala
20 25 30

Lys Asp Gly Asp Arg Phe Ser Lys Phe Ser Ala Thr Phe Asp Asp Gln
35 40 45

Met Leu Val Asp Tyr Ser Lys Asn Arg Ile Thr Glu Glu Thr Leu Ala
50 55 60

Lys Leu Gln Asp Leu Ala Lys Glu Cys Asp Leu Ala Gly Ala Ile Lys
65 70 75 80

Ser Met Phe Ser Gly Glu Lys Ile Asn Arg Thr Glu Asn Arg Ala Val

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85

90

95

Leu His Val Ala Leu Arg Asn Arg Ser Asn Thr Pro Ile Leu Val Asp
 100 105 110

Gly Lys Asp Val Met Pro Glu Val Asn Ala Val Leu Glu Lys Met Lys
 115 120 125

Thr Phe Ser Glu Ala Ile Ile Ser Gly Glu Trp Lys Gly Tyr Thr Gly
 130 135 140

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

Gly Pro Tyr Met Val Thr Glu Ala Leu Arg Pro Tyr Lys Asn His Leu
 165 170 175

Asn Met His Phe Val Ser Asn Val Asp Gly Thr His Ile Ala Glu Val
 180 185 190

Leu Lys Lys Val Asn Pro Glu Thr Thr Leu Phe Leu Val Ala Ser Lys
 195 200 205

Thr Phe Thr Thr Gln Glu Thr Met Thr Asn Ala His Ser Ala Arg Asp
 210 215 220

Trp Phe Leu Lys Ala Ala Gly Asp Glu Lys His Val Ala Lys His Phe
 225 230 235 240

Ala Ala Leu Ser Thr Asn Ala Lys Ala Val Gly Glu Phe Gly Ile Asp
 245 250 255

Thr Ala Asn Met Phe Glu Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser
 260 265 270

Leu Trp Ser Ala Ile Gly Leu Ser Ile Val Leu Ser Ile Gly Phe Asp

G083070013W000-SEQLISTING-CHB

275

280

285

Asn Phe Val Glu Leu Leu Ser Gly Ala His Ala Met Asp Lys His Phe
 290 295 300

Ser Thr Thr Pro Ala Glu Lys Asn Leu Pro Val Leu Leu Ala Leu Ile
 305 310 315 320

Gly Ile Trp Tyr Asn Asn Phe Phe Gly Ala Glu Thr Glu Ala Ile Leu
 325 330 335

Pro Tyr Asp Gln Tyr Met His Arg Phe Ala Ala Tyr Phe Gln Gln Gly
 340 345 350

Asn Met Glu Ser Asn Gly Lys Tyr Val Asp Arg Asn Gly Asn Val Val
 355 360 365

Asp Tyr Gln Thr Gly Pro Ile Ile Trp Gly Glu Pro Gly Thr Asn Gly
 370 375 380

Gln His Ala Phe Tyr Gln Leu Ile His Gln Gly Thr Lys Met Val Pro
 385 390 395 400

Cys Asp Phe Ile Ala Pro Ala Ile Thr His Asn Pro Leu Ser Asp His
 405 410 415

His Gln Lys Leu Leu Ser Asn Phe Phe Ala Gln Thr Glu Ala Leu Ala
 420 425 430

Phe Gly Lys Ser Arg Glu Val Val Glu Gln Glu Tyr Arg Asp Gln Gly
 435 440 445

Lys Asp Pro Ala Thr Leu Asp Tyr Val Val Pro Phe Lys Val Phe Glu
 450 455 460

Gly Asn Arg Pro Thr Asn Ser Ile Leu Leu Arg Glu Ile Thr Pro Phe

465 470 475 480

Met Leu Val Asp Tyr Ser Lys Asn Arg Ile Thr Glu Glu Thr Leu Ala
50 55 60

G083070013W000-SEQLISTING-CHB

Lys Leu Gln Asp Leu Ala Lys Glu Cys Asp Leu Ala Gly Ala Ile Lys
65 70 75 80

Ser Met Phe Ser Gly Glu Lys Ile Asn Arg Thr Glu Asn Arg Ala Val
85 90 95

Leu His Val Ala Leu Arg Asn Arg Ser Asn Thr Pro Ile Leu Val Asp
100 105 110

Gly Lys Asp Val Met Pro Glu Val Asn Ala Val Leu Glu Lys Met Lys
115 120 125

Thr Phe Ser Glu Ala Ile Ile Ser Gly Glu Trp Lys Gly Tyr Thr Gly
130 135 140

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

Gly Pro Tyr Met Val Thr Glu Ala Leu Arg Pro Tyr Lys Asn His Leu
165 170 175

Asn Met His Phe Val Ser Asn Val Asp Gly Thr His Ile Ala Glu Val
180 185 190

Leu Lys Lys Val Asn Pro Glu Thr Thr Leu Phe Leu Val Ala Ser Lys
195 200 205

Thr Phe Thr Thr Gln Glu Thr Met Thr Asn Ala His Ser Ala Arg Asp
210 215 220

Trp Phe Leu Lys Ala Ala Gly Asp Glu Lys His Val Ala Lys His Phe
225 230 235 240

Ala Ala Leu Ser Thr Asn Ala Lys Ala Val Gly Glu Phe Gly Ile Asp
245 250 255

G083070013W000-SEQLISTING-CHB

Thr Ala Asn Met Phe Glu Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser
260 265 270

Leu Trp Ser Ala Ile Gly Leu Ser Ile Val Leu Ser Ile Gly Phe Asp
275 280 285

Asn Phe Val Glu Leu Leu Ser Gly Ala His Ala Met Asp Lys His Phe
290 295 300

Ser Thr Thr Pro Ala Glu Lys Asn Leu Pro Val Leu Leu Ala Leu Ile
305 310 315 320

Gly Ile Trp Tyr Asn Asn Phe Phe Gly Ala Glu Thr Glu Ala Ile Leu
325 330 335

Pro Tyr Asp Gln Tyr Met His Arg Phe Ala Ala Tyr Phe Gln Gln Gly
340 345 350

Asn Met Glu Ser Asn Gly Lys Tyr Val Asp Arg Asn Gly Asn Val Val
355 360 365

Asp Tyr Gln Thr Gly Pro Ile Ile Trp Gly Glu Pro Gly Thr Asn Gly
370 375 380

Gln His Ala Phe Tyr Gln Leu Ile His Gln Gly Thr Lys Met Val Pro
385 390 395 400

Cys Asp Phe Ile Ala Pro Ala Ile Thr His Asn Pro Leu Ser Asp His
405 410 415

His Gln Lys Leu Leu Ser Asn Phe Phe Ala Gln Thr Glu Ala Leu Ala
420 425 430

Phe Gly Lys Ser Arg Glu Val Val Glu Gln Glu Tyr Arg Asp Gln Gly
435 440 445

G083070013W000-SEQLISTING-CHB

Lys Asp Pro Ala Thr Leu Asp Tyr Val Val Pro Phe Lys Val Phe Glu
450 455 460

Gly Asn Arg Pro Thr Asn Ser Ile Leu Leu Arg Glu Ile Thr Pro Phe
465 470 475 480

Ser Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Lys Ile Phe Thr Gln
485 490 495

Gly Val Ile Leu Asn Ile Phe Thr Phe Asp Gln Trp Gly Val Glu Leu
500 505 510

Gly Lys Gln Leu Ala Asn Arg Ile Leu Pro Glu Leu Lys Asp Leu Glu
515 520 525

Val Leu Phe Gln Gly Pro Asp Lys Glu Ile Ser Ser His Asp Ser Ser
530 535 540

Thr Asn Gly Leu Ile Asn Arg Tyr Lys Ala Trp Arg Gly
545 550 555

<210> 26
<211> 557
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 26

Met Lys Asn Ile Asn Pro Thr Gln Thr Ala Ala Trp Gln Ala Leu Gln
1 5 10 15

Lys His Phe Asp Glu Met Lys Asp Val Thr Ile Ala Asp Leu Phe Ala
20 25 30

Lys Asp Gly Asp Arg Phe Ser Lys Phe Ser Ala Thr Phe Asp Asp Gln

G083070013W000-SEQLISTING-CHB

35

40

45

Met Leu Val Asp Tyr Ser Lys Asn Arg Ile Thr Glu Glu Thr Leu Ala
 50 55 60

Lys Leu Gln Asp Leu Ala Lys Glu Cys Asp Leu Ala Gly Ala Ile Lys
 65 70 75 80

Ser Met Phe Ser Gly Glu Lys Ile Asn Arg Thr Glu Asn Arg Ala Val
 85 90 95

Leu His Val Ala Leu Arg Asn Arg Ser Asn Thr Pro Ile Leu Val Asp
 100 105 110

Gly Lys Asp Val Met Pro Glu Val Asn Ala Val Leu Glu Lys Met Lys
 115 120 125

Thr Phe Ser Glu Ala Ile Ile Ser Gly Glu Trp Lys Gly Tyr Thr Gly
 130 135 140

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

Gly Pro Tyr Met Val Thr Glu Ala Leu Arg Pro Tyr Lys Asn His Leu
 165 170 175

Asn Met His Phe Val Ser Asn Val Asp Gly Thr His Ile Ala Glu Val
 180 185 190

Leu Lys Lys Val Asn Pro Glu Thr Thr Leu Phe Leu Val Ala Ser Lys
 195 200 205

Thr Phe Thr Thr Gln Glu Thr Met Thr Asn Ala His Ser Ala Arg Asp
 210 215 220

Trp Phe Leu Lys Ala Ala Gly Asp Glu Lys His Val Ala Lys His Phe

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

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420

425

430

Phe Gly Lys Ser Arg Glu Val Val Glu Gln Glu Tyr Arg Asp Gln Gly
435 440 445

Lys Asp Pro Ala Thr Leu Asp Tyr Val Val Pro Phe Lys Val Phe Glu
450 455 460

Gly Asn Arg Pro Thr Asn Ser Ile Leu Leu Arg Glu Ile Thr Pro Phe
465 470 475 480

Ser Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Lys Ile Phe Thr Gln
485 490 495

Gly Val Ile Leu Asn Ile Phe Thr Phe Asp Gln Trp Gly Val Glu Leu
500 505 510

Gly Lys Gln Leu Ala Asn Arg Ile Leu Pro Glu Leu Lys Asp Asp Leu
515 520 525

Glu Val Leu Phe Gln Gly Pro Lys Glu Ile Ser Ser His Asp Ser Ser
530 535 540

Thr Asn Gly Leu Ile Asn Arg Tyr Lys Ala Trp Arg Gly
545 550 555

<210> 27

<211> 557

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 27

Met Lys Asn Ile Asn Pro Thr Gln Thr Ala Ala Trp Gln Ala Leu Gln
1 5 10 15

G083070013W000-SEQLISTING-CHB

Lys His Phe Asp Glu Met Lys Asp Val Thr Ile Ala Asp Leu Phe Ala
20 25 30

Lys Asp Gly Asp Arg Phe Ser Lys Phe Ser Ala Thr Phe Asp Asp Gln
35 40 45

Met Leu Val Asp Tyr Ser Lys Asn Arg Ile Thr Glu Glu Thr Leu Ala
50 55 60

Lys Leu Gln Asp Leu Ala Lys Glu Cys Asp Leu Ala Gly Ala Ile Lys
65 70 75 80

Ser Met Phe Ser Gly Glu Lys Ile Asn Arg Thr Glu Asn Arg Ala Val
85 90 95

Leu His Val Ala Leu Arg Asn Arg Ser Asn Thr Pro Ile Leu Val Asp
100 105 110

Gly Lys Asp Val Met Pro Glu Val Asn Ala Val Leu Glu Lys Met Lys
115 120 125

Thr Phe Ser Glu Ala Ile Ile Ser Gly Glu Trp Lys Gly Tyr Thr Gly
130 135 140

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

Gly Pro Tyr Met Val Thr Glu Ala Leu Arg Pro Tyr Lys Asn His Leu
165 170 175

Asn Met His Phe Val Ser Asn Val Asp Gly Thr His Ile Ala Glu Val
180 185 190

Leu Lys Lys Val Asn Pro Glu Thr Thr Leu Phe Leu Val Ala Ser Lys
195 200 205

G083070013W000-SEQLISTING-CHB

Thr Phe Thr Thr Gln Glu Thr Met Thr Asn Ala His Ser Ala Arg Asp
210 215 220

Trp Phe Leu Lys Ala Ala Gly Asp Glu Lys His Val Ala Lys His Phe
225 230 235 240

Ala Ala Leu Ser Thr Asn Ala Lys Ala Val Gly Glu Phe Gly Ile Asp
245 250 255

Thr Ala Asn Met Phe Glu Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser
260 265 270

Leu Trp Ser Ala Ile Gly Leu Ser Ile Val Leu Ser Ile Gly Phe Asp
275 280 285

Asn Phe Val Glu Leu Leu Ser Gly Ala His Ala Met Asp Lys His Phe
290 295 300

Ser Thr Thr Pro Ala Glu Lys Asn Leu Pro Val Leu Leu Ala Leu Ile
305 310 315 320

Gly Ile Trp Tyr Asn Asn Phe Phe Gly Ala Glu Thr Glu Ala Ile Leu
325 330 335

Pro Tyr Asp Gln Tyr Met His Arg Phe Ala Ala Tyr Phe Gln Gln Gly
340 345 350

Asn Met Glu Ser Asn Gly Lys Tyr Val Asp Arg Asn Gly Asn Val Val
355 360 365

Asp Tyr Gln Thr Gly Pro Ile Ile Trp Gly Glu Pro Gly Thr Asn Gly
370 375 380

Gln His Ala Phe Tyr Gln Leu Ile His Gln Gly Thr Lys Met Val Pro
385 390 395 400

G083070013W000-SEQLISTING-CHB

Cys Asp Phe Ile Ala Pro Ala Ile Thr His Asn Pro Leu Ser Asp His
405 410 415

His Gln Lys Leu Leu Ser Asn Phe Phe Ala Gln Thr Glu Ala Leu Ala
420 425 430

Phe Gly Lys Ser Arg Glu Val Val Glu Gln Glu Tyr Arg Asp Gln Gly
435 440 445

Lys Asp Pro Ala Thr Leu Asp Tyr Val Val Pro Phe Lys Val Phe Glu
450 455 460

Gly Asn Arg Pro Thr Asn Ser Ile Leu Leu Arg Glu Ile Thr Pro Phe
465 470 475 480

Ser Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Lys Ile Phe Thr Gln
485 490 495

Gly Val Ile Leu Asn Ile Phe Thr Phe Asp Gln Trp Gly Val Glu Leu
500 505 510

Gly Lys Gln Leu Ala Asn Arg Ile Leu Pro Glu Leu Lys Asp Asp Lys
515 520 525

Leu Glu Val Leu Phe Gln Gly Pro Glu Ile Ser Ser His Asp Ser Ser
530 535 540

Thr Asn Gly Leu Ile Asn Arg Tyr Lys Ala Trp Arg Gly
545 550 555

<210> 28

<211> 557

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

G083070013W000-SEQLISTING-CHB

<400> 28

Met Lys Asn Ile Asn Pro Thr Gln Thr Ala Ala Trp Gln Ala Leu Gln
 1 5 10 15

Lys His Phe Asp Glu Met Lys Asp Val Thr Ile Ala Asp Leu Phe Ala
 20 25 30

Lys Asp Gly Asp Arg Phe Ser Lys Phe Ser Ala Thr Phe Asp Asp Gln
 35 40 45

Met Leu Val Asp Tyr Ser Lys Asn Arg Ile Thr Glu Glu Thr Leu Ala
 50 55 60

Lys Leu Gln Asp Leu Ala Lys Glu Cys Asp Leu Ala Gly Ala Ile Lys
 65 70 75 80

Ser Met Phe Ser Gly Glu Lys Ile Asn Arg Thr Glu Asn Arg Ala Val
 85 90 95

Leu His Val Ala Leu Arg Asn Arg Ser Asn Thr Pro Ile Leu Val Asp
 100 105 110

Gly Lys Asp Val Met Pro Glu Val Asn Ala Val Leu Glu Lys Met Lys
 115 120 125

Thr Phe Ser Glu Ala Ile Ile Ser Gly Glu Trp Lys Gly Tyr Thr Gly
 130 135 140

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

Gly Pro Tyr Met Val Thr Glu Ala Leu Arg Pro Tyr Lys Asn His Leu
 165 170 175

Asn Met His Phe Val Ser Asn Val Asp Gly Thr His Ile Ala Glu Val

G083070013W000-SEQLISTING-CHB

180

185

190

Leu Lys Lys Val Asn Pro Glu Thr Thr Leu Phe Leu Val Ala Ser Lys
 195 200 205

Thr Phe Thr Thr Gln Glu Thr Met Thr Asn Ala His Ser Ala Arg Asp
 210 215 220

Trp Phe Leu Lys Ala Ala Gly Asp Glu Lys His Val Ala Lys His Phe
 225 230 235 240

Ala Ala Leu Ser Thr Asn Ala Lys Ala Val Gly Glu Phe Gly Ile Asp
 245 250 255

Thr Ala Asn Met Phe Glu Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser
 260 265 270

Leu Trp Ser Ala Ile Gly Leu Ser Ile Val Leu Ser Ile Gly Phe Asp
 275 280 285

Asn Phe Val Glu Leu Leu Ser Gly Ala His Ala Met Asp Lys His Phe
 290 295 300

Ser Thr Thr Pro Ala Glu Lys Asn Leu Pro Val Leu Leu Ala Leu Ile
 305 310 315 320

Gly Ile Trp Tyr Asn Asn Phe Phe Gly Ala Glu Thr Glu Ala Ile Leu
 325 330 335

Pro Tyr Asp Gln Tyr Met His Arg Phe Ala Ala Tyr Phe Gln Gln Gly
 340 345 350

Asn Met Glu Ser Asn Gly Lys Tyr Val Asp Arg Asn Gly Asn Val Val
 355 360 365

Asp Tyr Gln Thr Gly Pro Ile Ile Trp Gly Glu Pro Gly Thr Asn Gly

G083070013W000-SEQLISTING-CHB

370

375

380

Gln His Ala Phe Tyr Gln Leu Ile His Gln Gly Thr Lys Met Val Pro
 385 390 395 400

Cys Asp Phe Ile Ala Pro Ala Ile Thr His Asn Pro Leu Ser Asp His
 405 410 415

His Gln Lys Leu Leu Ser Asn Phe Phe Ala Gln Thr Glu Ala Leu Ala
 420 425 430

Phe Gly Lys Ser Arg Glu Val Val Glu Gln Glu Tyr Arg Asp Gln Gly
 435 440 445

Lys Asp Pro Ala Thr Leu Asp Tyr Val Val Pro Phe Lys Val Phe Glu
 450 455 460

Gly Asn Arg Pro Thr Asn Ser Ile Leu Leu Arg Glu Ile Thr Pro Phe
 465 470 475 480

Ser Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Lys Ile Phe Thr Gln
 485 490 495

Gly Val Ile Leu Asn Ile Phe Thr Phe Asp Gln Trp Gly Val Glu Leu
 500 505 510

Gly Lys Gln Leu Ala Asn Arg Ile Leu Pro Glu Leu Lys Asp Asp Lys
 515 520 525

Glu Leu Glu Val Leu Phe Gln Gly Pro Ile Ser Ser His Asp Ser Ser
 530 535 540

Thr Asn Gly Leu Ile Asn Arg Tyr Lys Ala Trp Arg Gly
 545 550 555

<210> 29

G083070013W000-SEQLISTING-CHB

<211> 557
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 29

Met Lys Asn Ile Asn Pro Thr Gln Thr Ala Ala Trp Gln Ala Leu Gln
 1 5 10 15

Lys His Phe Asp Glu Met Lys Asp Val Thr Ile Ala Asp Leu Phe Ala
 20 25 30

Lys Asp Gly Asp Arg Phe Ser Lys Phe Ser Ala Thr Phe Asp Asp Gln
 35 40 45

Met Leu Val Asp Tyr Ser Lys Asn Arg Ile Thr Glu Glu Thr Leu Ala
 50 55 60

Lys Leu Gln Asp Leu Ala Lys Glu Cys Asp Leu Ala Gly Ala Ile Lys
 65 70 75 80

Ser Met Phe Ser Gly Glu Lys Ile Asn Arg Thr Glu Asn Arg Ala Val
 85 90 95

Leu His Val Ala Leu Arg Asn Arg Ser Asn Thr Pro Ile Leu Val Asp
 100 105 110

Gly Lys Asp Val Met Pro Glu Val Asn Ala Val Leu Glu Lys Met Lys
 115 120 125

Thr Phe Ser Glu Ala Ile Ile Ser Gly Glu Trp Lys Gly Tyr Thr Gly
 130 135 140

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

G083070013W000-SEQLISTING-CHB

Gly Pro Tyr Met Val Thr Glu Ala Leu Arg Pro Tyr Lys Asn His Leu
165 170 175

Asn Met His Phe Val Ser Asn Val Asp Gly Thr His Ile Ala Glu Val
180 185 190

Leu Lys Lys Val Asn Pro Glu Thr Thr Leu Phe Leu Val Ala Ser Lys
195 200 205

Thr Phe Thr Thr Gln Glu Thr Met Thr Asn Ala His Ser Ala Arg Asp
210 215 220

Trp Phe Leu Lys Ala Ala Gly Asp Glu Lys His Val Ala Lys His Phe
225 230 235 240

Ala Ala Leu Ser Thr Asn Ala Lys Ala Val Gly Glu Phe Gly Ile Asp
245 250 255

Thr Ala Asn Met Phe Glu Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser
260 265 270

Leu Trp Ser Ala Ile Gly Leu Ser Ile Val Leu Ser Ile Gly Phe Asp
275 280 285

Asn Phe Val Glu Leu Leu Ser Gly Ala His Ala Met Asp Lys His Phe
290 295 300

Ser Thr Thr Pro Ala Glu Lys Asn Leu Pro Val Leu Leu Ala Leu Ile
305 310 315 320

Gly Ile Trp Tyr Asn Asn Phe Phe Gly Ala Glu Thr Glu Ala Ile Leu
325 330 335

Pro Tyr Asp Gln Tyr Met His Arg Phe Ala Ala Tyr Phe Gln Gln Gly
340 345 350

G083070013W000-SEQLISTING-CHB

Asn Met Glu Ser Asn Gly Lys Tyr Val Asp Arg Asn Gly Asn Val Val
355 360 365

Asp Tyr Gln Thr Gly Pro Ile Ile Trp Gly Glu Pro Gly Thr Asn Gly
370 375 380

Gln His Ala Phe Tyr Gln Leu Ile His Gln Gly Thr Lys Met Val Pro
385 390 395 400

Cys Asp Phe Ile Ala Pro Ala Ile Thr His Asn Pro Leu Ser Asp His
405 410 415

His Gln Lys Leu Leu Ser Asn Phe Phe Ala Gln Thr Glu Ala Leu Ala
420 425 430

Phe Gly Lys Ser Arg Glu Val Val Glu Gln Glu Tyr Arg Asp Gln Gly
435 440 445

Lys Asp Pro Ala Thr Leu Asp Tyr Val Val Pro Phe Lys Val Phe Glu
450 455 460

Gly Asn Arg Pro Thr Asn Ser Ile Leu Leu Arg Glu Ile Thr Pro Phe
465 470 475 480

Ser Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Lys Ile Phe Thr Gln
485 490 495

Gly Val Ile Leu Asn Ile Phe Thr Phe Asp Gln Trp Gly Val Glu Leu
500 505 510

Gly Lys Gln Leu Ala Asn Arg Ile Leu Pro Glu Leu Lys Asp Asp Lys
515 520 525

Glu Ile Leu Glu Val Leu Phe Gln Gly Pro Ser Ser His Asp Ser Ser
530 535 540

G083070013W000-SEQLISTING-CHB

Thr Asn Gly Leu Ile Asn Arg Tyr Lys Ala Trp Arg Gly
545 550 555

<210> 30
<211> 557
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 30

Met Lys Asn Ile Asn Pro Thr Gln Thr Ala Ala Trp Gln Ala Leu Gln
1 5 10 15

Lys His Phe Asp Glu Met Lys Asp Val Thr Ile Ala Asp Leu Phe Ala
20 25 30

Lys Asp Gly Asp Arg Phe Ser Lys Phe Ser Ala Thr Phe Asp Asp Gln
35 40 45

Met Leu Val Asp Tyr Ser Lys Asn Arg Ile Thr Glu Glu Thr Leu Ala
50 55 60

Lys Leu Gln Asp Leu Ala Lys Glu Cys Asp Leu Ala Gly Ala Ile Lys
65 70 75 80

Ser Met Phe Ser Gly Glu Lys Ile Asn Arg Thr Glu Asn Arg Ala Val
85 90 95

Leu His Val Ala Leu Arg Asn Arg Ser Asn Thr Pro Ile Leu Val Asp
100 105 110

Gly Lys Asp Val Met Pro Glu Val Asn Ala Val Leu Glu Lys Met Lys
115 120 125

Thr Phe Ser Glu Ala Ile Ile Ser Gly Glu Trp Lys Gly Tyr Thr Gly

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130

135

140

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

Gly Pro Tyr Met Val Thr Glu Ala Leu Arg Pro Tyr Lys Asn His Leu
 165 170 175

Asn Met His Phe Val Ser Asn Val Asp Gly Thr His Ile Ala Glu Val
 180 185 190

Leu Lys Lys Val Asn Pro Glu Thr Thr Leu Phe Leu Val Ala Ser Lys
 195 200 205

Thr Phe Thr Thr Gln Glu Thr Met Thr Asn Ala His Ser Ala Arg Asp
 210 215 220

Trp Phe Leu Lys Ala Ala Gly Asp Glu Lys His Val Ala Lys His Phe
 225 230 235 240

Ala Ala Leu Ser Thr Asn Ala Lys Ala Val Gly Glu Phe Gly Ile Asp
 245 250 255

Thr Ala Asn Met Phe Glu Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser
 260 265 270

Leu Trp Ser Ala Ile Gly Leu Ser Ile Val Leu Ser Ile Gly Phe Asp
 275 280 285

Asn Phe Val Glu Leu Leu Ser Gly Ala His Ala Met Asp Lys His Phe
 290 295 300

Ser Thr Thr Pro Ala Glu Lys Asn Leu Pro Val Leu Leu Ala Leu Ile
 305 310 315 320

Gly Ile Trp Tyr Asn Asn Phe Phe Gly Ala Glu Thr Glu Ala Ile Leu

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325

330

335

Pro Tyr Asp Gln Tyr Met His Arg Phe Ala Ala Tyr Phe Gln Gln Gly
 340 345 350

Asn Met Glu Ser Asn Gly Lys Tyr Val Asp Arg Asn Gly Asn Val Val
 355 360 365

Asp Tyr Gln Thr Gly Pro Ile Ile Trp Gly Glu Pro Gly Thr Asn Gly
 370 375 380

Gln His Ala Phe Tyr Gln Leu Ile His Gln Gly Thr Lys Met Val Pro
 385 390 395 400

Cys Asp Phe Ile Ala Pro Ala Ile Thr His Asn Pro Leu Ser Asp His
 405 410 415

His Gln Lys Leu Leu Ser Asn Phe Phe Ala Gln Thr Glu Ala Leu Ala
 420 425 430

Phe Gly Lys Ser Arg Glu Val Val Glu Gln Glu Tyr Arg Asp Gln Gly
 435 440 445

Lys Asp Pro Ala Thr Leu Asp Tyr Val Val Pro Phe Lys Val Phe Glu
 450 455 460

Gly Asn Arg Pro Thr Asn Ser Ile Leu Leu Arg Glu Ile Thr Pro Phe
 465 470 475 480

Ser Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Lys Ile Phe Thr Gln
 485 490 495

Gly Val Ile Leu Asn Ile Phe Thr Phe Asp Gln Trp Gly Val Glu Leu
 500 505 510

Gly Lys Gln Leu Ala Asn Arg Ile Leu Pro Glu Leu Lys Asp Asp Lys

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515

520

525

Glu Ile Ser Leu Glu Val Leu Phe Gln Gly Pro Ser His Asp Ser Ser
 530 535 540

Thr Asn Gly Leu Ile Asn Arg Tyr Lys Ala Trp Arg Gly
 545 550 555

<210> 31

<211> 557

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 31

Met Lys Asn Ile Asn Pro Thr Gln Thr Ala Ala Trp Gln Ala Leu Gln
 1 5 10 15

Lys His Phe Asp Glu Met Lys Asp Val Thr Ile Ala Asp Leu Phe Ala
 20 25 30

Lys Asp Gly Asp Arg Phe Ser Lys Phe Ser Ala Thr Phe Asp Asp Gln
 35 40 45

Met Leu Val Asp Tyr Ser Lys Asn Arg Ile Thr Glu Glu Thr Leu Ala
 50 55 60

Lys Leu Gln Asp Leu Ala Lys Glu Cys Asp Leu Ala Gly Ala Ile Lys
 65 70 75 80

Ser Met Phe Ser Gly Glu Lys Ile Asn Arg Thr Glu Asn Arg Ala Val
 85 90 95

Leu His Val Ala Leu Arg Asn Arg Ser Asn Thr Pro Ile Leu Val Asp
 100 105 110

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Gly Lys Asp Val Met Pro Glu Val Asn Ala Val Leu Glu Lys Met Lys
115 120 125

Thr Phe Ser Glu Ala Ile Ile Ser Gly Glu Trp Lys Gly Tyr Thr Gly
130 135 140

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

Gly Pro Tyr Met Val Thr Glu Ala Leu Arg Pro Tyr Lys Asn His Leu
165 170 175

Asn Met His Phe Val Ser Asn Val Asp Gly Thr His Ile Ala Glu Val
180 185 190

Leu Lys Lys Val Asn Pro Glu Thr Thr Leu Phe Leu Val Ala Ser Lys
195 200 205

Thr Phe Thr Thr Gln Glu Thr Met Thr Asn Ala His Ser Ala Arg Asp
210 215 220

Trp Phe Leu Lys Ala Ala Gly Asp Glu Lys His Val Ala Lys His Phe
225 230 235 240

Ala Ala Leu Ser Thr Asn Ala Lys Ala Val Gly Glu Phe Gly Ile Asp
245 250 255

Thr Ala Asn Met Phe Glu Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser
260 265 270

Leu Trp Ser Ala Ile Gly Leu Ser Ile Val Leu Ser Ile Gly Phe Asp
275 280 285

Asn Phe Val Glu Leu Leu Ser Gly Ala His Ala Met Asp Lys His Phe
290 295 300

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Ser Thr Thr Pro Ala Glu Lys Asn Leu Pro Val Leu Leu Ala Leu Ile
305 310 315 320

Gly Ile Trp Tyr Asn Asn Phe Phe Gly Ala Glu Thr Glu Ala Ile Leu
325 330 335

Pro Tyr Asp Gln Tyr Met His Arg Phe Ala Ala Tyr Phe Gln Gln Gly
340 345 350

Asn Met Glu Ser Asn Gly Lys Tyr Val Asp Arg Asn Gly Asn Val Val
355 360 365

Asp Tyr Gln Thr Gly Pro Ile Ile Trp Gly Glu Pro Gly Thr Asn Gly
370 375 380

Gln His Ala Phe Tyr Gln Leu Ile His Gln Gly Thr Lys Met Val Pro
385 390 395 400

Cys Asp Phe Ile Ala Pro Ala Ile Thr His Asn Pro Leu Ser Asp His
405 410 415

His Gln Lys Leu Leu Ser Asn Phe Phe Ala Gln Thr Glu Ala Leu Ala
420 425 430

Phe Gly Lys Ser Arg Glu Val Val Glu Gln Glu Tyr Arg Asp Gln Gly
435 440 445

Lys Asp Pro Ala Thr Leu Asp Tyr Val Val Pro Phe Lys Val Phe Glu
450 455 460

Gly Asn Arg Pro Thr Asn Ser Ile Leu Leu Arg Glu Ile Thr Pro Phe
465 470 475 480

Ser Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Lys Ile Phe Thr Gln
485 490 495

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Gly Val Ile Leu Asn Ile Phe Thr Phe Asp Gln Trp Gly Val Glu Leu
500 505 510

Gly Lys Gln Leu Ala Asn Arg Ile Leu Pro Glu Leu Lys Asp Asp Lys
515 520 525

Glu Ile Ser Ser Leu Glu Val Leu Phe Gln Gly Pro His Asp Ser Ser
530 535 540

Thr Asn Gly Leu Ile Asn Arg Tyr Lys Ala Trp Arg Gly
545 550 555

<210> 32
<211> 557
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 32

Met Lys Asn Ile Asn Pro Thr Gln Thr Ala Ala Trp Gln Ala Leu Gln
1 5 10 15

Lys His Phe Asp Glu Met Lys Asp Val Thr Ile Ala Asp Leu Phe Ala
20 25 30

Lys Asp Gly Asp Arg Phe Ser Lys Phe Ser Ala Thr Phe Asp Asp Gln
35 40 45

Met Leu Val Asp Tyr Ser Lys Asn Arg Ile Thr Glu Glu Thr Leu Ala
50 55 60

Lys Leu Gln Asp Leu Ala Lys Glu Cys Asp Leu Ala Gly Ala Ile Lys
65 70 75 80

Ser Met Phe Ser Gly Glu Lys Ile Asn Arg Thr Glu Asn Arg Ala Val

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85

90

95

Leu His Val Ala Leu Arg Asn Arg Ser Asn Thr Pro Ile Leu Val Asp
 100 105 110

Gly Lys Asp Val Met Pro Glu Val Asn Ala Val Leu Glu Lys Met Lys
 115 120 125

Thr Phe Ser Glu Ala Ile Ile Ser Gly Glu Trp Lys Gly Tyr Thr Gly
 130 135 140

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

Gly Pro Tyr Met Val Thr Glu Ala Leu Arg Pro Tyr Lys Asn His Leu
 165 170 175

Asn Met His Phe Val Ser Asn Val Asp Gly Thr His Ile Ala Glu Val
 180 185 190

Leu Lys Lys Val Asn Pro Glu Thr Thr Leu Phe Leu Val Ala Ser Lys
 195 200 205

Thr Phe Thr Thr Gln Glu Thr Met Thr Asn Ala His Ser Ala Arg Asp
 210 215 220

Trp Phe Leu Lys Ala Ala Gly Asp Glu Lys His Val Ala Lys His Phe
 225 230 235 240

Ala Ala Leu Ser Thr Asn Ala Lys Ala Val Gly Glu Phe Gly Ile Asp
 245 250 255

Thr Ala Asn Met Phe Glu Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser
 260 265 270

Leu Trp Ser Ala Ile Gly Leu Ser Ile Val Leu Ser Ile Gly Phe Asp

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275

280

285

Asn Phe Val Glu Leu Leu Ser Gly Ala His Ala Met Asp Lys His Phe
 290 295 300

Ser Thr Thr Pro Ala Glu Lys Asn Leu Pro Val Leu Leu Ala Leu Ile
 305 310 315 320

Gly Ile Trp Tyr Asn Asn Phe Phe Gly Ala Glu Thr Glu Ala Ile Leu
 325 330 335

Pro Tyr Asp Gln Tyr Met His Arg Phe Ala Ala Tyr Phe Gln Gln Gly
 340 345 350

Asn Met Glu Ser Asn Gly Lys Tyr Val Asp Arg Asn Gly Asn Val Val
 355 360 365

Asp Tyr Gln Thr Gly Pro Ile Ile Trp Gly Glu Pro Gly Thr Asn Gly
 370 375 380

Gln His Ala Phe Tyr Gln Leu Ile His Gln Gly Thr Lys Met Val Pro
 385 390 395 400

Cys Asp Phe Ile Ala Pro Ala Ile Thr His Asn Pro Leu Ser Asp His
 405 410 415

His Gln Lys Leu Leu Ser Asn Phe Phe Ala Gln Thr Glu Ala Leu Ala
 420 425 430

Phe Gly Lys Ser Arg Glu Val Val Glu Gln Glu Tyr Arg Asp Gln Gly
 435 440 445

Lys Asp Pro Ala Thr Leu Asp Tyr Val Val Pro Phe Lys Val Phe Glu
 450 455 460

Gly Asn Arg Pro Thr Asn Ser Ile Leu Leu Arg Glu Ile Thr Pro Phe

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465 470 475 480

Ser Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Lys Ile Phe Thr Gln
485 490 495

Gly Val Ile Leu Asn Ile Phe Thr Phe Asp Gln Trp Gly Val Glu Leu
500 505 510

Gly Lys Gln Leu Ala Asn Arg Ile Leu Pro Glu Leu Lys Asp Asp Lys
515 520 525

Glu Ile Ser Ser His Asp Ser Ser Thr Asn Gly Leu Ile Asn Arg Tyr
530 535 540

Lys Leu Glu Val Leu Phe Gln Gly Pro Ala Trp Arg Gly
545 550 555

<210> 33
<211> 558
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 33
atgggcccag aagaagaatt cggcatgagc ctgatcaagc ataactcttg cgtcattacc 60
acggagaatg gtaagttcac gggcttgggc gtttatgacc gtttcgtcgt ggttccgacc 120
cacgctgacc cgggtaaaga aatccagggt gacggtatca cgaccaaagt gattgatagc 180
tatgatctct ataataagaa cggcatcaag ctggaaatca cggtgctgaa actggaccgt 240
aatgaaaagt ttcgtgatat ccgtcgctat attccgaata acgaggatga ctacccaaat 300
tgcaatctgg cgctgctggc aaatcagccg gaaccgacga tcatcaacgt gggtgacgtg 360
gtgagctatg gcaatatcct gctgagcggg aaccagaccg cgcgtatgct gaagtattcc 420
tatccgacga aaagcggcta ttgcggcggc gtgctctata agattggtca agtcctgggc 480

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atccacgtcg gcggaatgg ccgcgatggt ttcagcgcga tgctgctgcg tagctatttc 540

accgacgtcc agtgataa 558

<210> 34

<211> 184

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 34

Met Gly Pro Glu Glu Glu Phe Gly Met Ser Leu Ile Lys His Asn Ser
1 5 10 15

Cys Val Ile Thr Thr Glu Asn Gly Lys Phe Thr Gly Leu Gly Val Tyr
20 25 30

Asp Arg Phe Val Val Val Pro Thr His Ala Asp Pro Gly Lys Glu Ile
35 40 45

Gln Val Asp Gly Ile Thr Thr Lys Val Ile Asp Ser Tyr Asp Leu Tyr
50 55 60

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

Asn Glu Lys Phe Arg Asp Ile Arg Arg Tyr Ile Pro Asn Asn Glu Asp
85 90 95

Asp Tyr Pro Asn Cys Asn Leu Ala Leu Leu Ala Asn Gln Pro Glu Pro
100 105 110

Thr Ile Ile Asn Val Gly Asp Val Val Ser Tyr Gly Asn Ile Leu Leu
115 120 125

Ser Gly Asn Gln Thr Ala Arg Met Leu Lys Tyr Ser Tyr Pro Thr Lys

130

135

140

Ser Gly Tyr Cys Gly Gly Val Leu Tyr Lys Ile Gly Gln Val Leu Gly
 145 150 155 160

Ile His Val Gly Gly Asn Gly Arg Asp Gly Phe Ser Ala Met Leu Leu
 165 170 175

Arg Ser Tyr Phe Thr Asp Val Gln
 180

<210> 35

<211> 618

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 35

atgaaaaaaa cggcaattgc gatagcgggtt gcgctagctg gttttgccac ggtggcgcag 60
 gctggcccag aagaagaatt cggcatgagc ctgatcaagc ataactcttg cgtcattacc 120
 acggagaatg gtaagttcac gggcttgggc gtttatgacc gtttcgtcgt gggtccgacc 180
 cacgctgacc cgggtaaaga aatccagggtt gacggatatca cgaccaaagt gattgatagc 240
 tatgatctct ataataagaa cggcatcaag ctggaaatca cggtgctgaa actggaccgt 300
 aatgaaaagt ttcgtgatat ccgtcgctat attccgaata acgaggatga ctacccaaat 360
 tgcaatctgg cgctgctggc aaatcagccg gaaccgacga tcatcaacgt gggtgacgtg 420
 gtgagctatg gcaatatcct gctgagcgggt aaccagaccg cgcgtatgct gaagtattcc 480
 tatccgacga aaagcggcta ttgcggcggc gtgctctata agattgggtca agtcctgggc 540
 atccacgtcg gcggtaatgg ccgcgatggt ttcagcgcga tgctgctgcg tagctatttc 600
 accgacgtcc agtgataa 618

<210> 36

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<211> 204
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 36

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 1 5 10 15

Thr Val Ala Gln Ala Gly Pro Glu Glu Glu Phe Gly Met Ser Leu Ile
 20 25 30

Lys His Asn Ser Cys Val Ile Thr Thr Glu Asn Gly Lys Phe Thr Gly
 35 40 45

Leu Gly Val Tyr Asp Arg Phe Val Val Val Pro Thr His Ala Asp Pro
 50 55 60

Gly Lys Glu Ile Gln Val Asp Gly Ile Thr Thr Lys Val Ile Asp Ser
 65 70 75 80

Tyr Asp Leu Tyr Asn Lys Asn Gly Ile Lys Leu Glu Ile Thr Val Leu
 85 90 95

Lys Leu Asp Arg Asn Glu Lys Phe Arg Asp Ile Arg Arg Tyr Ile Pro
 100 105 110

Asn Asn Glu Asp Asp Tyr Pro Asn Cys Asn Leu Ala Leu Leu Ala Asn
 115 120 125

Gln Pro Glu Pro Thr Ile Ile Asn Val Gly Asp Val Val Ser Tyr Gly
 130 135 140

Asn Ile Leu Leu Ser Gly Asn Gln Thr Ala Arg Met Leu Lys Tyr Ser
 145 150 155 160

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Tyr Pro Thr Lys Ser Gly Tyr Cys Gly Gly Val Leu Tyr Lys Ile Gly
165 170 175

Gln Val Leu Gly Ile His Val Gly Gly Asn Gly Arg Asp Gly Phe Ser
180 185 190

Ala Met Leu Leu Arg Ser Tyr Phe Thr Asp Val Gln
195 200

<210> 37
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 37
ctggaagtgc tgtttcaggg tccg 24

<210> 38
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 38

Leu Glu Val Leu Phe Gln Gly Pro
1 5

<210> 39
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 39

Glu Val Leu Phe Gln Gly Pro
1 5

<210> 40
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 40

Val Leu Phe Gln Gly Pro
1 5

<210> 41
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 41

Leu Phe Gln Gly Pro
1 5

<210> 42
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 42

Leu Glu Val Leu Phe Gln Gly
1 5

<210> 43

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

 <220>
 <223> Synthetic Polypeptide

 <400> 43

Leu Glu Val Leu Phe Gln
 1 5

<210> 44
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic Polypeptide

 <400> 44

Leu Glu Val Leu Phe
 1 5

<210> 45
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic Polypeptide

 <400> 45

Glu Val Leu Phe Gln Gly
 1 5

<210> 46
 <211> 21
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic Polypeptide

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<400> 46

Met	Lys	Lys	Thr	Ala	Ile	Ala	Ile	Ala	Val	Ala	Leu	Ala	Gly	Phe	Ala
1				5					10					15	

Thr	Val	Ala	Gln	Ala
			20	

<210> 47

<211> 2145

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 47

gtgtcccgta ttattatgct gatccctacc ggaaccagcg tcggtctgac cagcgtcagc	60
cttggcgtga tccgtgcaat ggaacgcaaa ggcgttcgtc tgagcgtttt caaacctatc	120
gctcagccgc gtaccgggtgg cgatgcgccc gatcagacta cgactatcgt gcgtgcgaac	180
tcttccacca cgacggccgc tgaaccgctg aaaatgagct acgttgaagg tctgctttcc	240
agcaatcaga aagatgtgct gatggaagag atcgtcgcaa actaccacgc taacaccaaa	300
gacgctgaag tcgttctggt tgaaggctctg gtcccgcacac gtaagcacca gtttgcccag	360
tctctgaact acgaaatcgc taaaacgctg aatgcggaaa tcgtcttcgt tatgtctcag	420
ggcactgaca ccccgaaca gctgaaagag cgtatcgaac tgaccgcga cagcttcggc	480
ggtgccaaaa acaccaacat caccggcggt atcgttaaca aactgaacgc accggttgat	540
gaacagggtc gtactcgcgc ggatctgtcc gagattttcg acgactcttc caaagctaaa	600
gtaaacaatg ttgatccggc gaagctgcaa gaatccagcc cgctgccggg tctcggcgct	660
gtgccgtgga gctttgacct gatcgcgact cgtgcgatcg atatggctcg ccacctgaat	720
gcgaccatca tcaacgaagg cgacatcaat actcgcgcg ttaaatccgt cactttctgc	780
gcacgcagca ttccgcacat gctggagcac ttccgtgccg gttctctgct ggtgacttcc	840

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gcagaccgtc ctgacgtgct ggtggccgct tgcctggcag ccatgaacgg cgtagaaatc	900
ggtgccctgc tgctgactgg cggttacgaa atggacgcgc gcatttctaa actgtgcgaa	960
cgtgctttcg ctaccggcct gccggtatct atggtgaaca ccaacacctg gcagacctct	1020
ctgagcctgc agagcttcaa cctggaagtt ccggttgacg atcacgaacg tatcgagaaa	1080
gttcaggaat acgttgctaa ctacatcaac gctgactgga tcgaatctct gactgccact	1140
tctgagcgca gccgtcgtct gtctccgcct gcgttccggt atcagctgac tgaacttgcg	1200
cgcaaagcgg gcaaacgtat cgtactgccg gaagggtgacg aaccgcgtac cgtaaagca	1260
gccgctatct gtgctgaacg tggatcgca acttgctgac tgctgggtaa tccggcagag	1320
atcaaccgtg ttgcagcgtc tcagggtgta gaactgggtg cagggttgga aatcgttgat	1380
ccagaagtgg ttcgcgaaag ctatgttggg cgtctggctg aactgcgtaa gaacaaaggc	1440
atgaccgaaa ccgttgcccg cgaacagctg gaagacaacg tggtgctcgg tacgctgatg	1500
ctggaacagg atgaagtga tggcttggtt tccggtgctg ttcacactac cgcaaacacc	1560
atccgtccgc cgctgcagct gatcaaaact gcaccgggca gctccctggg atcttccgtg	1620
ttcttcatgc tgctgccgga acagggttac gtttacgggt actgtgcgat caaccggat	1680
ccgaccgtg aacagctggc agaaatcgcg attcagtcg ctgattccgc tgcggccttc	1740
ggtatcgaa cgcgcgttgc tatgctctcc tactccaccg gtacttctgg tgcaggtagc	1800
gacgtagaaa aagttcgca agcaactcgt ctggcgcagg aaaaacgtcc tgacctgatg	1860
atcgacggtc cgctgcagta cgacgctgcg gtaatggctg acgttgcgaa atccaaagcg	1920
ccgaactctc cggttgagg tcgcgctacc gtgttcatct tcccgatct gaacaccggt	1980
aacaccacct acaaagcggg acagcgttct gccgacctga tctccatcgg gccgatgctg	2040
cagggtatgc gcaagccggg taacgacctg tcccgtggcg cactgggtga cgatatcgtc	2100
tacaccatcg cgctgactgc gattcagtct gcacagcagc agtaa	2145

<210> 48
 <211> 714
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 48

Val Ser Arg Ile Ile Met Leu Ile Pro Thr Gly Thr Ser Val Gly Leu
 1 5 10 15

Thr Ser Val Ser Leu Gly Val Ile Arg Ala Met Glu Arg Lys Gly Val
 20 25 30

Arg Leu Ser Val Phe Lys Pro Ile Ala Gln Pro Arg Thr Gly Gly Asp
 35 40 45

Ala Pro Asp Gln Thr Thr Thr Ile Val Arg Ala Asn Ser Ser Thr Thr
 50 55 60

Thr Ala Ala Glu Pro Leu Lys Met Ser Tyr Val Glu Gly Leu Leu Ser
 65 70 75 80

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

Ala Asn Thr Lys Asp Ala Glu Val Val Leu Val Glu Gly Leu Val Pro
 100 105 110

Thr Arg Lys His Gln Phe Ala Gln Ser Leu Asn Tyr Glu Ile Ala Lys
 115 120 125

Thr Leu Asn Ala Glu Ile Val Phe Val Met Ser Gln Gly Thr Asp Thr
 130 135 140

Pro Glu Gln Leu Lys Glu Arg Ile Glu Leu Thr Arg Asn Ser Phe Gly
 145 150 155 160

Gly Ala Lys Asn Thr Asn Ile Thr Gly Val Ile Val Asn Lys Leu Asn

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165

170

175

Ala Pro Val Asp Glu Gln Gly Arg Thr Arg Pro Asp Leu Ser Glu Ile
 180 185 190

Phe Asp Asp Ser Ser Lys Ala Lys Val Asn Asn Val Asp Pro Ala Lys
 195 200 205

Leu Gln Glu Ser Ser Pro Leu Pro Val Leu Gly Ala Val Pro Trp Ser
 210 215 220

Phe Asp Leu Ile Ala Thr Arg Ala Ile Asp Met Ala Arg His Leu Asn
 225 230 235 240

Ala Thr Ile Ile Asn Glu Gly Asp Ile Asn Thr Arg Arg Val Lys Ser
 245 250 255

Val Thr Phe Cys Ala Arg Ser Ile Pro His Met Leu Glu His Phe Arg
 260 265 270

Ala Gly Ser Leu Leu Val Thr Ser Ala Asp Arg Pro Asp Val Leu Val
 275 280 285

Ala Ala Cys Leu Ala Ala Met Asn Gly Val Glu Ile Gly Ala Leu Leu
 290 295 300

Leu Thr Gly Gly Tyr Glu Met Asp Ala Arg Ile Ser Lys Leu Cys Glu
 305 310 315 320

Arg Ala Phe Ala Thr Gly Leu Pro Val Phe Met Val Asn Thr Asn Thr
 325 330 335

Trp Gln Thr Ser Leu Ser Leu Gln Ser Phe Asn Leu Glu Val Pro Val
 340 345 350

Asp Asp His Glu Arg Ile Glu Lys Val Gln Glu Tyr Val Ala Asn Tyr

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355

360

365

Ile Asn Ala Asp Trp Ile Glu Ser Leu Thr Ala Thr Ser Glu Arg Ser
 370 375 380

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

Arg Lys Ala Gly Lys Arg Ile Val Leu Pro Glu Gly Asp Glu Pro Arg
 405 410 415

Thr Val Lys Ala Ala Ala Ile Cys Ala Glu Arg Gly Ile Ala Thr Cys
 420 425 430

Val Leu Leu Gly Asn Pro Ala Glu Ile Asn Arg Val Ala Ala Ser Gln
 435 440 445

Gly Val Glu Leu Gly Ala Gly Ile Glu Ile Val Asp Pro Glu Val Val
 450 455 460

Arg Glu Ser Tyr Val Gly Arg Leu Val Glu Leu Arg Lys Asn Lys Gly
 465 470 475 480

Met Thr Glu Thr Val Ala Arg Glu Gln Leu Glu Asp Asn Val Val Leu
 485 490 495

Gly Thr Leu Met Leu Glu Gln Asp Glu Val Asp Gly Leu Val Ser Gly
 500 505 510

Ala Val His Thr Thr Ala Asn Thr Ile Arg Pro Pro Leu Gln Leu Ile
 515 520 525

Lys Thr Ala Pro Gly Ser Ser Leu Val Ser Ser Val Phe Phe Met Leu
 530 535 540

Leu Pro Glu Gln Val Tyr Val Tyr Gly Asp Cys Ala Ile Asn Pro Asp

545 550 555 560

Leu Thr Ala Ile Gln Ser Ala Gln Gln Gln
705 710

<220>

<223> Synthetic Oligonucleotide

<400> 49

gtgtcccgta ttattatgct gatccctacc ggaaccagcg tcggtctgac cagcgtcagc	60
cttggcgtga tccgtgcaat ggaacgcaaa ggcgttcgtc tgagcgtttt caaacctatc	120
gctcagccgc gtaccggtgg cgatgcgccc gatcagacta cgactatcgt gcgtgcgaac	180
tcttccacca cgacggccgc tgaaccgctg aaaatgagct acgttgaagg tctgctttcc	240
agcaatcaga aagatgtgct gatggaagag atcgtcgcaa actaccacgc taacaccaaaa	300
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 50

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Thr	Ser	Val	Ser	Leu	Gly	Val	Ile	Arg	Ala	Met	Glu	Arg	Lys	Gly	Val
			20					25					30		

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Arg Leu Ser Val Phe Lys Pro Ile Ala Gln Pro Arg Thr Gly Gly Asp
 35 40 45

Ala Pro Asp Gln Thr Thr Thr Ile Val Arg Ala Asn Ser Ser Thr Thr
 50 55 60

Thr Ala Ala Glu Pro Leu Lys Met Ser Tyr Val Glu Gly Leu Leu Ser
 65 70 75 80

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

Ala Asn Thr Lys Asp Ala Glu Val Val Leu Val Glu Gly Leu Val Pro
 100 105 110

Thr Arg Lys His Gln Phe Ala Gln Ser Leu Asn Tyr Glu Ile Ala Lys
 115 120 125

Thr Leu Asn Ala Glu Ile Val Phe Val Met Ser Gln Gly Thr Asp Thr
 130 135 140

Pro Glu Gln Leu Lys Glu Arg Ile Glu Leu Thr Arg Asn Ser Phe Gly
 145 150 155 160

Gly Ala Lys Asn Thr Asn Ile Thr Gly Val Ile Val Asn Lys Leu Asn
 165 170 175

Ala Pro Val Asp Glu Gln Gly Arg Thr Arg Pro Asp Leu Ser Glu Ile
 180 185 190

Phe Asp Asp Ser Ser Lys Ala Lys Val Asn Asn Val Asp Pro Ala Lys
 195 200 205

Leu Gln Glu Ser Ser Pro Leu Pro Val Leu Gly Ala Val Pro Trp Ser
 210 215 220

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Phe Asp Leu Ile Ala Thr Arg Ala Ile Asp Met Ala Arg His Leu Asn
225 230 235 240

Ala Thr Ile Ile Asn Glu Gly Asp Ile Asn Thr Arg Arg Val Lys Ser
245 250 255

Val Thr Phe Cys Ala Arg Ser Ile Pro His Met Leu Glu His Phe Arg
260 265 270

Ala Gly Ser Leu Leu Val Thr Ser Ala Asp Arg Pro Asp Val Leu Val
275 280 285

Ala Ala Cys Leu Ala Ala Met Asn Gly Val Glu Ile Gly Ala Leu Leu
290 295 300

Leu Thr Gly Gly Tyr Glu Met Asp Ala Arg Ile Ser Lys Leu Cys Glu
305 310 315 320

Arg Ala Phe Ala Thr Gly Leu Pro Val Phe Met Val Asn Thr Asn Thr
325 330 335

Trp Gln Thr Ser Leu Ser Leu Gln Ser Phe Asn Leu Glu Val Pro Val
340 345 350

Asp Asp His Glu Arg Ile Glu Lys Val Gln Glu Tyr Val Ala Asn Tyr
355 360 365

Ile Asn Ala Asp Trp Ile Glu Ser Leu Thr Ala Thr Ser Leu Glu Val
370 375 380

Leu Phe Gln Gly Pro Glu Arg Ser Arg Arg Leu Ser Pro Pro Ala Phe
385 390 395 400

Arg Tyr Gln Leu Thr Glu Leu Ala Arg Lys Ala Gly Lys Arg Ile Val
405 410 415

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Leu Pro Glu Gly Asp Glu Pro Arg Thr Val Lys Ala Ala Ala Ile Cys
420 425 430

Ala Glu Arg Gly Ile Ala Thr Cys Val Leu Leu Gly Asn Pro Ala Glu
435 440 445

Ile Asn Arg Val Ala Ala Ser Gln Gly Val Glu Leu Gly Ala Gly Ile
450 455 460

Glu Ile Val Asp Pro Glu Val Val Arg Glu Ser Tyr Val Gly Arg Leu
465 470 475 480

Val Glu Leu Arg Lys Asn Lys Gly Met Thr Glu Thr Val Ala Arg Glu
485 490 495

Gln Leu Glu Asp Asn Val Val Leu Gly Thr Leu Met Leu Glu Gln Asp
500 505 510

Glu Val Asp Gly Leu Val Ser Gly Ala Val His Thr Thr Ala Asn Thr
515 520 525

Ile Arg Pro Pro Leu Gln Leu Ile Lys Thr Ala Pro Gly Ser Ser Leu
530 535 540

Val Ser Ser Val Phe Phe Met Leu Leu Pro Glu Gln Val Tyr Val Tyr
545 550 555 560

Gly Asp Cys Ala Ile Asn Pro Asp Pro Thr Ala Glu Gln Leu Ala Glu
565 570 575

Ile Ala Ile Gln Ser Ala Asp Ser Ala Ala Ala Phe Gly Ile Glu Pro
580 585 590

Arg Val Ala Met Leu Ser Tyr Ser Thr Gly Thr Ser Gly Ala Gly Ser
595 600 605

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Asp Val Glu Lys Val Arg Glu Ala Thr Arg Leu Ala Gln Glu Lys Arg
610 615 620

Pro Asp Leu Met Ile Asp Gly Pro Leu Gln Tyr Asp Ala Ala Val Met
625 630 635 640

Ala Asp Val Ala Lys Ser Lys Ala Pro Asn Ser Pro Val Ala Gly Arg
645 650 655

Ala Thr Val Phe Ile Phe Pro Asp Leu Asn Thr Gly Asn Thr Thr Tyr
660 665 670

Lys Ala Val Gln Arg Ser Ala Asp Leu Ile Ser Ile Gly Pro Met Leu
675 680 685

Gln Gly Met Arg Lys Pro Val Asn Asp Leu Ser Arg Gly Ala Leu Val
690 695 700

Asp Asp Ile Val Tyr Thr Ile Ala Leu Thr Ala Ile Gln Ser Ala Gln
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Gln Gln

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<212> DNA
<213> Artificial Sequence

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<223> Synthetic Oligonucleotide

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gctcagccgc gtaccgggtgg cgatgcgccc gatcagacta cgactatcgt gcgtgcgaac 180

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gacgctgaag tcgttctggt tgaaggctctg gtcccgcacac gtaagcacca gtttgcccag	360
tctctgaact acgaaatcgc taaaacgctg aatgcggaaa tcgtcttcgt tatgtctcag	420
ggcactgaca ccccggaaca gctgaaagag cgtatcgaac tgacccgcaa cagcttcggc	480
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gaacagggtc gtactcgccc ggatctgtcc gagattttcg acgactcttc caaagctaaa	600
gtaaacaatg ttgatccggc gaagctgcaa gaatccagcc cgctgccggt tctcggcgct	660
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<210> 52
<211> 722
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Polypeptide

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<400> 52

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Thr Ser Val Ser Leu Gly Val Ile Arg Ala Met Glu Arg Lys Gly Val
          20          25          30

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Arg Leu Ser Val Phe Lys Pro Ile Ala Gln Pro Arg Thr Gly Gly Asp
          35          40          45

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

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Ala	Asn	Thr	Lys	Asp	Ala	Glu	Val	Val	Leu	Val	Glu	Gly	Leu	Val	Pro
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Thr	Arg	Lys	His	Gln	Phe	Ala	Gln	Ser	Leu	Asn	Tyr	Glu	Ile	Ala	Lys
		115					120					125			
Thr	Leu	Asn	Ala	Glu	Ile	Val	Phe	Val	Met	Ser	Gln	Gly	Thr	Asp	Thr
	130					135					140				
Pro	Glu	Gln	Leu	Lys	Glu	Arg	Ile	Glu	Leu	Thr	Arg	Asn	Ser	Phe	Gly
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Gly	Ala	Lys	Asn	Thr	Asn	Ile	Thr	Gly	Val	Ile	Val	Asn	Lys	Leu	Asn
			165						170					175	
Ala	Pro	Val	Asp	Glu	Gln	Gly	Arg	Thr	Arg	Pro	Asp	Leu	Ser	Glu	Ile
			180					185					190		
Phe	Asp	Asp	Ser	Ser	Lys	Ala	Lys	Val	Asn	Asn	Val	Asp	Pro	Ala	Lys
		195					200					205			
Leu	Gln	Glu	Ser	Ser	Pro	Leu	Pro	Val	Leu	Gly	Ala	Val	Pro	Trp	Ser
	210					215					220				
Phe	Asp	Leu	Ile	Ala	Thr	Arg	Ala	Ile	Asp	Met	Ala	Arg	His	Leu	Asn
225					230					235					240
Ala	Thr	Ile	Ile	Asn	Glu	Gly	Asp	Ile	Asn	Thr	Arg	Arg	Val	Lys	Ser
			245						250					255	
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265

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Ala Gly Ser Leu Leu Val Thr Ser Ala Asp Arg Pro Asp Val Leu Val
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Ala Ala Cys Leu Ala Ala Met Asn Gly Val Glu Ile Gly Ala Leu Leu
 290 295 300

Leu Thr Gly Gly Tyr Glu Met Asp Ala Arg Ile Ser Lys Leu Cys Glu
 305 310 315 320

Arg Ala Phe Ala Thr Gly Leu Pro Val Phe Met Val Asn Thr Asn Thr
 325 330 335

Trp Gln Thr Ser Leu Ser Leu Gln Ser Phe Asn Leu Glu Val Pro Val
 340 345 350

Asp Asp His Glu Arg Ile Glu Lys Val Gln Glu Tyr Val Ala Asn Tyr
 355 360 365

Ile Asn Ala Asp Trp Ile Glu Ser Leu Thr Ala Thr Ser Glu Leu Glu
 370 375 380

Val Leu Phe Gln Gly Pro Arg Ser Arg Arg Leu Ser Pro Pro Ala Phe
 385 390 395 400

Arg Tyr Gln Leu Thr Glu Leu Ala Arg Lys Ala Gly Lys Arg Ile Val
 405 410 415

Leu Pro Glu Gly Asp Glu Pro Arg Thr Val Lys Ala Ala Ala Ile Cys
 420 425 430

Ala Glu Arg Gly Ile Ala Thr Cys Val Leu Leu Gly Asn Pro Ala Glu
 435 440 445

Ile Asn Arg Val Ala Ala Ser Gln Gly Val Glu Leu Gly Ala Gly Ile

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450

455

460

Glu Ile Val Asp Pro Glu Val Val Arg Glu Ser Tyr Val Gly Arg Leu
 465 470 475 480

Val Glu Leu Arg Lys Asn Lys Gly Met Thr Glu Thr Val Ala Arg Glu
 485 490 495

Gln Leu Glu Asp Asn Val Val Leu Gly Thr Leu Met Leu Glu Gln Asp
 500 505 510

Glu Val Asp Gly Leu Val Ser Gly Ala Val His Thr Thr Ala Asn Thr
 515 520 525

Ile Arg Pro Pro Leu Gln Leu Ile Lys Thr Ala Pro Gly Ser Ser Leu
 530 535 540

Val Ser Ser Val Phe Phe Met Leu Leu Pro Glu Gln Val Tyr Val Tyr
 545 550 555 560

Gly Asp Cys Ala Ile Asn Pro Asp Pro Thr Ala Glu Gln Leu Ala Glu
 565 570 575

Ile Ala Ile Gln Ser Ala Asp Ser Ala Ala Ala Phe Gly Ile Glu Pro
 580 585 590

Arg Val Ala Met Leu Ser Tyr Ser Thr Gly Thr Ser Gly Ala Gly Ser
 595 600 605

Asp Val Glu Lys Val Arg Glu Ala Thr Arg Leu Ala Gln Glu Lys Arg
 610 615 620

Pro Asp Leu Met Ile Asp Gly Pro Leu Gln Tyr Asp Ala Ala Val Met
 625 630 635 640

Ala Asp Val Ala Lys Ser Lys Ala Pro Asn Ser Pro Val Ala Gly Arg

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645

650

655

Ala Thr Val Phe Ile Phe Pro Asp Leu Asn Thr Gly Asn Thr Thr Tyr
660 665 670

Lys Ala Val Gln Arg Ser Ala Asp Leu Ile Ser Ile Gly Pro Met Leu
675 680 685

Gln Gly Met Arg Lys Pro Val Asn Asp Leu Ser Arg Gly Ala Leu Val
690 695 700

Asp Asp Ile Val Tyr Thr Ile Ala Leu Thr Ala Ile Gln Ser Ala Gln
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Gln Gln

<210> 53
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<212> DNA
<213> Artificial Sequence

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<223> Synthetic Oligonucleotide

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<220>
 <223> Synthetic Polypeptide

<400> 54

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 20 25 30

Arg Leu Ser Val Phe Lys Pro Ile Ala Gln Pro Arg Thr Gly Gly Asp
 35 40 45

Ala Pro Asp Gln Thr Thr Thr Ile Val Arg Ala Asn Ser Ser Thr Thr
 50 55 60

Thr Ala Ala Glu Pro Leu Lys Met Ser Tyr Val Glu Gly Leu Leu Ser
 65 70 75 80

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

Ala Asn Thr Lys Asp Ala Glu Val Val Leu Val Glu Gly Leu Val Pro
 100 105 110

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Thr Arg Lys His Gln Phe Ala Gln Ser Leu Asn Tyr Glu Ile Ala Lys
 115 120 125

Thr Leu Asn Ala Glu Ile Val Phe Val Met Ser Gln Gly Thr Asp Thr
 130 135 140

Pro Glu Gln Leu Lys Glu Arg Ile Glu Leu Thr Arg Asn Ser Phe Gly
 145 150 155 160

Gly Ala Lys Asn Thr Asn Ile Thr Gly Val Ile Val Asn Lys Leu Asn
 165 170 175

Ala Pro Val Asp Glu Gln Gly Arg Thr Arg Pro Asp Leu Ser Glu Ile
 180 185 190

Phe Asp Asp Ser Ser Lys Ala Lys Val Asn Asn Val Asp Pro Ala Lys
 195 200 205

Leu Gln Glu Ser Ser Pro Leu Pro Val Leu Gly Ala Val Pro Trp Ser
 210 215 220

Phe Asp Leu Ile Ala Thr Arg Ala Ile Asp Met Ala Arg His Leu Asn
 225 230 235 240

Ala Thr Ile Ile Asn Glu Gly Asp Ile Asn Thr Arg Arg Val Lys Ser
 245 250 255

Val Thr Phe Cys Ala Arg Ser Ile Pro His Met Leu Glu His Phe Arg
 260 265 270

Ala Gly Ser Leu Leu Val Thr Ser Ala Asp Arg Pro Asp Val Leu Val
 275 280 285

Ala Ala Cys Leu Ala Ala Met Asn Gly Val Glu Ile Gly Ala Leu Leu
 290 295 300

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Leu Thr Gly Gly Tyr Glu Met Asp Ala Arg Ile Ser Lys Leu Cys Glu
 305 310 315 320

Arg Ala Phe Ala Thr Gly Leu Pro Val Phe Met Val Asn Thr Asn Thr
 325 330 335

Trp Gln Thr Ser Leu Ser Leu Gln Ser Phe Asn Leu Glu Val Pro Val
 340 345 350

Asp Asp His Glu Arg Ile Glu Lys Val Gln Glu Tyr Val Ala Asn Tyr
 355 360 365

Ile Asn Ala Asp Trp Ile Glu Ser Leu Thr Ala Thr Ser Glu Arg Ser
 370 375 380

Arg Arg Leu Glu Val Leu Phe Gln Gly Pro Ser Pro Pro Ala Phe Arg
 385 390 395 400

Tyr Gln Leu Thr Glu Leu Ala Arg Lys Ala Gly Lys Arg Ile Val Leu
 405 410 415

Pro Glu Gly Asp Glu Pro Arg Thr Val Lys Ala Ala Ala Ile Cys Ala
 420 425 430

Glu Arg Gly Ile Ala Thr Cys Val Leu Leu Gly Asn Pro Ala Glu Ile
 435 440 445

Asn Arg Val Ala Ala Ser Gln Gly Val Glu Leu Gly Ala Gly Ile Glu
 450 455 460

Ile Val Asp Pro Glu Val Val Arg Glu Ser Tyr Val Gly Arg Leu Val
 465 470 475 480

Glu Leu Arg Lys Asn Lys Gly Met Thr Glu Thr Val Ala Arg Glu Gln
 485 490 495

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Leu Glu Asp Asn Val Val Leu Gly Thr Leu Met Leu Glu Gln Asp Glu
 500 505 510

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

Arg Pro Pro Leu Gln Leu Ile Lys Thr Ala Pro Gly Ser Ser Leu Val
 530 535 540

Ser Ser Val Phe Phe Met Leu Leu Pro Glu Gln Val Tyr Val Tyr Gly
 545 550 555 560

Asp Cys Ala Ile Asn Pro Asp Pro Thr Ala Glu Gln Leu Ala Glu Ile
 565 570 575

Ala Ile Gln Ser Ala Asp Ser Ala Ala Ala Phe Gly Ile Glu Pro Arg
 580 585 590

Val Ala Met Leu Ser Tyr Ser Thr Gly Thr Ser Gly Ala Gly Ser Asp
 595 600 605

Val Glu Lys Val Arg Glu Ala Thr Arg Leu Ala Gln Glu Lys Arg Pro
 610 615 620

Asp Leu Met Ile Asp Gly Pro Leu Gln Tyr Asp Ala Ala Val Met Ala
 625 630 635 640

Asp Val Ala Lys Ser Lys Ala Pro Asn Ser Pro Val Ala Gly Arg Ala
 645 650 655

Thr Val Phe Ile Phe Pro Asp Leu Asn Thr Gly Asn Thr Thr Tyr Lys
 660 665 670

Ala Val Gln Arg Ser Ala Asp Leu Ile Ser Ile Gly Pro Met Leu Gln
 675 680 685

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Gly Met Arg Lys Pro Val Asn Asp Leu Ser Arg Gly Ala Leu Val Asp
690 695 700

Asp Ile Val Tyr Thr Ile Ala Leu Thr Ala Ile Gln Ser Ala Gln Gln
705 710 715 720

Gln

<210> 55
<211> 2163
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 55
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gtaaacaatg ttgatccggc gaagctgcaa gaatccagcc cgctgccggg tctcggcgct 660
gtgccgtgga gctttgacct gatcgcgact cgtgcgatcg atatggctcg ccacctgaat 720
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taa	2163

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<210> 56
 <211> 720
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 56

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Thr Ser Val Ser Leu Gly Val Ile Arg Ala Met Glu Arg Lys Gly Val
 20 25 30

Arg Leu Ser Val Phe Lys Pro Ile Ala Gln Pro Arg Thr Gly Gly Asp
 35 40 45

Ala Pro Asp Gln Thr Thr Thr Ile Val Arg Ala Asn Ser Ser Thr Thr
 50 55 60

Thr Ala Ala Glu Pro Leu Lys Met Ser Tyr Val Glu Gly Leu Leu Ser
 65 70 75 80

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

Ala Asn Thr Lys Asp Ala Glu Val Val Leu Val Glu Gly Leu Val Pro
 100 105 110

Thr Arg Lys His Gln Phe Ala Gln Ser Leu Asn Tyr Glu Ile Ala Lys
 115 120 125

Thr Leu Asn Ala Glu Ile Val Phe Val Met Ser Gln Gly Thr Asp Thr
 130 135 140

Pro Glu Gln Leu Lys Glu Arg Ile Glu Leu Thr Arg Asn Ser Phe Gly

145 150 155 160

Ala Pro Val Asp Glu Gln Gly Arg Thr Arg Pro Asp Leu Ser Glu Ile
180 185 190

Phe Asp Asp Ser Ser Lys Ala Lys Val Asn Asn Val Asp Pro Ala Lys
195 200 205

Leu Gln Glu Ser Ser Pro Leu Pro Val Leu Gly Ala Val Pro Trp Ser
210 215 220

Phe Asp Leu Ile Ala Thr Arg Ala Ile Asp Met Ala Arg His Leu Asn
225 230 235 240

Ala Thr Ile Ile Asn Glu Gly Asp Ile Asn Thr Arg Arg Val Lys Ser
245 250 255

Val Thr Phe Cys Ala Arg Ser Ile Pro His Met Leu Glu His Phe Arg
260 265 270

Ala Gly Ser Leu Leu Val Thr Ser Ala Asp Arg Pro Asp Val Leu Val
275 280 285

Ala Ala Cys Leu Ala Ala Met Asn Gly Val Glu Ile Gly Ala Leu Leu
290 295 300

Leu Thr Gly Gly Tyr Glu Met Asp Ala Arg Ile Ser Lys Leu Cys Glu
305 310 315 320

Arg Ala Phe Ala Thr Gly Leu Pro Val Phe Met Val Asn Thr Asn Thr
325 330 335

Trp Gln Thr Ser Leu Ser Leu Gln Ser Phe Asn Leu Glu Val Pro Val

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340

345

350

Asp Asp His Glu Arg Ile Glu Lys Val Gln Glu Tyr Val Ala Asn Tyr
 355 360 365

Ile Asn Ala Asp Trp Ile Glu Ser Leu Thr Ala Thr Ser Glu Arg Ser
 370 375 380

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

Arg Lys Ala Gly Lys Arg Ile Val Leu Glu Val Leu Phe Gln Gly Pro
 405 410 415

Glu Gly Asp Glu Pro Arg Thr Val Lys Ala Ala Ala Ile Cys Ala Glu
 420 425 430

Arg Gly Ile Ala Thr Cys Val Leu Leu Gly Asn Pro Ala Glu Ile Asn
 435 440 445

Arg Val Ala Ala Ser Gln Gly Val Glu Leu Gly Ala Gly Ile Glu Ile
 450 455 460

Val Asp Pro Glu Val Val Arg Glu Ser Tyr Val Gly Arg Leu Val Glu
 465 470 475 480

Leu Arg Lys Asn Lys Gly Met Thr Glu Thr Val Ala Arg Glu Gln Leu
 485 490 495

Glu Asp Asn Val Val Leu Gly Thr Leu Met Leu Glu Gln Asp Glu Val
 500 505 510

Asp Gly Leu Val Ser Gly Ala Val His Thr Thr Ala Asn Thr Ile Arg
 515 520 525

Pro Pro Leu Gln Leu Ile Lys Thr Ala Pro Gly Ser Ser Leu Val Ser

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530

535

540

Ser Val Phe Phe Met Leu Leu Pro Glu Gln Val Tyr Val Tyr Gly Asp
 545 550 555 560

Cys Ala Ile Asn Pro Asp Pro Thr Ala Glu Gln Leu Ala Glu Ile Ala
 565 570 575

Ile Gln Ser Ala Asp Ser Ala Ala Ala Phe Gly Ile Glu Pro Arg Val
 580 585 590

Ala Met Leu Ser Tyr Ser Thr Gly Thr Ser Gly Ala Gly Ser Asp Val
 595 600 605

Glu Lys Val Arg Glu Ala Thr Arg Leu Ala Gln Glu Lys Arg Pro Asp
 610 615 620

Leu Met Ile Asp Gly Pro Leu Gln Tyr Asp Ala Ala Val Met Ala Asp
 625 630 635 640

Val Ala Lys Ser Lys Ala Pro Asn Ser Pro Val Ala Gly Arg Ala Thr
 645 650 655

Val Phe Ile Phe Pro Asp Leu Asn Thr Gly Asn Thr Thr Tyr Lys Ala
 660 665 670

Val Gln Arg Ser Ala Asp Leu Ile Ser Ile Gly Pro Met Leu Gln Gly
 675 680 685

Met Arg Lys Pro Val Asn Asp Leu Ser Arg Gly Ala Leu Val Asp Asp
 690 695 700

Ile Val Tyr Thr Ile Ala Leu Thr Ala Ile Gln Ser Ala Gln Gln Gln
 705 710 715 720

<210> 57

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<211> 1992

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 57

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tggcgtgatt tcctgaaaca caaccgcag aatccgtcct gggctgaccg tgaccgcttc	180
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gatctgccga tggaagaact gaaaaacttc cgtcagctgc actctaaaac tccgggtcac	300
ccggaagtgg gttacaccgc tgggtgtggaa accaccaccg gtccgctggg tcagggtatt	360
gccaacgcag tcggtatggc gattgcagaa aaaacgctgg cggcgcagtt taaccgtccg	420
ggccacgaca ttgtcgacca ctacacctac gccttcattg gcgacggctg catgatggaa	480
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accgcaatgc gtttcgaagc ttacggctgg cacgttattc gcgacatcga cggcatgac	660
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cacggtgcgc cgctgggcga cgctgaaatt gccctgaccc gcgaacaact gggctggaaa	840
tatgcgccgt tcgaaatccc gtctgaaatc tatgctcagt gggatgcgaa agaagcaggc	900
caggcgaaaag aatccgcatg gaacgagaaa ttcgctgctt acgcgaaaagc ttatccgcag	960
gaagccgctg aatttaccgc ccgtatgaaa ggcgaaatgc cgtctgactt cgacgctaaa	1020
gcgaaagagt tcatcgctaa actgcaggct aatccggcga aaatcgccag ccgtaaagcg	1080
tctcagaatg ctatcgaagc gttcgggtccg ctgttgccgg aattcctcgg cggttctgct	1140
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gcacgtaacg ccgtacgtat ggctgcgctg atgaaacagc gtcaggatgat ggtttacacc	1380
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gaactgctgt aa	1992

<210> 58

<211> 2016

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 58

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tggcgtgatt tcctgaaaca caaccgcag aatccgtcct gggctgaccg tgaccgcttc	180
gtgctgtcca acggccacgg ctccatgctg atctacagcc tgctgcacct caccggttac	240
gatctgccga tggaagaact gaaaaacttc cgtcagctgc actctaaaac tccgggtcac	300

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ccggaagtgg gttacaccgc tgggtgtggaa accaccaccg gtccgctggg tcagggtatt	360
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ggccacgaca ttgtcgacca ctacacctac gccttcatgg gcgacggctg catgatggaa	480
ggcatctccc acgaagtttg ctctctggcg ggtacgctga agctgggtaa actgattgca	540
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gcggcatcta tcaaacgcgc agtagaagaa gcgcgcgcag tgactgacaa accttccctg	720
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aagtatgttg gcctgaacgg tgctatcgtc ggtatgacca ccttcctgga agtgctgttt	1920
cagggtccgg gtgaatctgc tccggcagag ctgctgtttg aagagttcgg cttcactgtt	1980
gataacgttg ttgcgaaagc aaaagaactg ctgtaa	2016

<210> 59

<211> 2016

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 59

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tggcgtgatt tcctgaaaca caaccgcag aatccgtcct gggctgaccg tgaccgcttc	180
gtgctgtcca acggccacgg ctccatgctg atctacagcc tgctgcacct caccggttac	240
gatctgccga tggaagaact gaaaaacttc cgtcagctgc actctaaaac tccgggtcac	300
ccggaagtgg gttacaccgc tgggtgggaa accaccaccg gtccgctggg tcagggtatt	360
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tttcagggtc cggaatctgc tccggcagag ctgctgtttg aagagttcgg cttcactgtt	1980
gataacgttg ttgcgaaagc aaaagaactg ctgtaa	2016

<210> 60

<211> 2016

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

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<400> 60

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gcggcatcta tcaaacgcgc agtagaagaa gcgcgcgcag tgactgacaa accttcctg	720
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cagaacctgg cgcagcagga acgaactgaa gagcaactgg caaacatcgc gcgcggtggt	1620
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ctgccgaaag cggttactgc acgcgttgct gtagaagcgg gtattgctga ctactggtac	1860
aagtatgttg gcctgaacgg tgctatcgtc ggtatgacca ctttcggtga actggaagtg	1920
ctgtttcagg gtccgtctgc tccggcagag ctgctgtttg aagagttcgg cttcactgtt	1980
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<210> 61

<211> 2016

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 61

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tggcgtgatt tcctgaaaca caaccgcag aatccgtcct gggctgaccg tgaccgcttc	180
gtgctgtcca acggccacgg ctccatgctg atctacagcc tgctgcacct caccggttac	240
gatctgccga tggaagaact gaaaaacttc cgtcagctgc actctaaaac tccgggtcac	300
ccggaagtgg gttacaccgc tgggtgtggaa accaccaccg gtccgctggg tcagggtatt	360
gccaacgcag tcggtatggc gattgcagaa aaaacgctgg cggcgcagtt taaccgtccg	420
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accgcaatgc gtttcgaagc ttacggctgg cacgttattc gcgacatcga cggtcacgac	660
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aagtatgttg gcctgaacgg tgctatcgtc ggtatgacca ccttcggtga atctctggaa	1920

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gtgctgtttc aggggtccggc tccggcagag ctgctgtttg aagagttcgg cttcactggt 1980
gataacgttg ttgcgaaaagc aaaagaactg ctgtaa 2016

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<211> 2016
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 62
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aagtatgttg gcctgaacgg tgctatcgtc ggtatgacca ctttcggtga atctgctccg	1920
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<210> 63
 <211> 663
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 63

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Asp Ala Val Gln Lys Ala Lys Ser Gly His Pro Gly Ala Pro Met Gly
20 25 30

Met Ala Asp Ile Ala Glu Val Leu Trp Arg Asp Phe Leu Lys His Asn
35 40 45

Pro Gln Asn Pro Ser Trp Ala Asp Arg Asp Arg Phe Val Leu Ser Asn
50 55 60

Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr
65 70 75 80

Asp Leu Pro Met Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys
85 90 95

Thr Pro Gly His Pro Glu Val Gly Tyr Thr Ala Gly Val Glu Thr Thr
100 105 110

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

Ala Glu Lys Thr Leu Ala Ala Gln Phe Asn Arg Pro Gly His Asp Ile
130 135 140

Val Asp His Tyr Thr Tyr Ala Phe Met Gly Asp Gly Cys Met Met Glu
145 150 155 160

Gly Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Lys Leu Gly
165 170 175

Lys Leu Ile Ala Phe Tyr Asp Asp Asn Gly Ile Ser Ile Asp Gly His
180 185 190

Val Glu Gly Trp Phe Thr Asp Asp Thr Ala Met Arg Phe Glu Ala Tyr
195 200 205

G083070013W000-SEQLISTING-CHB

Gly Trp His Val Ile Arg Asp Ile Asp Gly His Asp Ala Ala Ser Ile
210 215 220

Lys Arg Ala Val Glu Glu Ala Arg Ala Val Thr Asp Lys Pro Ser Leu
225 230 235 240

Leu Met Cys Lys Thr Ile Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly
245 250 255

Thr His Asp Ser His Gly Ala Pro Leu Gly Asp Ala Glu Ile Ala Leu
260 265 270

Thr Arg Glu Gln Leu Gly Trp Lys Tyr Ala Pro Phe Glu Ile Pro Ser
275 280 285

Glu Ile Tyr Ala Gln Trp Asp Ala Lys Glu Ala Gly Gln Ala Lys Glu
290 295 300

Ser Ala Trp Asn Glu Lys Phe Ala Ala Tyr Ala Lys Ala Tyr Pro Gln
305 310 315 320

Glu Ala Ala Glu Phe Thr Arg Arg Met Lys Gly Glu Met Pro Ser Asp
325 330 335

Phe Asp Ala Lys Ala Lys Glu Phe Ile Ala Lys Leu Gln Ala Asn Pro
340 345 350

Ala Lys Ile Ala Ser Arg Lys Ala Ser Gln Asn Ala Ile Glu Ala Phe
355 360 365

Gly Pro Leu Leu Pro Glu Phe Leu Gly Gly Ser Ala Asp Leu Ala Pro
370 375 380

Ser Asn Leu Thr Leu Trp Ser Gly Ser Lys Ala Ile Asn Glu Asp Ala
385 390 395 400

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Ala Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala
 405 410 415

Ile Ala Asn Gly Ile Ser Leu His Gly Gly Phe Leu Pro Tyr Thr Ser
 420 425 430

Thr Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Val Arg Met Ala
 435 440 445

Ala Leu Met Lys Gln Arg Gln Val Met Val Tyr Thr His Asp Ser Ile
 450 455 460

Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Gln Ile Ala
 465 470 475 480

Ser Leu Arg Val Thr Pro Asn Met Ser Thr Trp Arg Pro Cys Asp Gln
 485 490 495

Val Glu Ser Ala Val Ala Trp Lys Tyr Gly Val Glu Arg Gln Asp Gly
 500 505 510

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

Thr Glu Glu Gln Leu Ala Asn Ile Ala Arg Gly Gly Tyr Val Leu Lys
 530 535 540

Asp Cys Ala Gly Gln Pro Glu Leu Ile Phe Ile Ala Thr Gly Ser Glu
 545 550 555 560

Val Glu Leu Ala Val Ala Ala Tyr Glu Lys Leu Thr Ala Glu Gly Val
 565 570 575

Lys Ala Arg Val Val Ser Met Pro Ser Thr Asp Ala Phe Asp Lys Gln
 580 585 590

G083070013W000-SEQLISTING-CHB

Asp Ala Ala Tyr Arg Glu Ser Val Leu Pro Lys Ala Val Thr Ala Arg
595 600 605

Val Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly
610 615 620

Leu Asn Gly Ala Ile Val Gly Met Thr Thr Phe Gly Glu Ser Ala Pro
625 630 635 640

Ala Glu Gln Leu Phe Glu Glu Phe Gly Phe Thr Val Asp Asn Val Val
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Ala Lys Ala Lys Ala Leu Leu
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<210> 64
<211> 671
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 64

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

Met Ala Asp Ile Ala Glu Val Leu Trp Arg Asp Phe Leu Lys His Asn
35 40 45

Pro Gln Asn Pro Ser Trp Ala Asp Arg Asp Arg Phe Val Leu Ser Asn
50 55 60

Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr

G083070013W000-SEQLISTING-CHB

65		70		75		80
Asp	Leu	Pro	Met	Glu	Glu	Leu
			85			
				Lys	Asn	Phe
					90	
						Arg
						Gln
						Leu
						His
						Ser
						Lys
Thr	Pro	Gly	His	Pro	Glu	Val
			100			
				Gly	Tyr	Thr
					105	
						Ala
						Gly
						Val
						Glu
						Thr
						Thr
Thr	Gly	Pro	Leu	Gly	Gln	Gly
						115
						Ile
						120
						Ala
						Asn
						Ala
						Val
						Gly
						Met
						Ala
						Ile
Ala	Glu	Lys	Thr	Leu	Ala	Ala
						130
						Gln
						135
						Phe
						Asn
						Arg
						Pro
						Gly
						His
						Asp
						Ile
Val	Asp	His	Tyr	Thr	Tyr	Ala
						145
						Phe
						Met
						Gly
						Asp
						150
						Gly
						155
						Cys
						Met
						Met
						Glu
						160
Gly	Ile	Ser	His	Glu	Val	Cys
						165
						Ser
						Leu
						Ala
						Gly
						Thr
						Leu
						Lys
						Leu
						Gly
						170
						Asp
						175
Lys	Leu	Ile	Ala	Phe	Tyr	Asp
						180
						Asp
						185
						Asn
						Gly
						Ile
						Ser
						Ile
						Asp
						Gly
						His
						190
Val	Glu	Gly	Trp	Phe	Thr	Asp
						195
						Asp
						200
						Thr
						Ala
						Met
						Arg
						Phe
						Glu
						Ala
						Tyr
Gly	Trp	His	Val	Ile	Arg	Asp
						210
						Ile
						215
						Asp
						Gly
						His
						Asp
						Ala
						Ala
						Ser
						Ile
Lys	Arg	Ala	Val	Glu	Glu	Ala
						225
						Arg
						230
						Ala
						Val
						Thr
						Asp
						Lys
						Pro
						Ser
						Leu
						240
Leu	Met	Cys	Lys	Thr	Ile	Ile
						245
						Gly
						250
						Phe
						Gly
						Ser
						Pro
						Asn
						Lys
						Ala
						Gly
						255
Thr	His	Asp	Ser	His	Gly	Ala
						Pro
						Leu
						Gly
						Asp
						Ala
						Glu
						Ile
						Ala
						Leu

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260

265

270

Thr Arg Glu Gln Leu Gly Trp Lys Tyr Ala Pro Phe Glu Ile Pro Ser
 275 280 285

Glu Ile Tyr Ala Gln Trp Asp Ala Lys Glu Ala Gly Gln Ala Lys Glu
 290 295 300

Ser Ala Trp Asn Glu Lys Phe Ala Ala Tyr Ala Lys Ala Tyr Pro Gln
 305 310 315 320

Glu Ala Ala Glu Phe Thr Arg Arg Met Lys Gly Glu Met Pro Ser Asp
 325 330 335

Phe Asp Ala Lys Ala Lys Glu Phe Ile Ala Lys Leu Gln Ala Asn Pro
 340 345 350

Ala Lys Ile Ala Ser Arg Lys Ala Ser Gln Asn Ala Ile Glu Ala Phe
 355 360 365

Gly Pro Leu Leu Pro Glu Phe Leu Gly Gly Ser Ala Asp Leu Ala Pro
 370 375 380

Ser Asn Leu Thr Leu Trp Ser Gly Ser Lys Ala Ile Asn Glu Asp Ala
 385 390 395 400

Ala Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala
 405 410 415

Ile Ala Asn Gly Ile Ser Leu His Gly Gly Phe Leu Pro Tyr Thr Ser
 420 425 430

Thr Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Val Arg Met Ala
 435 440 445

Ala Leu Met Lys Gln Arg Gln Val Met Val Tyr Thr His Asp Ser Ile

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450

455

460

Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Gln Val Ala
 465 470 475 480

Ser Leu Arg Val Thr Pro Asn Met Ser Thr Trp Arg Pro Cys Asp Gln
 485 490 495

Val Glu Ser Ala Val Ala Trp Lys Tyr Gly Val Glu Arg Gln Asp Gly
 500 505 510

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

Thr Glu Glu Gln Leu Ala Asn Ile Ala Arg Gly Gly Tyr Val Leu Lys
 530 535 540

Asp Cys Ala Gly Gln Pro Glu Leu Ile Phe Ile Ala Thr Gly Ser Glu
 545 550 555 560

Val Glu Leu Ala Val Ala Ala Tyr Glu Lys Leu Thr Ala Glu Gly Val
 565 570 575

Lys Ala Arg Val Val Ser Met Pro Ser Thr Asp Ala Phe Asp Lys Gln
 580 585 590

Asp Ala Ala Tyr Arg Glu Ser Val Leu Pro Lys Ala Val Thr Ala Arg
 595 600 605

Val Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly
 610 615 620

Leu Asn Gly Ala Ile Val Gly Met Thr Thr Phe Leu Glu Val Leu Phe
 625 630 635 640

Gln Gly Pro Gly Glu Ser Ala Pro Ala Glu Leu Leu Phe Glu Glu Phe

G083070013W000-SEQLISTING-CHB

645

650

655

Gly Phe Thr Val Asp Asn Val Val Ala Lys Ala Lys Glu Leu Leu
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<210> 65

<211> 671

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 65

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

Met Ala Asp Ile Ala Glu Val Leu Trp Arg Asp Phe Leu Lys His Asn
 35 40 45

Pro Gln Asn Pro Ser Trp Ala Asp Arg Asp Arg Phe Val Leu Ser Asn
 50 55 60

Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr
 65 70 75 80

Asp Leu Pro Met Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys
 85 90 95

Thr Pro Gly His Pro Glu Val Gly Tyr Thr Ala Gly Val Glu Thr Thr
 100 105 110

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

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Ala Glu Lys Thr Leu Ala Ala Gln Phe Asn Arg Pro Gly His Asp Ile
 130 135 140

Val Asp His Tyr Thr Tyr Ala Phe Met Gly Asp Gly Cys Met Met Glu
 145 150 155 160

Gly Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Lys Leu Gly
 165 170 175

Lys Leu Ile Ala Phe Tyr Asp Asp Asn Gly Ile Ser Ile Asp Gly His
 180 185 190

Val Glu Gly Trp Phe Thr Asp Asp Thr Ala Met Arg Phe Glu Ala Tyr
 195 200 205

Gly Trp His Val Ile Arg Asp Ile Asp Gly His Asp Ala Ala Ser Ile
 210 215 220

Lys Arg Ala Val Glu Glu Ala Arg Ala Val Thr Asp Lys Pro Ser Leu
 225 230 235 240

Leu Met Cys Lys Thr Ile Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly
 245 250 255

Thr His Asp Ser His Gly Ala Pro Leu Gly Asp Ala Glu Ile Ala Leu
 260 265 270

Thr Arg Glu Gln Leu Gly Trp Lys Tyr Ala Pro Phe Glu Ile Pro Ser
 275 280 285

Glu Ile Tyr Ala Gln Trp Asp Ala Lys Glu Ala Gly Gln Ala Lys Glu
 290 295 300

Ser Ala Trp Asn Glu Lys Phe Ala Ala Tyr Ala Lys Ala Tyr Pro Gln
 305 310 315 320

G083070013W000-SEQLISTING-CHB

Glu Ala Ala Glu Phe Thr Arg Arg Met Lys Gly Glu Met Pro Ser Asp
 325 330 335

Phe Asp Ala Lys Ala Lys Glu Phe Ile Ala Lys Leu Gln Ala Asn Pro
 340 345 350

Ala Lys Ile Ala Ser Arg Lys Ala Ser Gln Asn Ala Ile Glu Ala Phe
 355 360 365

Gly Pro Leu Leu Pro Glu Phe Leu Gly Gly Ser Ala Asp Leu Ala Pro
 370 375 380

Ser Asn Leu Thr Leu Trp Ser Gly Ser Lys Ala Ile Asn Glu Asp Ala
 385 390 395 400

Ala Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala
 405 410 415

Ile Ala Asn Gly Ile Ser Leu His Gly Gly Phe Leu Pro Tyr Thr Ser
 420 425 430

Thr Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Val Arg Met Ala
 435 440 445

Ala Leu Met Lys Gln Arg Gln Val Met Val Tyr Thr His Asp Ser Ile
 450 455 460

Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Gln Val Ala
 465 470 475 480

Ser Leu Arg Val Thr Pro Asn Met Ser Thr Trp Arg Pro Cys Asp Gln
 485 490 495

Val Glu Ser Ala Val Ala Trp Lys Tyr Gly Val Glu Arg Gln Asp Gly
 500 505 510

G083070013W000-SEQLISTING-CHB

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

Thr Glu Glu Gln Leu Ala Asn Ile Ala Arg Gly Gly Tyr Val Leu Lys
530 535 540

Asp Cys Ala Gly Gln Pro Glu Leu Ile Phe Ile Ala Thr Gly Ser Glu
545 550 555 560

Val Glu Leu Ala Val Ala Ala Tyr Glu Lys Leu Thr Ala Glu Gly Val
565 570 575

Lys Ala Arg Val Val Ser Met Pro Ser Thr Asp Ala Phe Asp Lys Gln
580 585 590

Asp Ala Ala Tyr Arg Glu Ser Val Leu Pro Lys Ala Val Thr Ala Arg
595 600 605

Val Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly
610 615 620

Leu Asn Gly Ala Ile Val Gly Met Thr Thr Phe Gly Leu Glu Val Leu
625 630 635 640

Phe Gln Gly Pro Glu Ser Ala Pro Ala Glu Leu Leu Phe Glu Glu Phe
645 650 655

Gly Phe Thr Val Asp Asn Val Val Ala Lys Ala Lys Glu Leu Leu
660 665 670

<210> 66

<211> 671

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

G083070013W000-SEQLISTING-CHB

<400> 66

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

Met Ala Asp Ile Ala Glu Val Leu Trp Arg Asp Phe Leu Lys His Asn
 35 40 45

Pro Gln Asn Pro Ser Trp Ala Asp Arg Asp Arg Phe Val Leu Ser Asn
 50 55 60

Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr
 65 70 75 80

Asp Leu Pro Met Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys
 85 90 95

Thr Pro Gly His Pro Glu Val Gly Tyr Thr Ala Gly Val Glu Thr Thr
 100 105 110

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

Ala Glu Lys Thr Leu Ala Ala Gln Phe Asn Arg Pro Gly His Asp Ile
 130 135 140

Val Asp His Tyr Thr Tyr Ala Phe Met Gly Asp Gly Cys Met Met Glu
 145 150 155 160

Gly Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Lys Leu Gly
 165 170 175

Lys Leu Ile Ala Phe Tyr Asp Asp Asn Gly Ile Ser Ile Asp Gly His

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180

185

190

Val Glu Gly Trp Phe Thr Asp Asp Thr Ala Met Arg Phe Glu Ala Tyr
 195 200 205

Gly Trp His Val Ile Arg Asp Ile Asp Gly His Asp Ala Ala Ser Ile
 210 215 220

Lys Arg Ala Val Glu Glu Ala Arg Ala Val Thr Asp Lys Pro Ser Leu
 225 230 235 240

Leu Met Cys Lys Thr Ile Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly
 245 250 255

Thr His Asp Ser His Gly Ala Pro Leu Gly Asp Ala Glu Ile Ala Leu
 260 265 270

Thr Arg Glu Gln Leu Gly Trp Lys Tyr Ala Pro Phe Glu Ile Pro Ser
 275 280 285

Glu Ile Tyr Ala Gln Trp Asp Ala Lys Glu Ala Gly Gln Ala Lys Glu
 290 295 300

Ser Ala Trp Asn Glu Lys Phe Ala Ala Tyr Ala Lys Ala Tyr Pro Gln
 305 310 315 320

Glu Ala Ala Glu Phe Thr Arg Arg Met Lys Gly Glu Met Pro Ser Asp
 325 330 335

Phe Asp Ala Lys Ala Lys Glu Phe Ile Ala Lys Leu Gln Ala Asn Pro
 340 345 350

Ala Lys Ile Ala Ser Arg Lys Ala Ser Gln Asn Ala Ile Glu Ala Phe
 355 360 365

Gly Pro Leu Leu Pro Glu Phe Leu Gly Gly Ser Ala Asp Leu Ala Pro

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370

375

380

Ser Asn Leu Thr Leu Trp Ser Gly Ser Lys Ala Ile Asn Glu Asp Ala
 385 390 395 400

Ala Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala
 405 410 415

Ile Ala Asn Gly Ile Ser Leu His Gly Gly Phe Leu Pro Tyr Thr Ser
 420 425 430

Thr Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Val Arg Met Ala
 435 440 445

Ala Leu Met Lys Gln Arg Gln Val Met Val Tyr Thr His Asp Ser Ile
 450 455 460

Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Gln Val Ala
 465 470 475 480

Ser Leu Arg Val Thr Pro Asn Met Ser Thr Trp Arg Pro Cys Asp Gln
 485 490 495

Val Glu Ser Ala Val Ala Trp Lys Tyr Gly Val Glu Arg Gln Asp Gly
 500 505 510

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

Thr Glu Glu Gln Leu Ala Asn Ile Ala Arg Gly Gly Tyr Val Leu Lys
 530 535 540

Asp Cys Ala Gly Gln Pro Glu Leu Ile Phe Ile Ala Thr Gly Ser Glu
 545 550 555 560

Val Glu Leu Ala Val Ala Ala Tyr Glu Lys Leu Thr Ala Glu Gly Val

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565

570

575

Lys Ala Arg Val Val Ser Met Pro Ser Thr Asp Ala Phe Asp Lys Gln
580 585 590

Asp Ala Ala Tyr Arg Glu Ser Val Leu Pro Lys Ala Val Thr Ala Arg
595 600 605

Val Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly
610 615 620

Leu Asn Gly Ala Ile Val Gly Met Thr Thr Phe Gly Glu Leu Glu Val
625 630 635 640

Leu Phe Gln Gly Pro Ser Ala Pro Ala Glu Leu Leu Phe Glu Glu Phe
645 650 655

Gly Phe Thr Val Asp Asn Val Val Ala Lys Ala Lys Glu Leu Leu
660 665 670

<210> 67

<211> 671

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 67

Met Ser Ser Arg Lys Glu Leu Ala Asn Ala Ile Arg Ala Leu Ser Met
1 5 10 15

Asp Ala Val Gln Lys Ala Lys Ser Gly His Pro Gly Ala Pro Met Gly
20 25 30

Met Ala Asp Ile Ala Glu Val Leu Trp Arg Asp Phe Leu Lys His Asn
35 40 45

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Pro Gln Asn Pro Ser Trp Ala Asp Arg Asp Arg Phe Val Leu Ser Asn
50 55 60

Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr
65 70 75 80

Asp Leu Pro Met Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys
85 90 95

Thr Pro Gly His Pro Glu Val Gly Tyr Thr Ala Gly Val Glu Thr Thr
100 105 110

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

Ala Glu Lys Thr Leu Ala Ala Gln Phe Asn Arg Pro Gly His Asp Ile
130 135 140

Val Asp His Tyr Thr Tyr Ala Phe Met Gly Asp Gly Cys Met Met Glu
145 150 155 160

Gly Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Lys Leu Gly
165 170 175

Lys Leu Ile Ala Phe Tyr Asp Asp Asn Gly Ile Ser Ile Asp Gly His
180 185 190

Val Glu Gly Trp Phe Thr Asp Asp Thr Ala Met Arg Phe Glu Ala Tyr
195 200 205

Gly Trp His Val Ile Arg Asp Ile Asp Gly His Asp Ala Ala Ser Ile
210 215 220

Lys Arg Ala Val Glu Glu Ala Arg Ala Val Thr Asp Lys Pro Ser Leu
225 230 235 240

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Leu Met Cys Lys Thr Ile Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly
 245 250 255

Thr His Asp Ser His Gly Ala Pro Leu Gly Asp Ala Glu Ile Ala Leu
 260 265 270

Thr Arg Glu Gln Leu Gly Trp Lys Tyr Ala Pro Phe Glu Ile Pro Ser
 275 280 285

Glu Ile Tyr Ala Gln Trp Asp Ala Lys Glu Ala Gly Gln Ala Lys Glu
 290 295 300

Ser Ala Trp Asn Glu Lys Phe Ala Ala Tyr Ala Lys Ala Tyr Pro Gln
 305 310 315 320

Glu Ala Ala Glu Phe Thr Arg Arg Met Lys Gly Glu Met Pro Ser Asp
 325 330 335

Phe Asp Ala Lys Ala Lys Glu Phe Ile Ala Lys Leu Gln Ala Asn Pro
 340 345 350

Ala Lys Ile Ala Ser Arg Lys Ala Ser Gln Asn Ala Ile Glu Ala Phe
 355 360 365

Gly Pro Leu Leu Pro Glu Phe Leu Gly Gly Ser Ala Asp Leu Ala Pro
 370 375 380

Ser Asn Leu Thr Leu Trp Ser Gly Ser Lys Ala Ile Asn Glu Asp Ala
 385 390 395 400

Ala Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala
 405 410 415

Ile Ala Asn Gly Ile Ser Leu His Gly Gly Phe Leu Pro Tyr Thr Ser
 420 425 430

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Thr Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Val Arg Met Ala
 435 440 445

Ala Leu Met Lys Gln Arg Gln Val Met Val Tyr Thr His Asp Ser Ile
 450 455 460

Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Gln Val Ala
 465 470 475 480

Ser Leu Arg Val Thr Pro Asn Met Ser Thr Trp Arg Pro Cys Asp Gln
 485 490 495

Val Glu Ser Ala Val Ala Trp Lys Tyr Gly Val Glu Arg Gln Asp Gly
 500 505 510

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

Thr Glu Glu Gln Leu Ala Asn Ile Ala Arg Gly Gly Tyr Val Leu Lys
 530 535 540

Asp Cys Ala Gly Gln Pro Glu Leu Ile Phe Ile Ala Thr Gly Ser Glu
 545 550 555 560

Val Glu Leu Ala Val Ala Ala Tyr Glu Lys Leu Thr Ala Glu Gly Val
 565 570 575

Lys Ala Arg Val Val Ser Met Pro Ser Thr Asp Ala Phe Asp Lys Gln
 580 585 590

Asp Ala Ala Tyr Arg Glu Ser Val Leu Pro Lys Ala Val Thr Ala Arg
 595 600 605

Val Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly
 610 615 620

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Leu Asn Gly Ala Ile Val Gly Met Thr Thr Phe Gly Glu Ser Leu Glu
625 630 635 640

Val Leu Phe Gln Gly Pro Ala Pro Ala Glu Leu Leu Phe Glu Glu Phe
645 650 655

Gly Phe Thr Val Asp Asn Val Val Ala Lys Ala Lys Glu Leu Leu
660 665 670

<210> 68

<211> 671

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 68

Met Ser Ser Arg Lys Glu Leu Ala Asn Ala Ile Arg Ala Leu Ser Met
1 5 10 15

Asp Ala Val Gln Lys Ala Lys Ser Gly His Pro Gly Ala Pro Met Gly
20 25 30

Met Ala Asp Ile Ala Glu Val Leu Trp Arg Asp Phe Leu Lys His Asn
35 40 45

Pro Gln Asn Pro Ser Trp Ala Asp Arg Asp Arg Phe Val Leu Ser Asn
50 55 60

Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr
65 70 75 80

Asp Leu Pro Met Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys
85 90 95

Thr Pro Gly His Pro Glu Val Gly Tyr Thr Ala Gly Val Glu Thr Thr

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100

105

110

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

Ala Glu Lys Thr Leu Ala Ala Gln Phe Asn Arg Pro Gly His Asp Ile
 130 135 140

Val Asp His Tyr Thr Tyr Ala Phe Met Gly Asp Gly Cys Met Met Glu
 145 150 155 160

Gly Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Lys Leu Gly
 165 170 175

Lys Leu Ile Ala Phe Tyr Asp Asp Asn Gly Ile Ser Ile Asp Gly His
 180 185 190

Val Glu Gly Trp Phe Thr Asp Asp Thr Ala Met Arg Phe Glu Ala Tyr
 195 200 205

Gly Trp His Val Ile Arg Asp Ile Asp Gly His Asp Ala Ala Ser Ile
 210 215 220

Lys Arg Ala Val Glu Glu Ala Arg Ala Val Thr Asp Lys Pro Ser Leu
 225 230 235 240

Leu Met Cys Lys Thr Ile Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly
 245 250 255

Thr His Asp Ser His Gly Ala Pro Leu Gly Asp Ala Glu Ile Ala Leu
 260 265 270

Thr Arg Glu Gln Leu Gly Trp Lys Tyr Ala Pro Phe Glu Ile Pro Ser
 275 280 285

Glu Ile Tyr Ala Gln Trp Asp Ala Lys Glu Ala Gly Gln Ala Lys Glu

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290

295

300

Ser Ala Trp Asn Glu Lys Phe Ala Ala Tyr Ala Lys Ala Tyr Pro Gln
 305 310 315 320

Glu Ala Ala Glu Phe Thr Arg Arg Met Lys Gly Glu Met Pro Ser Asp
 325 330 335

Phe Asp Ala Lys Ala Lys Glu Phe Ile Ala Lys Leu Gln Ala Asn Pro
 340 345 350

Ala Lys Ile Ala Ser Arg Lys Ala Ser Gln Asn Ala Ile Glu Ala Phe
 355 360 365

Gly Pro Leu Leu Pro Glu Phe Leu Gly Gly Ser Ala Asp Leu Ala Pro
 370 375 380

Ser Asn Leu Thr Leu Trp Ser Gly Ser Lys Ala Ile Asn Glu Asp Ala
 385 390 395 400

Ala Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala
 405 410 415

Ile Ala Asn Gly Ile Ser Leu His Gly Gly Phe Leu Pro Tyr Thr Ser
 420 425 430

Thr Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Val Arg Met Ala
 435 440 445

Ala Leu Met Lys Gln Arg Gln Val Met Val Tyr Thr His Asp Ser Ile
 450 455 460

Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Gln Val Ala
 465 470 475 480

Ser Leu Arg Val Thr Pro Asn Met Ser Thr Trp Arg Pro Cys Asp Gln

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485

490

495

Val Glu Ser Ala Val Ala Trp Lys Tyr Gly Val Glu Arg Gln Asp Gly
 500 505 510

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

Thr Glu Glu Gln Leu Ala Asn Ile Ala Arg Gly Gly Tyr Val Leu Lys
 530 535 540

Asp Cys Ala Gly Gln Pro Glu Leu Ile Phe Ile Ala Thr Gly Ser Glu
 545 550 555 560

Val Glu Leu Ala Val Ala Ala Tyr Glu Lys Leu Thr Ala Glu Gly Val
 565 570 575

Lys Ala Arg Val Val Ser Met Pro Ser Thr Asp Ala Phe Asp Lys Gln
 580 585 590

Asp Ala Ala Tyr Arg Glu Ser Val Leu Pro Lys Ala Val Thr Ala Arg
 595 600 605

Val Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly
 610 615 620

Leu Asn Gly Ala Ile Val Gly Met Thr Thr Phe Gly Glu Ser Ala Pro
 625 630 635 640

Leu Glu Val Leu Phe Gln Gly Pro Ala Glu Leu Leu Phe Glu Glu Phe
 645 650 655

Gly Phe Thr Val Asp Asn Val Val Ala Lys Ala Lys Glu Leu Leu
 660 665 670

<210> 69

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

<220>
 <223> Synthetic Oligonucleotide

<400> 69
 ctggaagtgc tgtttcaggg tccg

24

<210> 70
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 70

Met Lys Asn Ile Asn Pro Thr Gln Thr Ala Ala
 1 5 10

<210> 71
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide

<400> 71
 atgaaaaaca tcaatccaac gcagaccgct gcc

33

<210> 72
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 72

Met Leu Glu Val Leu Phe Gln Gly Pro Lys Asn Ile Asn Pro Thr Gln

1 5 10 15

Thr Ala Ala

<210> 73
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide

<400> 73
 atgctggaag tgctgtttca ggggccgaaa aacatcaatc caacgcagac cgctgcc 57

<210> 74
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 74

Met Lys Leu Glu Val Leu Phe Gln Gly Pro Asn Ile Asn Pro Thr Gln
 1 5 10 15

Thr Ala Ala

<210> 75
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide

<400> 75
 atgaaactgg aagtgctgtt tcagggtccg aacatcaatc caacgcagac cgctgcc 57

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<210> 76
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 76

Met Lys Asn Leu Glu Val Leu Phe Gln Gly Pro Ile Asn Pro Thr Gln
 1 5 10 15

Thr Ala Ala

<210> 77
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide

<400> 77
 atgaaaaacc tggaagtgt gtttcagggt ccgatcaatc caacgcagac cgctgcc 57

<210> 78
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 78

Met Leu Glu Val Leu Phe Gln Gly Pro Ala Ala
 1 5 10

<210> 79
 <211> 33
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 79

atgctggaag tgctgtttca ggggccggct gcc

33

<210> 80

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 80

Met Lys Leu Glu Val Leu Phe Gln Gly Pro Ala
1 5 10

<210> 81

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 81

atgaaactgg aagtgtgtt tcagggtccg gcc

33

<210> 82

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 82

Met Lys Asn Leu Glu Val Leu Phe Gln Gly Pro
1 5 10

<210> 83
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide

<400> 83
 atgaaaaacc tggaagtgct gtttcagggt ccg 33

<210> 84
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 84

Met	Lys	Asn	Ile	Asn	Leu	Glu	Val	Leu	Phe	Gln	Gly	Pro	Thr	Gln	Thr
1				5				10						15	

Ala Ala

<210> 85
 <211> 54
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide

<400> 85
 atgaaaaaca tcaatctgga agtgctgttt cagggtccaa cgcagaccgc tgcc 54

<210> 86
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 86

Thr	Ala	Ala	Trp	Gln	Ala	Leu	Glu	Val	Leu	Phe	Gln	Gly	Pro	Gln	Lys
1				5					10					15	

His

<210> 87

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 87

accgctgcct ggcaggcact agaagtgctg tttcagggtc cgcagaaaca c

51