

SEQUENCE LISTING

<110> The Trustees of The University of Pennsylvania

<120> QUANTITATIVE CONTROL OF ACTIVITY OF ENGINEERED CELLS EXPRESSING UNIVERSAL IMMUNE RECEPTORS

<130> 046483-7294W01(02460)

<150> 62/965,593

<151> 2020-01-24

<160> 30

<170> PatentIn version 3.5

<210> 1

<211> 1869

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized

<400> 1

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tacagtgaga ttgggatgaa aggcgagcgc cggaggggca aggggcacga tggcctttac	1800
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cctcgctaa	1869

<210> 2
 <211> 528
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Artificially Synthesized

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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Arg
 225 230 235 240

Ser Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
 245 250 255

Glu Glu Asn Pro Gly Pro Arg Met Ala Leu Pro Val Thr Ala Leu Leu
 260 265 270

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Gly Ser Ala His
 275 280 285

Ile Val Met Val Asp Ala Tyr Lys Pro Thr Lys Ala Ser Thr Thr Thr
 290 295 300

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
 305 310 315 320

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
 325 330 335

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp Val Leu Val Val
 340 345 350

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
 355 360 365

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
 370 375 380

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
385 390 395 400

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Ile Asp
405 410 415

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
420 425 430

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
435 440 445

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
450 455 460

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
465 470 475 480

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
485 490 495

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
500 505 510

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
515 520 525

<210> 3
<211> 1650
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 3
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ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc 180
ctcgtgacca ccctgaccta cggcgtgcag tgcttcagcc gctaccccga ccacatgaag 240
cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg caccatcttc 300
ttcaaggacg acggcaacta caagaccgc gccgaggtga agttcgaggg cgacaccctg 360
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 420
aagctggagt acaactacaa cagccacaac gtctatatca tggccgacaa gcagaagaac 480
ggcatcaagg tgaacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc 540
gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac 600

tacctgagca cccagtccgc cctgagcaaa gacccaacg agaagcgga tcacatggtc 660
 ctgctggagt tcgtgaccgc cgccgggac actctcggca tggacgagct gtacaagaga 720
 tctggcagcg gagagggcag aggaagtctt ctaacatgcg gtgacgtgga ggagaatccc 780
 ggccctagaa tggccttacc agtgaccgcc ttgctcctgc cgctggcctt gctgctccac 840
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 tatagcttgc tagtaacagt ggcctttatt attttctggg tgaggagtaa gaggagcagg 1200
 ctctgcaca gtgactacat gaacatgact cccgccgcc ccggggccac ccgcaagcat 1260
 taccagccct atgccccacc acgcgacttc gcagcctatc gctccatcga tagagtgaag 1320
 ttcagcagga gcgcagacgc cccgcgtac cagcagggcc agaaccagct ctataacgag 1380
 ctcaatctag gacgaagaga ggagtacgat gttttggaca agagacgtgg ccgggaccct 1440
 gagatggggg gaaagccgag aaggaagaac cctcaggaag gcctgtacaa tgaactgcag 1500
 aaagataaga tggcggaggc ctacagttag attgggatga aaggcgagcg ccggaggggc 1560
 aaggggcacg atggccttta ccagggtctc agtacagcca ccaaggacac ctacgacgcc 1620
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<210> 4
 <211> 549
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized

<400> 4

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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys

65					70						75				80
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
			85						90					95	
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
			100					105					110		
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
		115					120					125			
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
	130					135					140				
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
145					150					155					160
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
			165					170						175	
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
			180					185					190		
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu
		195					200					205			
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe
	210					215					220				
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Arg
225					230					235					240
Ser	Gly	Ser	Gly	Glu	Gly	Arg	Gly	Ser	Leu	Leu	Thr	Cys	Gly	Asp	Val
				245					250					255	
Glu	Glu	Asn	Pro	Gly	Pro	Arg	Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu
			260					265					270		
Leu	Pro	Leu	Ala	Leu	Leu	Leu	His	Ala	Ala	Arg	Pro	Gly	Ser	Ala	His
		275					280					285			
Ile	Val	Met	Val	Asp	Ala	Tyr	Lys	Pro	Thr	Lys	Gly	Gly	Ser	Gly	Gly
	290					295					300				
Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser
305					310					315					320
Ala	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr
				325					330					335	

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
340 345 350

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe
355 360 365

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
370 375 380

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
385 390 395 400

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
405 410 415

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
420 425 430

Tyr Arg Ser Ile Asp Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
435 440 445

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
450 455 460

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

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
485 490 495

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

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
515 520 525

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
530 535 540

Ala Leu Pro Pro Arg
545

<210> 5
<211> 1017
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 5
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ggcaaagagc tggctggcgc caccatggaa ctgcgggata gcagcggcaa gaccatcagc 180
acctggatca gcgacggcca ggtcaaagac ttctacctgt accccggcaa gtacaccttc 240
gtggaaacag ccgccctga cggctatgag gtggccacag ccatcacctt caccgtgaac 300
gagcagggac aggtcacagt gaacggcgct agcaccacga cgccagcgcc gcgaccacca 360
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gcctatcgct ccatcgatag agtgaagttc agcaggagcg cagacgcccc cggtaccag 720
cagggccaga accagctcta taacgagctc aatctaggac gaagagagga gtacgatgtt 780
ttggacaaga gacgtggccg ggaccctgag atggggggaa agccgagaag gaagaaccct 840
caggaaggcc tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgaatt 900
gggatgaaag gcgagcgccg gaggggcaag gggcacgatg gcctttacca ggtctcagt 960
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<210> 6
<211> 338
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 6

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gly Ser Gly Ser Gly Asp Ser Ala Thr His Ile
20 25 30

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

Met Glu Leu Arg Asp Ser Ser Gly Lys Thr Ile Ser Thr Trp Ile Ser
50 55 60

Asp Gly Gln Val Lys Asp Phe Tyr Leu Tyr Pro Gly Lys Tyr Thr Phe
65 70 75 80

Val Glu Thr Ala Ala Pro Asp Gly Tyr Glu Val Ala Thr Ala Ile Thr
 85 90 95

Phe Thr Val Asn Glu Gln Gly Gln Val Thr Val Asn Gly Ala Ser Thr
 100 105 110

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
 115 120 125

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
 130 135 140

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp Val Leu
 145 150 155 160

Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val
 165 170 175

Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His
 180 185 190

Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys
 195 200 205

His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
 210 215 220

Ile Asp Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
 225 230 235 240

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
 245 250 255

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
 260 265 270

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
 275 280 285

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
 290 295 300

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
 305 310 315 320

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
 325 330 335

Pro Arg

<210> 7
<211> 1080
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 7
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ggcaaagagc tggctggcgc caccatggaa ctgcgggaca gcagcggcaa gaccatcagc 180
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gagcagggac aggtcacagt gaacggcggc ggacgaggcg gcagcggcgg cagcggcggc 360
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ccaacaccgg cgcccacat cgcgtcgcag cccctgtccc tgcgcccaga ggctgcccgg 480
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ctggtggtgg ttggtggagt cctggcttgc tatagcttgc tagtaacagt ggcctttatt 600
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cagcagggcc agaaccagct ctataacgag ctcaatctag gacgaagaga ggagtacgat 840
gttttggaca agagacgtgg ccgggaccct gagatggggg gaaagccgag aaggaagaac 900
cctcaggaag gcctgtacaa tgaactgcag aaagataaga tggcggaggc ctacagttag 960
attgggatga aaggcgagcg ccggaggggc aaggggcacg atggccttta ccagggtctc 1020
agtacagcca ccaaggacac ctacgacgcc cttcacatgc aggcctgcc ccctcgctaa 1080

<210> 8
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 8

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gly Ser Gly Ser Gly Asp Ser Ala Thr His Ile
 20 25 30

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

Met Glu Leu Arg Asp Ser Ser Gly Lys Thr Ile Ser Thr Trp Ile Ser
 50 55 60

Asp Gly Gln Val Lys Asp Phe Tyr Leu Tyr Pro Gly Lys Tyr Thr Phe
 65 70 75 80

Val Glu Thr Ala Ala Pro Asp Gly Tyr Glu Val Ala Thr Ala Ile Thr
 85 90 95

Phe Thr Val Asn Glu Gln Gly Gln Val Thr Val Asn Gly Gly Gly Ser
 100 105 110

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
 115 120 125

Gly Ser Ala Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
 130 135 140

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
 145 150 155 160

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
 165 170 175

Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
 180 185 190

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
 195 200 205

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
 210 215 220

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
 225 230 235 240

Ala Ala Tyr Arg Ser Ile Asp Arg Val Lys Phe Ser Arg Ser Ala Asp
 245 250 255

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
 260 265 270

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg

275

280

285

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
 290 295 300

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
 305 310 315 320

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
 325 330 335

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
 340 345 350

Met Gln Ala Leu Pro Pro Arg
 355

<210> 9
 <211> 798
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized

<400> 9
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 acgccagcgc cgcgaccacc aacaccggcg cccaccatcg cgtcgcagcc cctgtccctg 180
 cgcccagagg cgtgccggcc agcggcgggg ggcgcagtgc acacgagggg gctggacttc 240
 gcctgtgatt tttgggtgct ggtggtggtt ggtggagtcc tggcttgcta tagcttgcta 300
 gtaacagtgg cttttattat tttctgggtg aggagtaaga ggagcaggct cctgcacagt 360
 gactacatga acatgactcc ccgccgcccc gggccacccc gcaagcatta ccagccctat 420
 gccccaccac gcgacttcgc agcctatcgc tccatcgata gagtgaagtt cagcaggagc 480
 gcagacgccc ccgcgtacca gcagggccag aaccagctct ataacgagct caatctagga 540
 cgaagagagg agtacgatgt tttggacaag agacgtggcc gggaccctga gatgggggga 600
 aagccgagaa ggaagaaccc tcaggaaggc ctgtacaatg aactgcagaa agataaatg 660
 gcggaggcct acagtgatg tgggatgaaa ggcgagcgcc ggaggggcaa ggggcacgat 720
 ggccctttacc agggctctcag tacagccacc aaggacacct acgacgccct tcacatgcag 780
 gccctgcccc ctcgctaa 798

<210> 10
 <211> 265
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Artificially Synthesized

<400> 10

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gly Ser Ala His Ile Val Met Val Asp Ala Tyr
20 25 30

Lys Pro Thr Lys Ala Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
35 40 45

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
50 55 60

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
65 70 75 80

Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
85 90 95

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
100 105 110

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
115 120 125

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
130 135 140

Asp Phe Ala Ala Tyr Arg Ser Ile Asp Arg Val Lys Phe Ser Arg Ser
145 150 155 160

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
165 170 175

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
180 185 190

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
195 200 205

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
210 215 220

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
225 230 235 240

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
 245 250 255

Leu His Met Gln Ala Leu Pro Pro Arg
 260 265

<210> 11
 <211> 861
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized

<400> 11
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 ccgggatccg cccacatcgt gatggtggac gcctacaagc ccaccaaggg cggcagcggc 120
 ggcagcggcg gcagcggcgg cagcggcggc agcggcggca gcggcggcag cgctagcacc 180
 acgacgccag cgccgcgacc accaacaccg gcgcccacca tcgcgtcgca gcccctgtcc 240
 ctgcgcccag aggcgtgccg gccagcggcg gggggcgagcag tgcacacgag ggggctggac 300
 ttcgcctgtg atttttgggt gctggtggtg gttggtggag tcctggcttg ctatagcttg 360
 ctagtaacag tggcctttat tattttctgg gtgaggagta agaggagcag gctcctgcac 420
 agtgactaca tgaacatgac tccccgccgc cccgggccca cccgaagca ttaccagccc 480
 tatgccccac cagcgcactt cgcagcctat cgctccatcg atagagtga gttcagcagg 540
 agcgcagacg ccccgcgcta ccagcagggc cagaaccagc tctataacga gctcaatcta 600
 ggacgaagag aggagtacga tgttttggac aagagacgtg gccgggaccc tgagatgggg 660
 ggaaagccga gaaggaagaa ccctcaggaa ggcctgtaca atgaactgca gaaagataag 720
 atggcggagg cctacagtga gattgggatg aaaggcagc gccggagggg caaggggcac 780
 gatggccttt accagggtct cagtacagcc accaaggaca cctacgacgc cttcacatg 840
 caggccctgc cccctcgcta a 861

<210> 12
 <211> 286
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized

<400> 12

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gly Ser Ala His Ile Val Met Val Asp Ala Tyr
 20 25 30

Lys Pro Thr Lys Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
 35 40 45

Gly Gly Ser Gly Gly Ser Gly Gly Ser Ala Ser Thr Thr Thr Pro Ala
 50 55 60

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
 65 70 75 80

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
 85 90 95

Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp Val Leu Val Val Val Gly
 100 105 110

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
 115 120 125

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
 130 135 140

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
 145 150 155 160

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Ile Asp Arg Val
 165 170 175

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
 180 185 190

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
 195 200 205

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
 210 215 220

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
 225 230 235 240

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
 245 250 255

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
 260 265 270

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 275 280 285

<210> 13
<211> 1806
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 13
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ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc 180
ctcgtgacca ccctgaccta cggcgtgcag tgcttcagcc gctaccccga ccacatgaag 240
cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg caccatcttc 300
ttcaaggacg acggcaacta caagaccgcg gccgaggtga agttcgaggg cgacaccctg 360
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 420
aagctggagt acaactacaa cagccacaac gtctatatca tggccgacaa gcagaagaac 480
ggcatcaagg tgaacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc 540
gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac 600
tacctgagca cccagtccgc cctgagcaaa gacccaacg agaagcgcga tcacatggtc 660
ctgctggagt tcgtgaccgc cgccgggatc actctcggca tggacgagct gtacaagaga 720
tctggcagcg gagagggcag aggaagtctt ctaacatgcg gtgacgtgga ggagaatccc 780
ggccctagaa tggccttacc agtgaccgcc ttgctcctgc cgctggcctt gctgctccac 840
gccgccaggc cgggatccgg aagcggagat agcgccaccc acatcaagtt cagcaagcgg 900
gacgaggacg gcaaagagct ggctggcgcc accatggaac tgcgggatag cagcggcaag 960
accatcagca cctggatcag cgacggccag gtcaaagact tctacctgta cccgggcaag 1020
tacaccttcg tggaaacagc cgcccctgac ggctatgagg tggccacagc catcaccttc 1080
accgtgaacg agcagggaca ggtcacagtg aacggcgcta gcaccacgac gccagcgccg 1140
cgaccaccaa caccggcgcc caccatcgcg tcgcagcccc tgtccctgcg cccagaggcg 1200
tgccggccag cggcgggggg cgcagtgcac acgagggggc tggacttcgc ctgtgatttt 1260
tgggtgctgg tgggtggttg tggagtcctg gcttgctata gcttgctagt aacagtggcc 1320
tttattatatt tctgggtgag gagtaagagg agcaggctcc tgcacagtga ctacatgaac 1380
atgactcccc gccgccccgg gccacccgc aagcattacc agccctatgc cccaccacgc 1440
gacttcgcag cctatcgctc catcgataga gtgaagttca gcaggagcgc agacgcccc 1500
gcgtaccagc agggccagaa ccagctctat aacgagctca atctaggacg aagagaggag 1560
tacgatgttt tggacaagag acgtggccgg gaccctgaga tggggggaaa gccgagaagg 1620
aagaaccctc aggaaggcct gtacaatgaa ctgcagaaag ataagatggc ggaggcctac 1680

agtgagattg ggatgaaagg cgagcgccgg aggggcaagg ggcacgatgg cctttaccag 1740
 ggtctcagta cagccaccaa ggacacctac gacgcccttc acatgcaggc cctgccccct 1800
 cgctaa 1806

<210> 14
 <211> 601
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Artificially Synthesized

 <400> 14

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Arg
 225 230 235 240

Ser Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
 245 250 255

Glu Glu Asn Pro Gly Pro Arg Met Ala Leu Pro Val Thr Ala Leu Leu
 260 265 270

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Gly Ser Gly Ser
 275 280 285

Gly Asp Ser Ala Thr His Ile Lys Phe Ser Lys Arg Asp Glu Asp Gly
 290 295 300

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

Thr Ile Ser Thr Trp Ile Ser Asp Gly Gln Val Lys Asp Phe Tyr Leu
 325 330 335

Tyr Pro Gly Lys Tyr Thr Phe Val Glu Thr Ala Ala Pro Asp Gly Tyr
 340 345 350

Glu Val Ala Thr Ala Ile Thr Phe Thr Val Asn Glu Gln Gly Gln Val
 355 360 365

Thr Val Asn Gly Ala Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
 370 375 380

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

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
 405 410 415

Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
 420 425 430

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
 435 440 445

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
450 455 460

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
465 470 475 480

Asp Phe Ala Ala Tyr Arg Ser Ile Asp Arg Val Lys Phe Ser Arg Ser
485 490 495

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
500 505 510

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
515 520 525

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
530 535 540

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
545 550 555 560

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
565 570 575

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
580 585 590

Leu His Met Gln Ala Leu Pro Pro Arg
595 600

<210> 15
<211> 1869
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 15
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ggcgacgtaa acggccacaa gttcagcgtg tccggcgagg gcgagggcga tgccacctac 120
ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc 180
ctcgtgacca ccctgaccta cggcgtgcag tgcttcagcc gctaccccga ccacatgaag 240
cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg caccatcttc 300
ttcaaggacg acggcaacta caagaccgc gccgaggtga agttcgaggg cgacaccctg 360
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 420
aagctggagt acaactacaa cagccacaac gtctatatca tggccgacaa gcagaagaac 480

ggcatcaagg tgaacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc	540
gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac	600
tacctgagca cccagtccgc cctgagcaaa gaccccaacg agaagcgcga tcacatggtc	660
ctgctggagt tcgtgaccgc cgccggggtc actctcggca tggacgagct gtacaagaga	720
tctggcagcg gagagggcag aggaagtctt ctaacatgcg gtgacgtgga ggagaatccc	780
ggccctagaa tggccttacc agtgaccgcc ttgctcctgc cgctggcctt gctgctccac	840
gccgccaggc cgggatccgg aagcggcgat agcgccaccc acatcaagtt cagcaagcgg	900
gacgaggacg gcaaagagct ggctggcgcc accatggaac tgcgggacag cagcggcaag	960
accatcagca cctggatcag cgacggccag gtcaaagact tctacctgta ccccggaag	1020
tacaccttcg tggaaacagc cgcccctgac ggctacgagg tggccacagc catcaccttc	1080
accgtgaacg agcagggaca ggtcacagtg aacggcggcg gcagcggcgg cagcggcggc	1140
agcggcggca gcggcggcag cggcggcagc ggcggcagcg ctagcaccac gacgccagcg	1200
ccgcgaccac caacaccggc gcccaccatc gcgtcgcagc ccctgtccct gcgcccagag	1260
gcgtgccggc cagcggcggg gggcgagtg cacacgaggg ggctggactt cgctgtgat	1320
ttttgggtgc tgggtggtgt tgggtgagtc ctggcttgct atagcttgct agtaacagtg	1380
gcctttatta ttttctgggt gaggagtaag aggagcaggc tcctgcacag tgactacatg	1440
aacatgactc cccgccgcc cgggccacc cgcaagcatt accagcccta tgccccacca	1500
cgcgacttcg cagcctatcg ctccatcgat agagtgaagt tcagcaggag cgagacgcc	1560
cccgcgtacc agcagggcca gaaccagctc tataacgagc tcaatctagg acgaagagag	1620
gagtacgatg ttttggacaa gagacgtggc cgggaccctg agatgggggg aaagccgaga	1680
aggaagaacc ctcaggaagg cctgtacaat gaactgcaga aagataagat ggcggaggcc	1740
tacagtgaga ttgggatgaa aggcgagcgc cggaggggca aggggcacga tggcctttac	1800
caggttctca gtacagccac caaggacacc tacgacgcc ttcatatgca ggccctgccc	1860
cctcgctaa	1869

<210> 16
 <211> 622
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Artificially Synthesized

 <400> 16

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
			20					25					30		

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Arg
 225 230 235 240

Ser Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
 245 250 255

Glu Glu Asn Pro Gly Pro Arg Met Ala Leu Pro Val Thr Ala Leu Leu
 260 265 270

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Gly Ser Gly Ser
 275 280 285

Gly Asp Ser Ala Thr His Ile Lys Phe Ser Lys Arg Asp Glu Asp Gly
 290 295 300

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

Thr Ile Ser Thr Trp Ile Ser Asp Gly Gln Val Lys Asp Phe Tyr Leu
 325 330 335

Tyr Pro Gly Lys Tyr Thr Phe Val Glu Thr Ala Ala Pro Asp Gly Tyr
 340 345 350

Glu Val Ala Thr Ala Ile Thr Phe Thr Val Asn Glu Gln Gly Gln Val
 355 360 365

Thr Val Asn Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
 370 375 380

Gly Gly Ser Gly Gly Ser Gly Gly Ser Ala Ser Thr Thr Thr Pro Ala
 385 390 395 400

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
 405 410 415

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
 420 425 430

Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp Val Leu Val Val Val Gly
 435 440 445

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
 450 455 460

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
 465 470 475 480

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
 485 490 495

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Ile Asp Arg Val
 500 505 510

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
 515 520 525

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
 530 535 540

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
545 550 555 560

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
565 570 575

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
580 585 590

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
595 600 605

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
610 615 620

<210> 17
<211> 609
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 17
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gaagcagcac gtgcaggatca ggatgatgaa gttcgtattc tgatggcaaa tggatgcagat 120
gttaacgcc aagattttta tggattattaca ccgctgcatc tggcagcagc ctatgggtcat 180
ctggaaattg ttgaagtctt gctgaaacat ggtgccgatg tgaatgcaca tgattggaat 240
ggttggaccc cggttacacct ggcagcaaaa tatggccatt tagaaatcgt ggaagtgcgt 300
ttaaaacatg gcgcagacgt taatgcaatt gataatgcag gtaaaacccc tctgcattta 360
gcagccgcac atggccacct ggaaatcgta gaggttttac tgaaatacgg tgcggatgta 420
aacgcgcagg ataaatttgg taaaaccgcc ttcgatatta gcatcgataa tggtaatgag 480
gacctggcag aaattctgca agaggcatgc ggtgggtggg gtagtgggtg cggatggttca 540
gcaagcgcac atattgttat ggttgatgca tataaaccga ccaaactgga acatcatcat 600
caccattaa 609

<210> 18
<211> 202
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 18

Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly Ser Asp Leu Gly
1 5 10 15

Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
20 25 30

Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Phe Tyr Gly
35 40 45

Ile Thr Pro Leu His Leu Ala Ala Ala Tyr Gly His Leu Glu Ile Val
50 55 60

Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala His Asp Trp Asn
65 70 75 80

Gly Trp Thr Pro Leu His Leu Ala Ala Lys Tyr Gly His Leu Glu Ile
85 90 95

Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala Ile Asp Asn
100 105 110

Ala Gly Lys Thr Pro Leu His Leu Ala Ala Ala His Gly His Leu Glu
115 120 125

Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala Gln Asp
130 135 140

Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu
145 150 155 160

Asp Leu Ala Glu Ile Leu Gln Glu Ala Cys Gly Gly Gly Gly Ser Gly
165 170 175

Gly Gly Gly Ser Ala Ser Ala His Ile Val Met Val Asp Ala Tyr Lys
180 185 190

Pro Thr Lys Leu Glu His His His His His
195 200

<210> 19
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 19
atggaacaga aactgatcag cgaagaagat ctgggttctg atctgggtaa aaaactgctg 60
gaagcagcac gtgcagggtca ggatgatgaa gttcgtattc tgatggcaaa tgggtgcagat 120
gttaatgcag atgatacctg gggttggaca ccgctgcata tggcagcata tcagggtcat 180
ctggaaattg ttgaagtgt gctgaaaaac ggtgccgatg tgaatgccta tgattatatt 240

ggttggaccc ctctgcactt agcagcagat ggccatttag aaatcgtgga agttttactg	300
aaaaatggcg cagacgtgaa cgcaagcgat tatatcgggtg ataccccgtt acacctggca	360
gcacataatg gccacctgga aatcgtagag gttctgttaa aacatgggtgc ggacgtgaat	420
gcacaggata aatttggtaa aaccgccttc gatatcagca ttgataatgg caatgaggat	480
ctggcagaaa ttctgcaaga agcatgtctc gagggtaggta gtggtggctc tggcggttct	540
ggtggcagtg gcggtagcgg tggtagtggg ggcagtagag gcgtgccaca catcgtgatg	600
gtggacgcct acaagcggta caagggcggg tctggtggca gtctgccgga aaccggtggg	660
ggtagtgggt gctctggcgg ttctggtggc agtggcggta gccaaagctaa acctcaaatt	720
ccgaaagata aatcaaaagt ggcaggctat attgaaattc cagatgctga tattaaagaa	780
ccagtatatc caggaccagc aacacctgaa caattaaata gaggtgtaag ctttgcagaa	840
gaaaaatgaat cactagatga tcaaaatatt tcaattgcag gacacacttt cattgaccgt	900
ccgaactatc aattttacaaa tcttaaagca gccaaaaaag gtagtatggg gtactttaaa	960
gttggtaatg aaacacgtaa gtataaaatg acaagtataa gagatgttaa gccaacagat	1020
gtagaagttc tagatgaaca aaaaggtaaa gataaacaat taacattaat tacttgtgat	1080
gattacaatg aaaagacagg cgtttgggaa aaacgtaaaa tctttgtagc tacagaagtc	1140
aaacatcacc accatcatca ctaa	1164

<210> 20
 <211> 387
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized

<400> 20

Met	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Gly	Ser	Asp	Leu	Gly
1				5					10					15	

Lys	Lys	Leu	Leu	Glu	Ala	Ala	Arg	Ala	Gly	Gln	Asp	Asp	Glu	Val	Arg
		20						25					30		

Ile	Leu	Met	Ala	Asn	Gly	Ala	Asp	Val	Asn	Ala	Asp	Asp	Thr	Trp	Gly
		35					40					45			

Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Tyr	Gln	Gly	His	Leu	Glu	Ile	Val
	50					55					60				

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

Gly	Trp	Thr	Pro	Leu	His	Leu	Ala	Ala	Asp	Gly	His	Leu	Glu	Ile	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85

90

95

Glu Val Leu Leu Lys Asn Gly Ala Asp Val Asn Ala Ser Asp Tyr Ile
 100 105 110

Gly Asp Thr Pro Leu His Leu Ala Ala His Asn Gly His Leu Glu Ile
 115 120 125

Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala Gln Asp Lys
 130 135 140

Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu Asp
 145 150 155 160

Leu Ala Glu Ile Leu Gln Glu Ala Cys Leu Glu Gly Gly Ser Gly Gly
 165 170 175

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
 180 185 190

Arg Gly Val Pro His Ile Val Met Val Asp Ala Tyr Lys Arg Tyr Lys
 195 200 205

Gly Gly Ser Gly Gly Ser Leu Pro Glu Thr Gly Gly Gly Ser Gly Gly
 210 215 220

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gln Ala Lys Pro Gln Ile
 225 230 235 240

Pro Lys Asp Lys Ser Lys Val Ala Gly Tyr Ile Glu Ile Pro Asp Ala
 245 250 255

Asp Ile Lys Glu Pro Val Tyr Pro Gly Pro Ala Thr Pro Glu Gln Leu
 260 265 270

Asn Arg Gly Val Ser Phe Ala Glu Glu Asn Glu Ser Leu Asp Asp Gln
 275 280 285

Asn Ile Ser Ile Ala Gly His Thr Phe Ile Asp Arg Pro Asn Tyr Gln
 290 295 300

Phe Thr Asn Leu Lys Ala Ala Lys Lys Gly Ser Met Val Tyr Phe Lys
 305 310 315 320

Val Gly Asn Glu Thr Arg Lys Tyr Lys Met Thr Ser Ile Arg Asp Val
 325 330 335

Lys Pro Thr Asp Val Glu Val Leu Asp Glu Gln Lys Gly Lys Asp Lys
 340 345 350

Gln Leu Thr Leu Ile Thr Cys Asp Asp Tyr Asn Glu Lys Thr Gly Val
 355 360 365

Trp Glu Lys Arg Lys Ile Phe Val Ala Thr Glu Val Lys His His His
 370 375 380

His His His
 385

<210> 21
 <211> 1164
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized

<400> 21
 atggaacaga aactgatacag cgaagaagat ctgggttctg atctgggtaa aaaactgctg 60
 gaagcagcac gtgcaggatca ggatgatgaa gttcgtattc tgatggcaaa tggatgcagat 120
 gttaacgcca aagattttta tggatattaca ccgctgcatc tggcagcagc ctatggatcat 180
 ctggaaattg ttgaagttct gctgaaacat ggtgccgatg tgaatgcaca tgattggaat 240
 ggttggaacc cgttacacct ggcagcaaaa tatggccatt tagaaatcgt ggaagtgcctg 300
 ttaaaacatg gcgcagacgt taatgcaatt gataatgcag gtaaaacccc tctgcattta 360
 gcagccgcac atggccacct ggaaatcgta gaggttttac tgaaatacgg tgcggatgta 420
 aacgcgcagg ataaatttgg taaacacgcc ttcgatatta gcatcgataa tggtaatgag 480
 gacctggcag aaattctgca agaggcactc gaggggtgta gtgggtggctc tggcggttct 540
 ggtggcagtg gcggtagcgg tggtagtggt ggcagtagag gcgtgccaca catcgtgatg 600
 gtggacgcct acaagcggta caagggcggg tctggtggca gtctgccgga aaccggtggt 660
 ggtagtggtg gctctggcgg ttctggtggc agtggcgta gccaaagctaa acctcaaatt 720
 ccgaaagata aatcaaaagt ggcaggctat attgaaattc cagatgctga tattaagaa 780
 ccagtatatc caggaccagc aacacctgaa caattaaata gaggtgtaag ctttgcagaa 840
 gaaaatgaat cactagatga tcaaatatt tcaattgcag gacacacttt cattgaccgt 900
 ccgaactatc aatttataaa tcttaaagca gccaaaaaag gtagtatggt gtactttaaa 960
 gttggtaatg aaacacgtaa gtataaaatg acaagtataa gagatgttaa gccaacagat 1020
 gtagaagttc tagatgaaca aaaaggtaaa gataaacaat taacattaat tacttgtgat 1080
 gattacaatg aaaagacagg cgtttgggaa aaacgtaaaa tctttgtagc tacagaagtc 1140
 aaacatcacc accatcatca ctaa 1164

<210> 22

<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 22

Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly Ser Asp Leu Gly
1 5 10 15

Lys Lys Leu Leu Glu Ala Ala Arg Ala Gly Gln Asp Asp Glu Val Arg
20 25 30

Ile Leu Met Ala Asn Gly Ala Asp Val Asn Ala Lys Asp Phe Tyr Gly
35 40 45

Ile Thr Pro Leu His Leu Ala Ala Ala Tyr Gly His Leu Glu Ile Val
50 55 60

Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala His Asp Trp Asn
65 70 75 80

Gly Trp Thr Pro Leu His Leu Ala Ala Lys Tyr Gly His Leu Glu Ile
85 90 95

Val Glu Val Leu Leu Lys His Gly Ala Asp Val Asn Ala Ile Asp Asn
100 105 110

Ala Gly Lys Thr Pro Leu His Leu Ala Ala Ala His Gly His Leu Glu
115 120 125

Ile Val Glu Val Leu Leu Lys Tyr Gly Ala Asp Val Asn Ala Gln Asp
130 135 140

Lys Phe Gly Lys Thr Ala Phe Asp Ile Ser Ile Asp Asn Gly Asn Glu
145 150 155 160

Asp Leu Ala Glu Ile Leu Gln Glu Ala Leu Glu Gly Gly Ser Gly Gly
165 170 175

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
180 185 190

Arg Gly Val Pro His Ile Val Met Val Asp Ala Tyr Lys Arg Tyr Lys
195 200 205

Gly Gly Ser Gly Gly Ser Leu Pro Glu Thr Gly Gly Gly Ser Gly Gly
210 215 220

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gln Ala Lys Pro Gln Ile
225 230 235 240

Pro Lys Asp Lys Ser Lys Val Ala Gly Tyr Ile Glu Ile Pro Asp Ala
245 250 255

Asp Ile Lys Glu Pro Val Tyr Pro Gly Pro Ala Thr Pro Glu Gln Leu
260 265 270

Asn Arg Gly Val Ser Phe Ala Glu Glu Asn Glu Ser Leu Asp Asp Gln
275 280 285

Asn Ile Ser Ile Ala Gly His Thr Phe Ile Asp Arg Pro Asn Tyr Gln
290 295 300

Phe Thr Asn Leu Lys Ala Ala Lys Lys Gly Ser Met Val Tyr Phe Lys
305 310 315 320

Val Gly Asn Glu Thr Arg Lys Tyr Lys Met Thr Ser Ile Arg Asp Val
325 330 335

Lys Pro Thr Asp Val Glu Val Leu Asp Glu Gln Lys Gly Lys Asp Lys
340 345 350

Gln Leu Thr Leu Ile Thr Cys Asp Asp Tyr Asn Glu Lys Thr Gly Val
355 360 365

Trp Glu Lys Arg Lys Ile Phe Val Ala Thr Glu Val Lys His His His
370 375 380

His His His
385

<210> 23
<211> 825
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 23
atgaccttta aactgattat taacggcaaa accctgaaag gcgaaattac cattgaagcg 60
gtggatgcgt aggaagcgga aaaaattttt aaacagtatg cgaacgatta tggcattgat 120
ggcgaatgga cctatgatga tgcgacaaa acctttaccg tgaccgaact cgagggtggt 180
agtgttggt ctggcggttc tggtagtcagt ggcggtagcg gtgtagtggt tggcagtaga 240
ggcgtgccac acatcgtgat ggtggacgcc tacaagcggg acaagggcgg ttctggtggc 300
agtctgccgg aaaccggtgg tggtagtggt ggctctggcg gttctggtgg cagtggcggt 360

agccaagcta aacctcaaat tccgaaagat aaatcaaaag tggcaggcta tattgaaatt 420
ccagatgctg atattaaaga accagtatat ccaggaccag caacacctga acaattaaat 480
agagggtgtaa gctttgcaga agaaaatgaa tcactagatg atcaaaatat ttcaattgca 540
ggacacactt tcattgaccg tccgaactat caatttaca atcttaaagc agccaaaaaa 600
ggtagtatgg tgtactttta agttggtaat gaaacacgta agtataaaat gacaagtata 660
agagatgtta agccaacaga tgtagaagtt ctagatgaac aaaaaggtaa agataaacia 720
ttaacattaa ttacttgtga tgattacaat gaaaagacag gcgtttggga aaaacgtaaa 780
atctttgtag ctacagaagt caaacatcac caccatcatc actaa 825

<210> 24
<211> 273
<212> PRT
<213> Artificial Sequence
<220>
<223> Artificially Synthesized
<400> 24

Met Thr Phe Lys Leu Ile Ile Asn Gly Lys Thr Leu Lys Gly Glu Ile
1 5 10 15
Thr Ile Glu Ala Val Asp Ala Glu Ala Glu Lys Ile Phe Lys Gln Tyr
20 25 30
Ala Asn Asp Tyr Gly Ile Asp Gly Glu Trp Thr Tyr Asp Asp Ala Thr
35 40 45
Lys Thr Phe Thr Val Thr Glu Leu Glu Gly Gly Ser Gly Gly Ser Gly
50 55 60
Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Arg Gly
65 70 75 80
Val Pro His Ile Val Met Val Asp Ala Tyr Lys Arg Tyr Lys Gly Gly
85 90 95
Ser Gly Gly Ser Leu Pro Glu Thr Gly Gly Gly Ser Gly Gly Ser Gly
100 105 110
Gly Ser Gly Gly Ser Gly Gly Ser Gln Ala Lys Pro Gln Ile Pro Lys
115 120 125
Asp Lys Ser Lys Val Ala Gly Tyr Ile Glu Ile Pro Asp Ala Asp Ile
130 135 140
Lys Glu Pro Val Tyr Pro Gly Pro Ala Thr Pro Glu Gln Leu Asn Arg
145 150 155 160

Gly Val Ser Phe Ala Glu Glu Asn Glu Ser Leu Asp Asp Gln Asn Ile
165 170 175

Ser Ile Ala Gly His Thr Phe Ile Asp Arg Pro Asn Tyr Gln Phe Thr
180 185 190

Asn Leu Lys Ala Ala Lys Lys Gly Ser Met Val Tyr Phe Lys Val Gly
195 200 205

Asn Glu Thr Arg Lys Tyr Lys Met Thr Ser Ile Arg Asp Val Lys Pro
210 215 220

Thr Asp Val Glu Val Leu Asp Glu Gln Lys Gly Lys Asp Lys Gln Leu
225 230 235 240

Thr Leu Ile Thr Cys Asp Asp Tyr Asn Glu Lys Thr Gly Val Trp Glu
245 250 255

Lys Arg Lys Ile Phe Val Ala Thr Glu Val Lys His His His His His
260 265 270

His

<210> 25
<211> 1086
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 25
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60
ccgggatccg tgacaacact gagcggactg tctggcgagc aaggcccttc tggcgatatg 120
accaccgaag aggatagcgc cacacacatc aagttcagca agcgcgacga ggacggcaga 180
gaacttgctg gcgctacat ggaactgaga gacagcagcg gcaagaccat cagcacctgg 240
atctctgacg gccacgtgaa ggacttctat ctgtaccccg gcaagtacac cttcgtggaa 300
accgccgctc ctgacggcta cgaagtggcc acacctatcg agttcaccgt gaacgaggat 360
ggccaagtga ccgtggatgg cgaagctaca gaaggcgacg cccatacagc tagcaccacg 420
acgccagcgc cgcgaccacc aacaccggcg cccaccatcg cgtcgcagcc cctgtccctg 480
cgcccagagg cgtgccggcc agcggcgggg ggcgcagtcg acacgagggg gctggacttc 540
gcctgtgata tctacatctg ggccgccctg gccgggactt gtggggtcct tctcctgtca 600
ctggttatca ccctttactg caaacggggc agaaagaaac tcctgtatat attcaaacia 660

ccatttatga gaccagtaca aactactcaa gaggaagatg gctgtagctg ccgatttcca	720
gaagaagaag aaggaggatg tgaactgaga gtgaagtca gcaggagcgc agacgcccc	780
gcgtacaagc agggccagaa ccagctctat aacgagctca atctaggacg aagagaggag	840
tacgatgttt tggacaagag acgtggccgg gaccctgaga tggggggaaa gccgagaagg	900
aagaaccctc aggaaggcct gtacaatgaa ctgcagaaag ataagatggc ggaggcctac	960
agtgagattg ggatgaaagg cgagcgccgg aggggcaagg ggcacgatgg cctttaccag	1020
ggtctcagta cagccaccaa ggacacctac gacgcccttc acatgcaggc cctgccccct	1080
cgctaa	1086

<210> 26
 <211> 361
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Artificially Synthesized

 <400> 26

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu
1			5					10					15	

His	Ala	Ala	Arg	Pro	Gly	Ser	Val	Thr	Thr	Leu	Ser	Gly	Leu	Ser	Gly
			20					25					30		

Glu	Gln	Gly	Pro	Ser	Gly	Asp	Met	Thr	Thr	Glu	Glu	Asp	Ser	Ala	Thr
		35					40					45			

His	Ile	Lys	Phe	Ser	Lys	Arg	Asp	Glu	Asp	Gly	Arg	Glu	Leu	Ala	Gly
	50					55					60				

Ala	Thr	Met	Glu	Leu	Arg	Asp	Ser	Ser	Gly	Lys	Thr	Ile	Ser	Thr	Trp
65					70					75					80

Ile	Ser	Asp	Gly	His	Val	Lys	Asp	Phe	Tyr	Leu	Tyr	Pro	Gly	Lys	Tyr
				85					90					95	

Thr	Phe	Val	Glu	Thr	Ala	Ala	Pro	Asp	Gly	Tyr	Glu	Val	Ala	Thr	Pro
			100					105					110		

Ile	Glu	Phe	Thr	Val	Asn	Glu	Asp	Gly	Gln	Val	Thr	Val	Asp	Gly	Glu
		115					120					125			

Ala	Thr	Glu	Gly	Asp	Ala	His	Thr	Ala	Ser	Thr	Thr	Thr	Pro	Ala	Pro
	130					135						140			

Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu
145					150					155					160

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
165 170 175

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
180 185 190

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys
195 200 205

Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg
210 215 220

Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro
225 230 235 240

Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser
245 250 255

Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu
260 265 270

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
275 280 285

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
290 295 300

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
305 310 315 320

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
325 330 335

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
340 345 350

Leu His Met Gln Ala Leu Pro Pro Arg
355 360

<210> 27
<211> 1098
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially Synthesized

<400> 27
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg

60

ccgggatccg tgacaacact gagcggactg tctggcgagc aaggcccttc tggcgatatg	120
accaccgaag aggatagcgc cacacacatc aagttcagca agcgcgacga ggacggcaga	180
gaacttgctg gcgctacat ggaactgaga gacagcagcg gcaagaccat cagcacctgg	240
atctctgacg gccacgtgaa ggacttctat ctgtaccccc gcaagtacac cttcgtggaa	300
accgccgctc ctgacggcta cgaagtggcc acacctatcg agttcaccgt gaacgaggat	360
ggccaagtga ccgtggatgg cgaagctaca gaaggcgacg cccatacagc tagcaccacg	420
acgccagcgc cgcgaccacc aacaccggcg cccaccatcg cgtcgcagcc cctgtccctg	480
cgcccagagg cgtgccggcc agcggcgggg ggcgagtgac acacgagggg gctggacttc	540
gcctgtgatt tttgggtgct ggtggtggtt ggtggagtcc tggcttgcta tagcttgcta	600
gtaacagtgg cttttattat tttctgggtg aggagtaaga ggagcaggct cctgcacagt	660
gactacatga acatgactcc ccgccgcccc gggccacccc gcaagcatta ccagccctat	720
gccccaccac gcgacttcgc agcctatcgc tccatcgata gagtgaagtt cagcaggagc	780
gcagacgccc ccgcgtacaa gcagggccag aaccagctct ataacgagct caatctagga	840
cgaagagagg agtacgatgt tttggacaag agacgtggcc gggaccctga gatgggggga	900
aagccgagaa ggaagaaccc tcaggaaggc ctgtacaatg aactgcagaa agataaatg	960
gcggaggcct acagtgaatg tgggatgaaa ggcgagcgcc ggaggggcaa ggggcacgat	1020
ggcctttacc aggggtctcag tacagccacc aaggacacct acgacgccct tcacatgcag	1080
gccctgcccc ctcgctaa	1098

<210> 28
 <211> 365
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Artificially Synthesized

 <400> 28

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		
His	Ala	Ala	Arg	Pro	Gly	Ser	Val	Thr	Thr	Leu	Ser	Gly	Leu	Ser	Gly
			20					25					30		
Glu	Gln	Gly	Pro	Ser	Gly	Asp	Met	Thr	Thr	Glu	Glu	Asp	Ser	Ala	Thr
		35					40					45			
His	Ile	Lys	Phe	Ser	Lys	Arg	Asp	Glu	Asp	Gly	Arg	Glu	Leu	Ala	Gly
	50					55					60				
Ala	Thr	Met	Glu	Leu	Arg	Asp	Ser	Ser	Gly	Lys	Thr	Ile	Ser	Thr	Trp
65					70					75					80

Ile Ser Asp Gly His Val Lys Asp Phe Tyr Leu Tyr Pro Gly Lys Tyr
 85 90 95

Thr Phe Val Glu Thr Ala Ala Pro Asp Gly Tyr Glu Val Ala Thr Pro
 100 105 110

Ile Glu Phe Thr Val Asn Glu Asp Gly Gln Val Thr Val Asp Gly Glu
 115 120 125

Ala Thr Glu Gly Asp Ala His Thr Ala Ser Thr Thr Thr Pro Ala Pro
 130 135 140

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
 145 150 155 160

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
 165 170 175

Gly Leu Asp Phe Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly
 180 185 190

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
 195 200 205

Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
 210 215 220

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
 225 230 235 240

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Ile Asp Arg Val Lys
 245 250 255

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln
 260 265 270

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
 275 280 285

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
 290 295 300

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
 305 310 315 320

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
 325 330 335

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
 340 345 350

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 355 360 365

<210> 29
 <211> 648
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized

<400> 29
 atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60
 ccgggatccg tgacaacact gagcggactg tctggcgagc aaggcccttc tggcgatatg 120
 accaccgaag aggatagcgc cacacacatc aagttcagca agcgcgacga ggacggcaga 180
 gaacttgctg gcgctaccat ggaactgaga gacagcagcg gcaagaccat cagcacctgg 240
 atctctgacg gccacgtgaa ggacttctat ctgtaccccg gcaagtacac cttcgtggaa 300
 accgccgctc ctgacggcta cgaagtggcc acacctatcg agttcacctg gaacgaggat 360
 ggccaagtga ccgtggatgg cgaagctaca gaaggcgacg cccatacagc tagcaccacg 420
 acgccagcgc cgcgaccacc aacaccggcg cccaccatcg cgtcgcagcc cctgtccctg 480
 cgcccagagg cgtgccggcc agcggcgggg ggcgagtgac acacgagggg gctggacttc 540
 gcctgtgatt tttgggtgct ggtggtggtt ggtggagtcc tggcttgcta tagcttgcta 600
 gtaacagtgg cctttattat tttctgggtg aggagtaaga ggagctaa 648

<210> 30
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificially Synthesized

<400> 30

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gly Ser Val Thr Thr Leu Ser Gly Leu Ser Gly
 20 25 30

Glu Gln Gly Pro Ser Gly Asp Met Thr Thr Glu Glu Asp Ser Ala Thr
 35 40 45

His Ile Lys Phe Ser Lys Arg Asp Glu Asp Gly Arg Glu Leu Ala Gly
 50 55 60

Ala Thr Met Glu Leu Arg Asp Ser Ser Gly Lys Thr Ile Ser Thr Trp
65 70 75 80

Ile Ser Asp Gly His Val Lys Asp Phe Tyr Leu Tyr Pro Gly Lys Tyr
85 90 95

Thr Phe Val Glu Thr Ala Ala Pro Asp Gly Tyr Glu Val Ala Thr Pro
100 105 110

Ile Glu Phe Thr Val Asn Glu Asp Gly Gln Val Thr Val Asp Gly Glu
115 120 125

Ala Thr Glu Gly Asp Ala His Thr Ala Ser Thr Thr Thr Pro Ala Pro
130 135 140

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
145 150 155 160

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
165 170 175

Gly Leu Asp Phe Ala Cys Asp Phe Trp Val Leu Val Val Val Gly Gly
180 185 190

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
195 200 205

Trp Val Arg Ser Lys Arg Ser
210 215